

OY	704	GTTATTCCATCGTGGTATCATGATGCCGTACGGTAATTCAGTAGTGCTCATGGCCCTCAAG	763
Db	704	GTCCTTTTCCATGCGTGTATACTAAATGTCGGGAATTCGATTTNCCATGGGCCTAATACC	763
OY	764	AATGCCAAGTGTGGCGCTCACCAAGGCCAACGCTGTTGGCTATAAGGAGAGACAAATG	823
Db	764	AATGTACAATGTGCTCCTTCACTTAGCCAAATTTGGACGGCTCTAAGGGGTGAGATTAAG	823
OY	824	AAAAAGATATCCTGSAATTCCTTAATGAAAAGCAATCCCCTATGATTTGGATCAAAAGAGAC	883
Db	824	ATAAGAGATGTTTTGGANNTTCTTNAGAAGCAACCCACAGGATTTAATAAATCTTAGG	883
OY	884	CACAAGTTTGGACCCGCAAGAATGCAAAAATAAGTCATGTTTCTTTGGACCCACTG	943
Db	884	AAAAAGTTTAACTCTTAGAAGAGCGTACCAATTAAGGTCATGTTTCTTTGGTCCACTG	943
OY	944	TGAAACCATPACCAGACAGCCGACTGTGTGGTACCACCAACCATACAGAGAAATGTAAGA	1003
Db	944	TTGANACCATACACACCGCTGATGTGTCTTACCCAAATCTCTGGGAATAGGTTAAAN	1003
OY	1004	GGCGCTGGGGAAATTCGATACCCACATTCATAGGCATATACCTCTACGAAAGTTTGCTTT	1063
Db	1004	NTCGTTGGGGTAATTCATACCCAGATATAGGTGTACCTTCATATAGAGGTCATATTT	1063
OY	1064	CCAATCATTTGCCAAACAATATCCGAGGTTGTAAAAAGTTGGAATTCGCTGCAATT	1123
Db	1064	TCACCTCTNNTTCTTAAACAATTCCTATGCTTTTAAAGAAATGGAACCTGTCTCAATT	1123
OY	1124	ATGTGCTTGGGAGTTGGCTGCAGACGACGATGCCGCCGAAACCCCTGGAGAGGCTG	1183
Db	1124	TTGGCCAAATGTAATTTGCTGATNCTGAAGCACCGCCCCAGACACCTTGGAAATGGGTG	1183
OY	1184	CCATTTGTAAAAAGGCCCATGTGTGATGGGGAAACCTACTCTGATTAATTTATGAGAC	1243
Db	1184	CTAAATTAATAAAGGCTCATGTTTAAGAGGAACAACCAACGACGATTAATTTATGAGAC	1243
OY	1244	TTTGCTCTATTTCTATTTTCTCTTCCCATGATCGCTTCTCAATTCGCTTAAC	1303
Db	1244	TTTGCTCTCATCTATATTTCTTGTTCCCATGCAATCGTTTNTGCAATTAACGTTTCATC	1303
OY	1304	ACACAGCTGGCACTCCCATTTATTTGTATCGTTTCGATTCGATTCGGAAGAAATATTA	1363
Db	1304	ACNCCTCCGGTACACCCGCTACTGTATGCTTCGACTTGATNGATNGAAGATCTTATTA	1363
OY	1364	ACCCCATGCTATTAATGCGTTTGGCGCTGGCGTTAAAGGTGTAAAGCATGCGCATGAGC	1423
Db	1364	ATCCCATGCTATTAATTAATGCGTGTAGGAGCTGTGTTAAGSGTGTACTCAATGCTGAT	1423
OY	1424	TAACTATCTCTTCGGAACAATTTGTTCGAAAGCGCTGCCAAAGGAACCCGCAATACA	1483
Db	1424	TAACTATTTCTTCGGAATCAATTTGGCCAAAGCTATGCTTAAAGATATNCCTGAAATACA	1483
OY	1484	AAACCATGAACGCAATGGTTGGCAATTTGGAAGGAATTCGCCACACCGGCAACATACA	1543
Db	1484	AAACCATGAACGTAATGACGTGTATATGATTAACAATTTGCCACACCTGGTATTCCTTATA	1543
OY	1544	GCAATGATATAGCGGATGAGAAACCTCACCGGGATCCCAATAAAAAATTCGATGATG	1603
Db	1544	GCAATGAATGTAAGGATATGAAATGTTTCCGGGATCAATTAAGAAATCCCANAG	1603
OY	1604	TCTATTAATGTTTAATATGCGCGATGAATTGAAATTAATGATTTGGCAGAAATGATATA	1663
Db	1604	TMTCAAGTGTGTAATTAATTAAGANGAATTTGAATGATGATGATGCTTAAATTTGATATA	1663
OY	1664	AAATTAACAATGGGCAAGTATTTGATTAATAAAAAAGAGAAATGTTT	1710
Db	1664	AGATTAACAATGGCAATGATGTTTGAATAAACATAGAGATTTATTT	1710
RESULT 11			
ARI53440			
LOCUS	AR153440	1713 bp DNA linear	PAT 08-AUG-2001

DEFINITION	Sequence 5 from patent US 6235515.
ACCESSION	ARI53440
VERSION	ARI53440.1
KEYWORDS	GI:15120972
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified. 1 (bases 1 to 1713)
AUTHORS	Russell, R. Joyce., Newcomb, R. David., Campbell, P. Malcolm., Robin, G. Charles., Quetleville, J., Claudianos, C., Smyth, K., A., Boyer, T. Mark., Oakeshott, J. Graham, and Brownlie, J. Colin. Malathion carboxylesterase Patent: US 6235515-A 5 22-May-2001;
TITLE	Location/Qualifiers
JOURNAL	1..1713
FEATURES	/organism="unknown"
BASE COUNT	516 a 305 c 369 g 523 t
ORIGIN	
Query Match	55.7%, Score 951.8; DB 6; Length 1713;
Best Local Similarity	73.2%; Pred. No. 9,9e-269;
Matches 1220; Conservative	0; Mismatches 447; Indels 0; Gaps 0.
44	TTAAATGATGCTCATTAATACAAACTACGCTCGATGACAAATGAACCAATAA 103
44	TTAAATGATGAAATATAAGTTTAAACTATGCTTAATACCAATGAACCGTGTAG 103
104	TGATATGATATGACAAATTAAGGCTTTAAGCAATGACCGCTACGATGATCTT 163
104	CTGAATGATATGACAAATGAAAGCGTTAAAGCTTAACGTTAACGTGTACGATGATCT 163
164	ACTACAGTTTGAAGATATACCCATCTTAAGCTTCAGTGGTGAGATTCAAG 223
164	ACTACAGTTTGAAGATATACCCATCTTAAGCTTCAGTGGTGAGATTCAAG 223
224	CACCCAGCGGCTGTACCATGAGAGGCTGACGATGTTCTGTGGCCAGCAACAGT 283
224	CACCCAGCGGCTGTACCATGAGAGGCTGACGATGTTCTGTGGCCAGCAACAGT 283
284	CGATACGACAGATTCATTAAGTGGAAACCCAGAGTTGGAGATTTGCTTAACCTGA 343
284	CAGTACAGATTTGATTTTATACGGGAAAGTGTGGCTCAGAGATTTGCTTAACCTGA 343
344	ATGTGATACCAATGACTTGAACCCAGCAAAAGCGTCTGTATGGTTTCAATTCATG 403
344	GTGTCTATACGAATATCTAAATCCGGAACCTAAACGTCCTTTAGTATACATACATG 403
404	GCGAGATTTTATTTTGGCGGAAAGCAATCGTACTGTTGGTCCGACTACTTATGA 463
404	GTTGTGTTTATTTATGCGTGAATATCATGCAATATGATATGATGCTGATATTAATGA 463
464	AGAAACCCGTGCTTGTGAACCGTGAATATGCTTGGTGGTGTGGGTTTCCCTAGCC 523
464	AAAAGATGTGTTGTTGATTAACATACAAATTCGTTTGGAGCTTGAAGTTTCTAAGTT 523
524	TGAAATCGGAAATTCATGATGCTCCCGCAACGCTGGCTCAAGATCAAGTATGGCTT 583
524	TAAATTCAGAAACCTTAATGTCGCGTAAATGCGGCTTAAAGATCAAGTATGGCTT 583
584	TGAGATGGGTCAGAGTATATTCGCAATTTTGGTGGCGATGTAAGCAATATACCGTCT 643
584	TGCATTTGATTAATAATTAATTGGCCAACTTTGGTGGCAATCCCGATTAATATACAGT 643
644	TGGGGAAGAGTGTGGTGGGCTTCACCACTTACATGATGATTAACGAAAGACCGCTG 703
644	TTGCTGAAGAGTGGGCTGGCTTCACCACTTACATGATGATTAACGAAAGACCGCTG 703
704	GTTATTTCCATCGTGTATCATGATGTCGGTATTCATTCATGCTATGGGCTTCAAG 763
704	GTTATTTCCATCGTGTATCATGATGTCGGTATTCATTCATGCTATGGGCTTCAAG 763
764	ATATCCAAAGTGTGGCTTACCATGAGCAACGTTTGGCTATTAAGGAGAGGCAATG 823

Db 764 AATGCAACATCGTGCCTTACCTTACCCAAATTTGGCCGCTATTAAGGTGAGATATATG 823
 Oy 824 AAAAGATATCCCTGGAATTCCTATATGAAGCAATCCCTATGATTTGATCAAGAGAC 883
 Db 824 ATAGGATGTTTGAATTTCTTATGAAGCCAAAGCCACGAGATTTAGTAAACTGAG 883
 Oy 884 CACAAGTTTGAACCCGAAAGAAATGAATAAGTATGTTCTTTTGAACCACTG 943
 Db 884 AAAAGTTTAACTCTAGAGAGGCTACAAATTAAGTATGTTCTTTTGGTCCACTG 943
 Oy 944 TAGAACAATACAGACAGCCAGCTGTGTGATCCCAACCAATCAATAGAGAAATGTTAGA 1003
 Db 944 TTGAGCCATATCAGACCCCTGATGTGCTTACCAACATCTCTGGGAGGTTTAAA 1003
 Oy 1004 GGGCGTGGGAATTCGATTCACCATGTATGACATACCTCTCTAGAGGTTTCTT 1063
 Db 1004 CTGCTTGGGTTATTCGATACCCACTATGATGGGTAACTCATATGAGGCTATTTT 1063
 Oy 1064 CCAATTCATTTGCCAAGATATCCGAGGTTTAAAGAGTTGGAATCTCTGTGATTT 1123
 Db 1064 TCACCTTCATTTCTTAAAGCAATGCTTATGCTTAAAGAAATTTGAAACTTGTCAATT 1123
 Oy 1124 ATGTGCTTGGAGTTGGCTGACATGAAAGAGTGGCCGAAACCTGAGAGGCTG 1183
 Db 1124 TTGTGCAAGTAAATTTGCTGATGCTGAAAGCAGCCGCCAGACACTTGAATGGGTG 1183
 Oy 1184 CCAATTCGAAAGAGCCATGATGAGGAAACACCTACTCTGATATTTTATGAGC 1243
 Db 1184 CTAATTTAAAGAGCTATGATGAGGAAACACCAACAGCTATATTTATGATC 1243
 Oy 1244 TTGTGCTTATTTCTATTTCTCTTCCCATGATCGCTCTCTACATTTGGGCTCAAC 1303
 Db 1244 TTGTGCTTATTTCTATTTCTCTTCCCATGATCGCTCTCTACATTTGGGCTCAAC 1303
 Oy 1304 ACACAGTGGACCTCCATTTATTTATGATTTGATTTGATTTGATTTGATTTGATTT 1363
 Db 1304 ACACAGTGGACCTCCATTTATTTATGATTTGATTTGATTTGATTTGATTTGATTT 1363
 Oy 1364 ACCCTATGCTATTTATGCTTTTGGCCGCTTAAAGGTGTAAGCCATGCCGATGAGC 1423
 Db 1364 ATCCCTATGCTATTTATGCTTTTGGCCGCTTAAAGGTGTAAGGTGTAAGGTGTAAGT 1423
 Oy 1424 TAACTATCTCTTCTGGAATTTTGTGCAAGGCTGCAAGGAAAGCCGCAATACA 1483
 Db 1424 TAACTATCTCTTCTGGAATTTTGTGCAAGGCTGCAAGGAAAGCCGCAATACA 1483
 Oy 1484 AAACCATTTGAAGCATGATGCTTGAAGCATTTGCAAGGATTTGCCACACCCGCAATACA 1543
 Db 1484 AAACCATTTGAAGCATGATGCTTGAAGCATTTGCAAGGATTTGCCACACCCGCAATACA 1543
 Oy 1544 GCAATGATATGCGGCGATGGAAGCACTCACTGGGATCCCAATAAATCCGATGATG 1603
 Db 1544 GCAATGATATGGAAGGATGGAAGCACTCACTGGGATCCCAATAAATCCGATGATG 1603
 Oy 1604 TCTATTAATGTTTAAATGATGCGGATGGAAGGATTTGCAAGGATTTGCCAGAAATGATA 1663
 Db 1604 TATACAGTGTGTAATATTAAGTATGGAAGGATTTGCAAGGATTTGCCAGAAATGATA 1663
 Oy 1664 AAATTAACAATGCGCAAGTATATTCATTAAGGAAAGGATTTGTTT 1710
 Db 1664 AGATTAAACAATGCGAGTATGTTGAAAGCAATGAGATTTATTT 1710

RESULT 12
 AT051473 2017 bp mRNA linear INV 27-AUG-2001
 LOCUS AY051473
 DEFINITION Drosophila melanogaster GH13950 full length cDNA.
 ACCESSION AY051473
 VERSION AY051473.1 GI:15291256
 KEYWORDS
 SOURCE Drosophila melanogaster.
 ORGANISM Drosophila melanogaster.
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

Neoptera: Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 2017)
 Stapleton, M., Broksstein, P., Hong, L., Agbayani, A., Carlson, J., Champe, M., Chavez, C., Dorsett, V., Farrant, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Li, P., Liao, G., Miranda, A., Mungall, C. J., Nunoo, J., Paclet, J., Paragas, V., Park, S., Phouanavong, S., Wan, K., Yu, C., Lewis, S. E., Rubin, G. M. and Celnikier, S.
 Direct Submission
 Submitted (10-AUG-2001) Berkeley Drosophila Genome Project, Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley, CA 94720, USA
 Sequence submitted by:
 Lawrence Berkeley National Laboratory
 Berkeley Drosophila Genome Project
 Berkeley National Laboratory

FEATURES
 source

1..2017
 /organism="Drosophila melanogaster"
 /strain="y: cn bw sp"
 /db_xref="taxon:7227"
 /map="84D5-84D5"
 1..2017
 /gene="alpha-Est7"
 /note="alignment with genomic scaffold AE003671"
 /db_xref="FLYBASE:FBgn0015575"
 91..1809
 /gene="alpha-Est7"
 /note="Longest ORF"
 /product="GH13950p"
 /protein_id="AAK92897.1"
 /db_xref="GI:15291257"
 /protein_id="AAK92897.1"
 /db_xref="FLYBASE:FBgn0015575"
 /translation="MNKNGFVERLRMLKTEHVOYRSTNETVAVDEYGOVNG
 IRLSLIDVPTFSFEIIPAPQPVGEILPFKAPORPIPERYRDCDSOPDKAVQVFE
 DKVEGSEDLVLTNTNNKPKAPRWYWHGGFTITGEANREMGDPVEMKEDVYL
 VTIOYRLGALGFMNSLSPKLVNPNAGLKDVLAKMLKNNKASFGDPNCTYFGS
 AGASFTYVMMLIDOTGLFHRGILLOSGLCPWAVNSDITNPRILALVSKEDND
 KADLEFLONVKKAKDLIYVENVLTLEERNNKIMFPGSLFSPTECVLSKPKEMK
 KTAWSNSIMFGTNGTSEGLVWPVKLMPVOYLQDLGTFPIRELATVSPSEKLD
 SWSAOIRVDHNGSESTPNYMDLSIYFVLPALVHSHAAVAVYFVETD
 SEELITPYRIMHGRGVKVSADLSIOFSLARLPKRSREVRNERTVGIWTF
 AATGNPYSEKINGMDTLITDYPKRSDEYIKCLINISDLKFLIDLPWPKLWSELYDD
 NKDLIF"

BASE COUNT
 ORIGIN

Query Match 37.8%; Score 646.6; DB 3; Length 2017;
 Best Local Similarity 61.9%; Pred. No. 8.4e-179;
 Matches 1043; Conservative 0; Mismatches 639; Indels 3; Gaps 1;
 Oy 28 GCGCTGAACATGCTTTAATGATGATCAATAATACCAACTACGCTTGATATA 87
 Db 118 CGCTTGGCGTGGCGCTCAAAACCATGAGATTAAGTCCAGAGATCGCCAGTGACC 177
 Oy 88 AATGAACCCAAATATGATGATATGATGACAAATTAAGGTGTTAAGCATGACC 147
 Db 118 AATGAACCCAAATATGATGATATGATGACAAATTAAGGTGTTAAGCATGACC 147

Db 178 AATGAACAGTGTGCGCCGACGAGAGTACGGCCAGTGGGGTATCAAGCGTCTACT 237
 QY 148 GTCTAGAGATGATTTACTACTACATTTGAGAGATACCCATAGCTAGCTCCATGGGT 207
 Db 238 CTCTAGAGATGATTTACTACTACATTTGAGAGATACCCATAGCTAGCTCCATGGGT 297
 QY 208 GATTTGAGATTTCAAGGACCCGACGCGCTGATGAGAGAGGAGTGTACGATTTGCTGT 267
 Db 298 GATTTGAGATTTCAAGGACCCGACGCGCTGATGAGAGAGGAGTGTACGATTTGCTGT 357
 QY 268 GGGCCAGCCAGATCGGTGTACAGACAGATTTCAATAGTGGGAAACCCAGAGTTGGAG 327
 Db 358 CACCCAGAGATGAGAGGCGCTCCAGAGTGTACGATTTGCTGATGAGAGAGGCGTGGAG 417
 QY 328 GATTTGATTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 387
 Db 418 GATTTGATTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 477
 QY 388 ATGTTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 447
 Db 478 ATGTTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 537
 QY 448 CCGGATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 507
 Db 538 CCGGATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 597
 QY 508 TTGGGTTTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 567
 Db 598 TTGGGTTTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 657
 QY 568 GATCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 627
 Db 658 GATCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 717
 QY 628 GATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 687
 Db 718 GATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 777
 QY 688 ACCGAAACAGCCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 747
 Db 778 ACCGAAACAGCCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 837
 QY 748 TCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 804
 Db 838 TCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 897
 QY 805 TATAGGAG 864
 Db 898 TATAGGAG 957
 QY 865 GATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 924
 Db 958 GATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1017
 QY 925 TTTTCTTTTGGACCACTGTAGAACATACAGACAGCCGAGTGTGTGTACCAACCA 984
 Db 1018 TTTTCTTTTGGACCACTGTAGAACATACAGACAGCCGAGTGTGTGTGTGTGTGTGT 1077
 QY 985 ATCAGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1044
 Db 1078 ATCAGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1137
 QY 1045 TCTTACAG 1104
 Db 1138 TCTTACAG 1197
 QY 1105 TTGGAGTCTGT 1164
 Db 1198 TTGGAGTCTGT 1257
 QY 1165 GAAACCTTGGAG 1224
 Db 1258 GAAACCTTGGAG 1317

QY 1225 CTGGAATATTTTATGAGAGCTTTGCTCCATTTTCTATTTTCTTCCCATGATCGCTTC 1284
 Db 1318 CCAGATATTTTATGAGAGCTTTGCTCCATTTTCTATTTTCTTCCCATGATCGCTTC 1377
 QY 1285 CTGGAATATTTTATGAGAGCTTTGCTCCATTTTCTATTTTCTTCCCATGATCGCTTC 1344
 Db 1378 CTGGAATATTTTATGAGAGCTTTGCTCCATTTTCTATTTTCTTCCCATGATCGCTTC 1437
 QY 1345 GATTTGAG 1404
 Db 1438 GATTTGAG 1497
 QY 1405 GATTTGAG 1464
 Db 1498 GATTTGAG 1557
 QY 1465 AAGGAAAG 1524
 Db 1558 AAGGAAAG 1617
 QY 1525 ACCAGCGGAG 1584
 Db 1618 ACCAGCGGAG 1677
 QY 1585 ATAAAG 1644
 Db 1678 ATAAAG 1737
 QY 1645 GATTTGAG 1704
 Db 1738 GATTTGAG 1797
 QY 1705 TTGTT 1709
 Db 1798 TTGTT 1802

RESULT 13
 LOCUS AY058637
 DEFINITION Drosophila melanogaster
 ACCESSION AY058637
 VERSION AY058637.1
 KEYWORDS GI:16198126
 SOURCE
 ORGANISM Drosophila melanogaster.
 Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Phylotrietales; Drosophilidae; Drosophila.
 REFERENCE 1 (bases 1 to 2122)
 STAPLETON, M., BROCKSTEIN, P., HONG, L., ABAYAN, A., CARLSON, J.,
 CHAMPE, M., CHAVEZ, C., DORSETT, V., FARFAN, D., FRISCH, E., GEORGE, R.,
 GONZALEZ, M., GUARDIA, H., LI, P., LIAO, G., MIRANDA, A., MUNGALL, C., J.,
 NUNO, J., PACHEL, J., PARAGAS, V., PARK, S., PHOUANAVONG, S., WAN, K.,
 YU, C., LEWIS, S. E., RUBIN, G. M. and CELINKER, S.
 Direct Submission
 Submitted (08-OCT-2001) Berkeley Drosophila Genome Project,
 Lawrence Berkeley National Laboratory, One Cyclotron Road,
 Berkeley, CA 94720, USA
 Sequence submitted by:
 Berkeley Drosophila Genome Project
 Lawrence Berkeley National Laboratory
 Berkeley, CA 94720

COMMENT
 This clone was sequenced as part of a high-throughput process to
 sequence clones from Drosophila Gene Collection 1 (Rubin et al.,
 Science 2000). The sequence has been subjected to integrity checks
 for sequence accuracy, presence of a polyA tail and contiguity
 within 100 kb in the genome. Thus we believe the sequence to
 reflect accurately this particular cDNA clone. However, there are
 artifacts associated with the generation of cDNA clones that may
 have not been detected in our initial analyses such as internal
 priming, priming from contaminating genomic DNA, retained introns

Db 1740 ACTAGTGA---GAAAGGCCGACAGATGTCATTAATATGGAAGAACATGAGTTCAT 11796
 QY 1644 GAATTTCCGAGAAATGATTAATTAACAAATGGCAGATTAATTCATTAATAA 1697
 Db 1797 TGTGTCGCGGAGTGAAGAAATGATTTGGATTAAGTATTAACATTAATAA 1850

RESULT 14
 AX260182
 LOCUS AX260182 1809 bp DNA linear PAT 26-OCT-2001
 DEFINITION Sequence 144 from Patent WO0172774.
 ACCESSION AX260182
 VERSION AX260182.1 GI:16509196
 KEYWORDS
 SOURCE fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 REFERENCE
 1. Deak P., Glover, D.M. and Midgley, C.
 TITLE Cell cycle progression proteins
 JOURNAL Patent: WO 0172774-A 144 04-OCT-2001;
 Cytoskeleton Limited (GB)
 FEATURES
 source location/Qualifiers
 1. 1809
 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"

Query Match 20.6%; Score 352.8; DB 6; Length 1809;
 Best Local Similarity 54.3%; Pred. No. 3e-92;
 Matches 876; Conservative 0; Mismatches 687; Indels 51; Gaps 6;

QY 101 TATTCATATCTGATATGACAAATTAAGGTTTAAGCATGACCTCTACGATGAT 160
 Db 239 TCTATTAAGCAATGAGTCTGTCGCGGAGTGAAGAAACAAATCTGGGAGGAA 298
 QY 161 CTATACAGTTTTCGAGATATACCTTATGTAAGCTCCGATGGGTAGTGAATCA 220
 Db 299 GCTACTTCACTTTCGAGAAATACCTTTCGAAAGCTCCGATGGGATCTGCGTTCA 358
 QY 221 AGGCAACCCAGGCGCTTACCATGGAGGATGATGATGCTGGGCAACCA 280
 Db 359 AGGCCCCGGAACAGTGGAGGATGGATGAGAAATGGATGATCTCCCGGAGACA 418
 QY 281 GATCGGTACAGACATTTCAATAGTGGCAACCCAGATGCGAGATGCTATAC 340
 Db 419 AGCCCTTCAGACACATGTTTTCAGAAATAGCGGCTCAGAGACTGCTCTAC 478
 QY 341 TGAATGTATACCAATGACTTGAACCAAGCAAGGCTCCGTTATGTTGATCATC 400
 Db 479 TAAATGTATGTCAAAAGATCTGACCGGATTAACCTGCTCCGATGATGTTGATCA 538
 QY 401 ATGGCGGATATTTATTTGGGGAACCAATGTAATGCTGTTGCTCCGACTACTTA 460
 Db 539 ACGAGGAGGATTAATGATTTGGGAACTTCTGAGGATTTGAT----- 582
 QY 461 TGAAGAAACCCGCTGTTGTAACCGTGAATGCTGTTGGTGTGTTGCTTCTTA 520
 Db 583 -----GTGTCATATGTCACCGTTGCTTATGACTGGGTGCTTGGCTTCTCA 631
 QY 521 GCCTGAATGGGAAATCTCAATGTCCTCCGCAAGCTGCTCAAGATCAAGTAATG 580
 Db 632 GCTGATGATGTCCTCAATGATGTCCTCCGAAATGCAAGTCTCAAGATCAATG 691
 QY 581 CTTGATGATGCTCAAGATGATGATGATGATGATGATGATGATGATGATGATG 640
 Db 692 CCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 751
 QY 641 TCTTGGCGGAAGTGTGCTGCTGCTGCTCAACCATTAATGATGATGATGATGATG 700

Db 752 TCTTTGGGGAAGTCCCGGAGAGCTGACACTTCTTGGACTAATGCTCCCAAGC 811
 QY 701 GTGTTTATTCATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 760
 Db 812 AAGTCTTATCCCAAAACATGCTGATGATGATGATGATGATGATGATGATGATGATG 871
 QY 761 CAGATGCGAAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 820
 Db 872 CACGAGAAATATATGAGCTTATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 931
 QY 821 ATGAAAAAGATATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 880
 Db 932 AGGCAAGGCGATCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATG 991
 QY 881 AGCCACAAAGTTTGGACACCCGAAAGATGCAAAATGATGATGATGATGATGATGATG 940
 Db 992 CCGCAACAGTTTCCAGAACAGATGAAAGATGATGATGATGATGATGATGATGATGATG 1051
 QY 941 CTGTAGAACATACAGACAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1000
 Db 1052 TCGTAGAACATATATACAGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1111
 QY 1001 AGAGCGCTGCGGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1060
 Db 1112 AGAATAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1171
 QY 1061 TTTCCAAATCAATTTGCCAAATATCCGAGGTTGTAAGATGATGATGATGATGATG 1120
 Db 1172 TATTTATCCAGAGTTTCAAGCGCGGACCAACCTCGATGATGATGATGATGATGATG 1231
 QY 1121 ATATATGCTGCTGCGGAGTGTGCTGATGATGATGATGATGATGATGATGATGATGATG 1180
 Db 1232 ATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1288
 QY 1181 CTGCAATTTGAAAGGCGCATGATGATGATGATGATGATGATGATGATGATGATGATG 1240
 Db 1289 GCTTGCAATGAAAGAGCGATTTTCGCGGAGCAACCTGATGATGATGATGATGATG 1348
 QY 1241 ACCTTGTGCTGATTTTATTTTCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1294
 Db 1349 AGTTTCTGAGGTATGCTATGATGATGATGATGATGATGATGATGATGATGATGATG 1408
 QY 1295 GCTTACACACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1354
 Db 1409 ACCGTGTCCGCAATCCAGCGCACCATGATGATGATGATGATGATGATGATGATGATG 1465
 QY 1355 AATATATTAACCCATGCTATGATGATGATGATGATGATGATGATGATGATGATGATG 1414
 Db 1466 AACTGTGCAACGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1525
 QY 1415 CCGATGAGCTAACCTATCTCTGCAACATTTTGTGCAAGCGCTGCAAGGAAAGCC 1474
 Db 1526 GTGAGATGCTGTGATATTTTTCACAGATGATGATGATGATGATGATGATGATGATG 1585
 QY 1475 GCGAATCAAAACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1534
 Db 1586 CCGAACAAGGTTATTAACCGGAATGTGAGCTTTGAGGATTTCCGAGCCACCGAG 1645
 QY 1535 AACCATACCAATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1594
 Db 1646 ATCCCAACCTGCAAAAGTATA-----AAATCACTCAAGTTTCCACCATGCAAAA-- 1694
 QY 1595 CCGATGATGCTATTAATGTTTAATATGATGATGATGATGATGATGATGATGATGATGATG 1654
 Db 1695 -CGTAACCACTTTAATGCTCAATATGATGATGATGATGATGATGATGATGATGATGATG 1753
 QY 1655 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1708
 Db 1754 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1807

RESULT 15

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 10, 2003, 22:58:21 ; Search time 246.473 Seconds
(without alignments)
15624.094 Million cell updates/sec

Title: US-09-776-910-14

Perfect score: 1710
Sequence: 1 atgaccttcttgagcaatt.....ataaaagaagaattgttt 1710

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

N.Geneseq_101002:*

- 1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
- 2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
- 3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
- 4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
- 5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
- 6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
- 7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
- 8: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
- 9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
- 10: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
- 11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
- 12: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
- 13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
- 14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
- 15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
- 16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
- 17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
- 18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
- 19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
- 20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
- 21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
- 22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
- 23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
- 24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1710	100.0	1710	18	AAT68597
2	956.6	55.9	1713	16	AAQ91561
3	956.6	55.9	1713	18	AAT68596
4	955	55.8	1713	16	AAQ91566
5	955	55.8	1713	16	AAQ91562
6	955	55.8	1713	16	AAQ91565
7	953.4	55.8	1713	16	AAQ91564
8	950.2	55.6	1713	16	AAQ91563
9	646.6	37.8	2001	23	ABL02067

10	399.2	23.3	1665	23	ABL02099	Drosophila melanog
11	398.8	23.3	1593	23	ABL02103	Drosophila melanog
12	353.2	20.7	1863	23	ABL01859	Drosophila melanog
13	352.8	20.6	1809	24	ABR90480	Drosophila cell cy
14	349.4	20.4	6175	23	ABL02066	Drosophila melanog
15	347.8	20.3	1791	23	ABL10333	Drosophila melanog
16	346.4	20.3	1704	23	ABL02081	Drosophila melanog
17	342	20.0	3856	23	ABL10332	Drosophila melanog
18	342	20.0	67279	23	ABL07668	Drosophila melanog
19	336.8	19.7	1719	23	ABL02101	Drosophila melanog
20	335	19.6	1792	23	ABL04689	Drosophila melanog
21	320.6	18.7	1878	23	ABL01947	Drosophila melanog
22	259	15.1	4242	23	ABL02102	Drosophila melanog
23	224.6	13.8	1727	23	ABL01943	Drosophila melanog
24	218.4	12.7	5008	23	ABL04688	Drosophila melanog
25	217.2	12.0	4294	23	ABL02098	Drosophila melanog
26	204.4	12.0	4294	23	ABL02100	Drosophila melanog
27	204.4	12.0	5132	23	ABL01858	Drosophila melanog
28	204.4	11.4	2613	23	ABL19064	Drosophila melanog
29	195.6	11.0	1626	23	ABL01945	Drosophila melanog
30	187.6	9.8	1987	19	AAV40762	Drosophila melanog
31	167.2	9.8	1987	19	AAV40763	Drosophila melanog
32	167.2	9.8	1590	19	AAV40764	Drosophila melanog
33	164.6	9.6	1590	19	AAV40765	Drosophila melanog
34	164.6	9.6	1590	19	AAV40766	Drosophila melanog
35	164	9.6	4288	23	ABL01942	Drosophila melanog
36	162.6	9.5	1540	19	AAV40756	Drosophila melanog
37	162.6	9.5	1584	19	AAV40757	Drosophila melanog
38	162.6	9.5	2007	19	AAV40754	Drosophila melanog
39	162.6	9.5	2007	22	AAV40755	Drosophila melanog
40	162.6	9.5	2007	22	AAV40756	Drosophila melanog
41	160.6	9.4	1783	23	ABL02029	Drosophila melanog
42	144.8	8.5	4283	23	ABL01946	Drosophila melanog
43	129.8	7.6	3357	23	ABL11072	Drosophila melanog
44	129.6	7.6	1584	23	ABL11073	Drosophila melanog
45	128	7.5	1774	23	ABL15783	Drosophila melanog

ALIGNMENTS

RESULT 1	
AAT68597	standard; DNA; 1710 BP.
ID	AAT68597
XX	
AC	AAT68597;
XX	
DT	08-AUG-1997 (first entry)
XX	
DE	Md-alpha-E7 gene.
XX	
KW	Malathion carboxylesterase; organophosphate; insecticide;
KW	pesticide; remediation; bioremediation; decontamination; ds.
XX	
OS	Musca domestica Rutgers strain.
XX	
FH	
FT	Key
FT	mutation
FT	Location/Qualifiers
FT	752
FT	/tag= a
FT	/note= "Trp-251 TGG codon is altered to a Ser
FT	codon in resistant mutants"
FN	
PD	W09719176-A1.
PD	29-MAY-1997.
XX	
PF	22-NOV-1996; 96NC-AU00746.
XX	
PR	23-NOV-1995; 95AU-0006751.
XX	
PA	(CSIR) COMMONWEALTH SCI & IND RES ORG.
XX	
PI	Boyce T, Brownlie JC, Campbell PM, Claudianos C;

PI Newcomb RD, Oakesholt JG, Robln GC, Russell RJ, Smyth K;
XX WPI: 1997-298113/27.
DR P-PSDB: AAM17767.
XX
XX DNA encoding enzyme that degrades organophosphate pesticides -
PI useful for decontamination of soil, water, food etc
XX
XX Claim 6: Fig 3: 52pp; English.

CC A 1710 bp DNA molecule (AAT68597) comprises the Md-alpha-E7
CC coding sequence of the Musca domestica Rutgers strain. It was
CC isolated by amplification of genomic DNA using alpha-esterase
CC consensus primers (see also AAT68598-99) and use of a 534 bp
CC amplicon to screen a genomic library of M. domestica. A
CC mutation of the gene, resulting in subst. of serine for tryptophan
CC at amino acid position 251 (see also AAM17767), confers malathion
CC resistance. The resistant enzyme acts as a malathion
CC carboxylesterase and can be formulated for use in degrading
CC environmental carboxylester or dimethyl general organophosphates.
XX
XX Sequence 1710 BP; 498 A; 369 C; 394 G; 449 T; 0 other;

Query Match 100.0%; Score 1710; DB 18; Length 1710;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1710; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACTTTTGAAGCAATTCATATTTCCGCTGAACATCTTAAATGATGATCAT 60
DB 1 ATGACTTTTGAAGCAATTCATATTTCCGCTGAACATCTTAAATGATGATCAT 60
QY 61 AAATACCAAACTACCTGTGAGTACAAATGAAGCAAAATATCGATCTGATATGGA 120
DB 61 AAATACCAAACTACCTGTGAGTACAAATGAAGCAAAATATCGATCTGATATGGA 120
QY 121 CAAATTAAGGGTGTAAAGCAATGACCGTCTACGATGATCTTACACAGTTTCGAGAGT 180
DB 121 CAAATTAAGGGTGTAAAGCAATGACCGTCTACGATGATCTTACACAGTTTCGAGAGT 180
QY 181 ATACCATGCTAAGCCTCCAGTGGGTGAGTTGAGTTCAAGGACCCGAGGCTGTGA 240
DB 181 ATACCATGCTAAGCCTCCAGTGGGTGAGTTGAGTTCAAGGACCCGAGGCTGTGA 240
QY 241 CCATGGAGGGTGTACGCTGATTTGCTGGGCCAGCCAGATCGGTACAGACATTTTC 300
DB 241 CCATGGAGGGTGTACGCTGATTTGCTGGGCCAGCCAGATCGGTACAGACATTTTC 300
QY 301 ATAGAGGCAAAACCCACAGGTTGGAGATTTGCTATACCTGAATGTGTATACCAATGAC 360
DB 301 ATAGAGGCAAAACCCACAGGTTGGAGATTTGCTATACCTGAATGTGTATACCAATGAC 360
QY 361 TTGAACCCAGACAAAGGGCTCTGTATGTTTCAATCCATGAGGAGATTTTATTTTC 420
DB 361 TTGAACCCAGACAAAGGGCTCTGTATGTTTCAATCCATGAGGAGATTTTATTTTC 420
QY 421 GGGGAAGCAAAATGTAAGTGTGGTCCGACTATTATGAAGAAACCCGTGGTCTTG 480
DB 421 GGGGAAGCAAAATGTAAGTGTGGTCCGACTATTATGAAGAAACCCGTGGTCTTG 480
QY 481 GTAACGCTCAATATGCTTTGGGTGTGGTCTTCTTACCTGGAATTCGGAATATCTC 540
DB 481 GTAACGCTCAATATGCTTTGGGTGTGGTCTTCTTACCTGGAATTCGGAATATCTC 540
QY 541 AATGTCCCGGCAACGCTGAGCTCAAGGATCAAGTAATGCTTGAAGTGGCTCAAGT 600
DB 541 AATGTCCCGGCAACGCTGAGCTCAAGGATCAAGTAATGCTTGAAGTGGCTCAAGT 600
QY 601 AATATGCTATTTGGTGGGAGTATAGACAATATTAACGCTTGGCGGAAGTCTGT 660
DB 601 AATATGCTATTTGGTGGGAGTATAGACAATATTAACGCTTGGCGGAAGTCTGT 660
QY 661 GGGGCTCAACCATTTATCATGATGATTAACGACAGCCGTGGTTATTCATCGTGT 720
DB 661 GGGGCTCAACCATTTATCATGATGATTAACGACAGCCGTGGTTATTCATCGTGT 720

DB 661 GGGGCTCAACCATTTATCATGATGATTAACGACAGCCGTGGTTATTCATCGTGT 720
QY 721 ATCATGATGTCGGTAATTCATGTCATGGGCTCTACAGATGCCAAATCGTGG 780
DB 721 ATCATGATGTCGGTAATTCATGTCATGGGCTCTACAGATGCCAAATCGTGG 780
QY 781 CTCACCATGCCAAACGTTGGCTATTAAGGAGAGACATGAAAAAGATTCGTGAA 840
DB 781 CTCACCATGCCAAACGTTGGCTATTAAGGAGAGACATGAAAAAGATTCGTGAA 840
QY 841 TTCCATATGAAGCAATCCATGATGATGATGATGATGATGATGATGATGATGATGAT 900
DB 841 TTCCATATGAAGCAATCCATGATGATGATGATGATGATGATGATGATGATGATGAT 900
QY 901 GAAAGATGCAAAATTAAGTGTATGTTTCTTTGAGCCCTGTACACATACCGAGCA 960
DB 901 GAAAGATGCAAAATTAAGTGTATGTTTCTTTGAGCCCTGTACACATACCGAGCA 960
QY 961 GCGGACGTGTGTGATGACCAACCAATGAGAAATGAGAGCGCTGGGAAATTCG 1020
DB 961 GCGGACGTGTGTGATGACCAACCAATGAGAAATGAGAGCGCTGGGAAATTCG 1020
QY 1021 ATACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
DB 1021 ATACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
QY 1081 CAAATATCGGAGGTGTGTAAGAGTGTGAATCTGTGTGAATTTGCTTGGAGTTG 1140
DB 1081 CAAATATCGGAGGTGTGTAAGAGTGTGAATCTGTGTGAATTTGCTTGGAGTTG 1140
QY 1141 GCTGACAGTGAAGCAAGTGTGCGGAAACCTGGAAGAGGCTGCAATGTAAGAGCC 1200
DB 1141 GCTGACAGTGAAGCAAGTGTGCGGAAACCTGGAAGAGGCTGCAATGTAAGAGCC 1200
QY 1201 CATGTGATGAGGGAACACCTACTCTGTGAATTTATGAGACCTTGTCTTATTTCTAT 1260
DB 1201 CATGTGATGAGGGAACACCTACTCTGTGAATTTATGAGACCTTGTCTTATTTCTAT 1260
QY 1261 TTCTCTTCCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
DB 1261 TTCTCTTCCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
QY 1321 ATTTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
DB 1321 ATTTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
QY 1381 CGTTTGGGCGGTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1440
DB 1381 CGTTTGGGCGGTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1440
QY 1441 AACATTTTGTGAAGAGCGCTGCAAGAGAAAGCCGCAATACCAATGTAAGAGCATG 1500
DB 1441 AACATTTTGTGAAGAGCGCTGCAAGAGAAAGCCGCAATACCAATGTAAGAGCATG 1500
QY 1501 GTTGGATTTGAAGAGGATTTGGCCACCAACCGGCAACCATACAGCAATGATAGCCGGC 1560
DB 1501 GTTGGATTTGAAGAGGATTTGGCCACCAACCGGCAACCATACAGCAATGATAGCCGGC 1560
QY 1561 ATGGAAGAACTCACCTGGGATCCATAAAAAATCCGATGTCATTAATGTTAAAT 1620
DB 1561 ATGGAAGAACTCACCTGGGATCCATAAAAAATCCGATGTCATTAATGTTAAAT 1620
QY 1621 ATCGGCGATGAATGAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
DB 1621 ATCGGCGATGAATGAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
QY 1681 AGTATATTCGATTAAGAAAGAGATTTGTT 1710
DB 1681 AGTATATTCGATTAAGAAAGAGATTTGTT 1710
RESULT 2
AA091561

ID AA091561 standard; cDNA; 1713 BP.
 AC AA091561;
 XX 22-DEC-1995 (first entry)
 XX OP-sensitive esterase E3 Lc743 clone.
 DE Esterase; E3; bioremediation; organophosphate; carbamate;
 XX Insecticide; pesticide; water decontamination; meat decontamination;
 KW ss.
 XX Lucilia cuprina.
 OS
 XX Key Location/Qualifiers
 FT CDS 1..1713
 FT /tag- a
 FT
 XX MO9519440-A1.
 XX 20-JUL-1995.
 XX 13-JAN-1995; 95MO-AU00016.
 XX 13-JAN-1994; 94AU-0003347.
 XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
 XX Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;
 PI Parker AG, Robin GC, Russell RJ, Smyth K;
 DR WPI; 1995-263870/34.
 DR P-PSDB; AAR78142.
 XX Pure E3 esterase from *Lucilia cuprina* and related DNA - used to
 PT eliminate residues of organophosphate and carbamate pesticides from
 PT water, meat etc.
 XX
 PS Claim 5; Page 12-17; 38pp; English.
 CC cDNA from organophosphate (OP)-sensitive *L. cuprina* pupa cDNA
 CC library was amplified using cluster-specific esterase primers.
 CC Isolated clone Lc743, a probable full-length cDNA, was expressed
 CC using a baculovirus vector in insect cells and shown to encode
 CC an OP-susceptible E3 esterase, useful in bioremediation.
 XX
 SQ Sequence 1713 BP; 516 A; 305 C; 370 G; 522 T; 0 other;
 Query Match 55.9%; Score 956.6; DB 16; Length 1713;
 Best Local Similarity 73.4%; Pred. No. 2e-285;
 Matches 1223; Conservative 0; Mismatches 444; Indels 0; Gaps 0;

Db 344 GTGTCTATACGATTAATTAATCCGAAACTAAACGTCCTTTAGTATACATACATG 403
 Qy 404 GCGAGATTTTATTTTCGCGCAAGCAATCTGACTGGTTGCTCCGACATCTTATGA 463
 Db 404 GTGTGTTTATTTATTCGGAATAATCATGATATGATGCTGCTGTTATTTTCAATA 463
 Qy 464 AGAAACCGGTGCTTGTGTAACCGTGCATATGCTTTGGGTGTGTTGCTTCTTACC 523
 Db 464 AAAAGCATGTGCTGTTGATTAACATACATATGCTTTGGAGCTCTAGTCTTAAAGT 523
 Qy 524 TGAATCGAAAAATCTCATGTCCTCCGCGCAAGCTGGCTCAAGATCAAGTAATGGCT 583
 Db 524 TAAATTCAGAAACCTTAATGTCGCGGTAAATGCCCTTAAGATCAAGTATGAGCT 583
 Qy 584 TGAATGGGTACAGATTAATGTCATTTTGGTGGCTAGACATATTTACGCTCT 643
 Db 584 TGCCTTGATTAATAAATAATTTGGCCCACTTTGGTGGCAATCCGATATATTTACAGT 643
 Qy 644 TCGCGAAAGTGTGCTGGGGCTCAACCCATTACATGATGATTAACGCAAGACCCGTG 703
 Db 644 TTGCTGAAAGTCCGCGGTGCTCTACCATACATGATGATTAACGCAAGACCCGTG 703
 Qy 704 GTTTATTCATGCTGATATGATGATGCTGCTAATTCATGCTCTATGAGGCTCTACAG 763
 Db 704 GTCTTTCCATGCTGATATGATGATGCTGCTAATTCATGCTCTATGAGGCTCTACAG 763
 Qy 764 AATGCCAAAGTGTGCTGGGGCTCAACCCATTACATGATGATTAACGCAAGACCCGTG 823
 Db 764 AATGCCAAAGTGTGCTGGGGCTCAACCCATTACATGATGATTAACGCAAGACCCGTG 823
 Qy 824 AAAAGATATCTGTAATTCCTTAATGAAGCAATCCCTTATGATTTGATCAAGAGAGAC 883
 Db 824 AATGCCAAAGTGTGCTGGGGCTCAACCCATTACATGATGATTAACGCAAGACCCGTG 883
 Qy 884 CACAAGTTTGAACCCCAAGATGCAATTAAGTCAATGCTTTGCTTTGACCCACTG 943
 Db 884 AAAAGTTTAACTCTAAGAGAGAGGATCAATTAAGTCAATGCTTTGCTTTGACCCACTG 943
 Qy 944 TAGAATCATACAGACAGCCGCTGCTGATACCAACCAATCAGAGAAAGGTGAGAG 1003
 Db 944 TTGACCATATACAGCCGCTGATGCTGATACCAACCAATCAGAGAAAGGTGAGAG 1003
 Qy 1004 GCGCTGGGGAATTCATACCCCATATGATGATGATGATGATGATGATGATGATG 1063
 Db 1004 GCGCTGGGGAATTCATACCCCATATGATGATGATGATGATGATGATGATGATG 1063
 Qy 1064 CCAATTCGAAAGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1123
 Db 1064 CCAATTCGAAAGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1123
 Qy 1124 ATGTGCTTGGAGTGGCTGACAGTGAAGCAGTGGCCCGGAAACCTTGAAGAGGCTG 1183
 Db 1124 ATGTGCTTGGAGTGGCTGACAGTGAAGCAGTGGCCCGGAAACCTTGAAGAGGCTG 1183
 Qy 1184 CCAATTCGAAAGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1243
 Db 1184 CCAATTCGAAAGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1243
 Qy 1244 TTTGCTCTATTTTCAATTTCTTCCCATGCTGCTTCCATATTTGGCTTCAAC 1303
 Db 1244 TTTGCTCTATTTTCAATTTCTTCCCATGCTGCTTCCATATTTGGCTTCAAC 1303
 Qy 1304 ACACAGTGGCACTCCCATTTATTTGATGATGATGATGATGATGATGATGATGATG 1363
 Db 1304 ACACAGTGGCACTCCCATTTATTTGATGATGATGATGATGATGATGATGATGATG 1363
 Qy 1364 ACCCTATGCTATTTATGCTTTTGGGCTGATTAAGGCTGATTAAGGCTGATTAAG 1423
 Db 1364 ACCCTATGCTATTTATGCTTTTGGGCTGATTAAGGCTGATTAAGGCTGATTAAG 1423
 Qy 1424 TAACCTATCTCTTGTGAACATTTTGTGAACAGCTTGTGAACAGGAGGAGGAGGAG 1483
 Db 1424 TAACCTATCTCTTGTGAACATTTTGTGAACAGCTTGTGAACAGGAGGAGGAGGAG 1483

Db 1424 TAACCTATTTCTTGGATCAATTCGCAAAAGCTATGCTTAAGATCGGTGATACA 1483
 QY 1484 AACCATTCAGACGATGGTGGATTTGGAGCAATTCGCCACCGGCAACCATACA 1543
 Db 1484 AACCATTCAGACGATGGTGGATTTGGAGCAATTCGCCACCGGCAACCATACA 1543
 QY 1544 GCAATGATATAGCCGCGATGAAAAACCTCACCCTGGATCCCATAAAAATCCGATGATG 1603
 Db 1544 GCAATGATATAGCCGCGATGAAAAACCTCACCCTGGATCCCATAAAAATCCGATGATG 1603
 QY 1604 TCTATTAATGTTTAATTCGCGCATGATTCGCAATTAAGATTTGGCAAAATGATA 1663
 Db 1604 TATCAATGTTTGAATTTAGTACGAAATGAAATGATTCGATGCTGCAATGATGATA 1663
 QY 1664 AAATTAACATGCGCAAGTATTCGATTAAGAAAGAAAGATTTGTT 1710
 Db 1664 AGATTAAACATGGAATTCGATTTTGAAGAAACATAGATTTTATTT 1710

RESULT 3

AAT68596
 ID AAT68596 standard; DNA; 1713 BP.

XX AAT68596;

DT 08-AUG-1997 (first entry)

DE Lc-alpha-E7 malathion susceptible esterase clone Lc743.

XX Malathion carboxylesterase; organophosphate; insecticide;
 KW pesticide; remediation; bioremediation; decontamination; esterase;
 KM ss.

XX Lucilia cuprinia.

EH key Location/Qualifiers
 FT primer_bind complement (1..26)
 FT /tag= a
 FT /note= "Lc743 5' primer"
 FT primer_bind 1686..1713
 FT /tag= b
 FT /note= "Lc743 3' primer"
 FT /tag= c
 FT /note= "base 752 is T in resistant clones
 (TTP to Leu mutation)"
 FT mutation 1344
 FT /tag= d
 FT /note= "base 1344 is C in resistant clones
 (silent mutation)"
 FT mutation 1362
 FT /tag= e
 FT /note= "base 1362 is C in resistant clones
 (silent mutation)"
 FT mutation 1599
 FT /tag= f
 FT /note= "base 1599 is T in resistant clones
 (silent mutation)"
 FT mutation 1629
 FT /tag= g
 FT /note= "base 1629 is T in resistant clones
 (silent mutation)"

PN W09719176-A1.

XX 29-MAY-1997.

XX 22-NOV-1996; 96WO-AU00746.

XX 23-NOV-1995; 95AU-0006751.

PA (CSIR) COMMONWEALTH SCI & IND RES ORG.

PI Boyce T, Brownlie JC, Campbell PM, Claudianos C;
 PT Newcomb RD, Oakeshott JC, Roblin GC, Russell RJ, Smyth K;
 DR WPI: 1997-298113/27.
 DR P-PsDB; AAM17765.
 XX
 PT DNA encoding enzyme that degrades organophosphate pesticides -
 PT useful for decontamination of soil, water, food etc
 PS
 PS Claim 4: Fig 1: 52pp; English.

Sequence 1713 BP; 516 A; 305 C; 370 G; 522 T; 0 other;

Query Match 55.9%; Score 956.6; DB 18; Length 1713;
 Best Local Similarity 73.4%; Pred. No. 2e-285;
 Matches 1223; Conservative 0; Mismatches 444; Indels 0; Gaps 0;

QY 44 TTAATGCAATGGTCAATTAATATACCAACACTACCGTCTGATGACAATGAAACCAATTA 103
 Db 44 TTAATGCAATGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 103
 QY 104 TCGATAGTGAATATGACCAATTAAGGCTTTAAGCCATGACCGTCTAGATATTCTT 163
 Db 104 CTGAACACTGAATATGCAAGATGAAAGGCTTTAATGCTTTAATGCTTTAATGCTTTAATGCTT 163
 QY 164 ACTACAGTTTGGAGAGATATACCTATGCTTAAGCTCCAGTGGGATGATGATTTCAAG 223
 Db 164 ACTACAGTTTGGAGAGATATACCTATGCTTAAGCTCCAGTGGGATGATGATTTCAAG 223
 QY 224 CACCCAGCGGCTGATACATGAGGAGGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 283
 Db 224 CACCCAGCGGCTGATACATGAGGAGGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 283
 QY 284 CGGTACAGACGATTTATCATAGTGAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 343
 Db 284 CAGTGAAGTGAATTTATATACGAGGCAAGTGTGCTGATGAGGATGCTGATATACCTAA 343
 QY 344 ATGTGTATACCAATGACTGAACCCAGCAAAAGGCTCCTGTTATGTTTATCATCATG 403
 Db 344 GTGTCTATACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 403
 QY 404 GCGGAGATTTTATTTTGGGGAAGCAATGCTAATGCTTTGCTCCGACTACTTATGA 463
 Db 404 GTGTGCTTTTATTTATGCTGAATATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCT 463
 QY 464 AGAAACCCGCT 523
 Db 464 AGAAACCCGCT 523
 QY 524 TGAATGGAATATTCATATGCTCCGCGCAACGCTGCTCAAGATCAAGATATGAGCT 583
 Db 524 TGAATGGAATATTCATATGCTCCGCGCAACGCTGCTCAAGATCAAGATATGAGCT 583
 QY 584 TGAATGGAATATTCATATGCTCCGCGCAACGCTGCTCAAGATCAAGATATGAGCT 643
 Db 584 TGAATGGAATATTCATATGCTCCGCGCAACGCTGCTCAAGATCAAGATATGAGCT 643
 QY 644 TCGGCAAGATGCT 703
 Db 644 TCGGCAAGATGCT 703
 QY 704 GTTATTCATGCT 763

Db 704 GTCTTTTCATCGTGTATTAATGTCGGTAATGCTATTTGCTCATTTGGGCTAATACC 763
 Qy 764 AATGCCAAAGTCGCGCTCAGCATGCGCAACGTTGGCTATTAAGGAGAGACATG 823
 Db 764 AATGTCAACATCGTCCTTACCTTACCAATTTGGCGGCTAATAAGGAGATATG 823
 Qy 824 AAAAGATATCTGGAATTCCTAATGAAGCAATCCCTATGATTTGATCAAGAGAGC 883
 Db 824 ATAAGGATGTTTGAATTTCTTATGAAGCAAGCCACAGGATTTAATAACCTGAGG 883
 Qy 884 CACAAGTTTGACACCGCAAGATGCAAAATAGTCATGTTCCCTTTGAGACCCAGC 943
 Db 884 AAAAGTTTAACTCTAAGAGAGCGTCAAAATAGTCATGTTCTTTTGGTCCACTG 943
 Qy 944 TAGAACCATACAGACAGCGCAGTGTGTACCCCAACCAATCAGAGAAATGCTGAGA 1003
 Db 944 TTGAGCCATACAGACCGCTGATTTGTCTTACCAACCAATCCTCGGGAATGCTTAAA 1003
 Qy 1004 GCGCTGGGGAATTCGATACCCCATTTGATAGCAATACCTCTACGAGAGTTGCTTT 1063
 Db 1004 CTGCTTGGGTAATTCGATACCCCATTTGATAGGAGTAACTCATATGAGGCTATTTT 1063
 Qy 1064 CCAATCAATTCGCAACCAATATCCGAGGTTGTAAAGATTTGGAATCCCTGTGATTT 1123
 Db 1064 TCACCTTCAATTTCTAAGCAAAATGCTTATCTTTTAAAGATTTGGAATCTGTCAATT 1123
 Qy 1124 ATGTGCTTGGAGTGTGCTGACAGTAAAGCAGTGCCTCCGAAACCTTGAGAGGCTG 1183
 Db 1124 TTGTGCCAAGTAAATTTGGCTGATGCTGAAGCAGCCGCGAGACCTTTGGAATGGGTC 1183
 Qy 1184 CCATTTGTAAGAGGCGCATGTGATGGGGAACACCTACTCTGATTAATTTTATGAGC 1243
 Db 1184 CTAAATTTAAAGGCTGATGTACAGAGAAACCAACAGCTGATTAATTTTATGATC 1243
 Qy 1244 TTGCTCTATTTCTATTTCTCTCCCATGATGCTGCTCAATTTGCTTCAAC 1303
 Db 1244 TTGCTCTATTTCTATTTCTCTCCCATGATGCTGCTCAATTTGCTTCAAC 1303
 Qy 1304 ACACAGCTGGACCTCCATTTATTTATGCTTGTGATTTGATTTGATTTGATTTA 1363
 Db 1304 ACACCTCGGTACACCCGCTGATGTTGCTTGTGATTTGATTTGATTTGATTTA 1363
 Qy 1364 ACCCTATGATTAATGCTTGTGCTGCTGCTTAAAGGTTAAGGATGCTGCTGATGC 1423
 Db 1364 ATCCCTATGATTAATGCTGCTGCTGCTGCTTAAAGGTTAAGGATGCTGCTGATGC 1423
 Qy 1424 TAACCTATCTTCTGGAACATTTTGTGGAACGCTGCTCCAAAGGAAGCCGCAATCA 1483
 Db 1424 TAACCTATTTCTTGTGGAATCAATTTGGCCAAACGATGCTTAAGAAATCGGCTGAATCA 1483
 Qy 1484 AAACCATTAAGCATGCTTGGCATTTGGACGGAATTTGCCACACCGGCAACCATCA 1543
 Db 1484 AAACCATTAAGCATGCTTGGCATTTGGACGGAATTTGCCACACCGGCAACCATCA 1543
 Qy 1544 GCAATGATATAGCGCGGCAAGCAACCTCACCTGGGATCCCATAAAAAATCCGATGATG 1603
 Db 1544 GCAATGATATAGCGCGGCAAGCAACCTCACCTGGGATCCCATAAAAAATCCGATGATG 1603
 Qy 1604 TCTATAATGTTTAAATATCGCGCATGATTTGAAAGTATGATTTGGCAGAAATGATTA 1663
 Db 1604 TATACAGGTTTGAATATTTATGAGCAATTTGAAATGATTTGATTTGCTGAATGATTA 1663
 Qy 1664 AAATTAACATGCGCAAGTATTTGATTAAGAAAGAGAGATTTT 1710
 Db 1664 AGATTAACATGCGCAATGATTTGATTAAGAAAGAGAGATTTT 1710

RESULT 4
 AA091566
 ID AA091566 standard; cDNA; 1713 BP.
 XX
 AC AA091566;

XX
 DT 22-DEC-1995 (first entry)
 DE OP-resistant esterase Lc7L103con.
 XX
 XX Esterase; E3; bioremediation; organophosphate; carbamate;
 KM Insecticide; pesticide; water decontamination; meat decontamination;
 KM ss.
 XX
 XX Lucilia cuprina.
 OS
 FH Key 1.1713
 FT CDS /tag= a
 FT
 PN W09519440-A1.
 PD 20-JUL-1995.
 XX
 XX 13-JAN-1995; 95MO-AU000016.
 PF 13-JAN-1994; 94AU-0003347.
 PR
 XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
 PA Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;
 PI Parker AG, Rodin GC, Russell RJ, Smyth K;
 XX WPI; 1995-263870/34.
 DR
 XX Pure E3 esterase from Lucilia cuprina and related DNA - used to
 PT eliminate residues of organo:phosphate and carbamate pesticides from
 PT water, meat etc.
 PS Example 4; Page 12-17; 38pp; English.
 XX RT-PCR was used to clone a cDNA allele of Lc-alpha-E7 (encoding
 CC OP-susceptible esterase E3 of L. cuprina) from a diazinon
 CC resistant strain, Llandillo 103. 4 isolated clones were
 CC sequenced (Lc7L103 A-D, AA091562-65) that encoded diazinon-resistant
 CC esterases; a consensus sequence is given in AA091566.
 XX
 SQ Sequence 1713 BP; 512 A; 307 C; 369 G; 525 T; 0 other;
 Query Match 55.8%; Score 955; DB 16; Length 1713;
 Best Local Similarity 73.3%; Pred. No. 6; le-285;
 Matches 1222; Conservative 0; Mismatches 445; Indels 0; Gaps 0;
 Qy 44 TTAATGATGTCATTAATTAACCAAACTACCTGTGATGATCAATGAACCAATAA 103
 Db 44 TTAATGATTAATTAATTAATTTTAACTATGATTAACCAATGAACCGTGTAG 103
 Qy 104 TCGATGATGATTAAGCAATTAAGGCTTAAAGCAATGACCGCTCTGATGATTTCT 163
 Db 104 CTGAAGCTGATTAAGCAAGTGAAGGCTTAAAGCTTAACTGATGATGATTTCT 163
 Qy 164 ACTACAGTTTGAGAGATATACCTATGCTTAAGCTCAGTGGGCTGATGATTTCAAG 223
 Db 164 ACTACAGTTTGAGAGATATACCTATGCTTAAGCTCAGTGGGCTGATGATTTCAAG 223
 Qy 224 CACCCAGCGCGCTGATCAATGAGAGGCTGATGATTTGCGCCAGCAAGAT 283
 Db 224 CACCCAGCGCGCAACACCTGATGATGCTGATTTGCTCAATCAATGAATGAAT 283
 Qy 284 CGGTACAGAGATTTTATTAAGTGCAACCCACAGGTTGGAGAGATTTGATTTACCTGA 343
 Db 284 CAGTGAAGTGTATTTATTAAGCAAGCAAGTGTGCTCAGAGAGATTTGATTTACCTGA 343
 Qy 344 ATGTATACCAATGATTTGATGACCCAGCAAAAGGCTCCTGATGATTTATGATTTATCCAG 403
 Db 344 GCGTCTATACCAATTAATTAATCCGAAACTAAGCTCCCGTTTATGATTTATACATCAG 403
 Qy 404 GCGAGATTTTATTTTGGGGAAGCAATGTAATGCTGATTTGCTCCGACTTATGATGA 463

PT water, meat etc.

XX Example 4: Page 12-17; 38pp; English.

CC RT-PCR was used to clone a cDNA allele of Lc-alpha-E7 (encoding
CC OP-susceptible esterase E3 of *L. cuprina*) from a diadion
CC resistant strain, Llandillo 103. 4 Isolated clones were
CC sequenced (LC7L103 A-D, A091562-65) that encoded diadion-resistant
CC esterases. The esterases, or cells expressing them, are used
CC in bioremediation.

XX Sequence 1713 BP; 513 A; 307 C; 369 G; 524 T; 0 other:

Query Match 55.8%; Score 955; DB 16; Length 1713;

Best Local Similarity 73.3%; Pred. No. 6,1e-285;
Matches 1222; Conservative 0; Mismatches 445; Indels 0; Gaps 0;

44 TTAATGATGTCATTAATACCAACCTGCTGATGACCAATGAAACCAATAA 103
44 TTAATGATGTCATTAATACCAACCTGCTGATGACCAATGAAACCAATAA 103
104 TCGATGATGTCATTAATACCAACCTGCTGATGACCAATGAAACCAATAA 163
104 TCGATGATGTCATTAATACCAACCTGCTGATGACCAATGAAACCAATAA 163
104 CTGATGATGTCATTAATACCAACCTGCTGATGACCAATGAAACCAATAA 163
164 ACTACAGTTTCGAGATGATACCTGATGCTGATGCTGATGCTGATGCTGAT 223
164 ACTACAGTTTCGAGATGATACCTGATGCTGATGCTGATGCTGATGCTGAT 223
224 CACCCAGCGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 283
224 CACCCAGCGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 283
284 CGGATACAGATGTCATTAATACCAACCTGCTGATGCTGATGCTGATGCTGAT 343
284 CGGATACAGATGTCATTAATACCAACCTGCTGATGCTGATGCTGATGCTGAT 343
344 ATGCTATACCAATGATGTCATTAATACCAACCTGCTGATGCTGATGCTGATGCT 403
344 ATGCTATACCAATGATGTCATTAATACCAACCTGCTGATGCTGATGCTGATGCT 403
404 GCGGATGATGTCATTAATACCAACCTGCTGATGCTGATGCTGATGCTGATGCT 463
404 GCGGATGATGTCATTAATACCAACCTGCTGATGCTGATGCTGATGCTGATGCT 463
404 GTGGATGATGTCATTAATACCAACCTGCTGATGCTGATGCTGATGCTGATGCT 463
464 AGAAGCCGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 523
464 AGAAGCCGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 523
524 TGAATGATGTCATTAATACCAACCTGCTGATGCTGATGCTGATGCTGATGCTGAT 583
524 TGAATGATGTCATTAATACCAACCTGCTGATGCTGATGCTGATGCTGATGCTGAT 583
584 TGAATGATGTCATTAATACCAACCTGCTGATGCTGATGCTGATGCTGATGCTGAT 643
584 TGAATGATGTCATTAATACCAACCTGCTGATGCTGATGCTGATGCTGATGCTGAT 643
644 TCGGCGAAGTGTGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 703
644 TCGGCGAAGTGTGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 703
704 GTTATGATGTCATTAATACCAACCTGCTGATGCTGATGCTGATGCTGATGCTGAT 763
704 GTTATGATGTCATTAATACCAACCTGCTGATGCTGATGCTGATGCTGATGCTGAT 763
764 AATGCCAAGTGTGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 823
764 AATGCCAAGTGTGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 823
824 AAAAGATGTCATTAATACCAACCTGCTGATGCTGATGCTGATGCTGATGCTGATGCT 883
824 AAAAGATGTCATTAATACCAACCTGCTGATGCTGATGCTGATGCTGATGCTGATGCT 883

QY 884 CACAGTTTGGACCCGGAAGAAATGCAATATAGGTCATGCTTTCGATGACCCAGT 943
DB 884 AAAAGTTTACCTGATGAAAGAGCTACAAATAGGTCATGCTTTCGATGACCCAGT 943
QY 944 TAGAATGATGTCATTAATACCAACCTGCTGATGCTGATGCTGATGCTGATGCT 1003
DB 944 TTAGGATGATGTCATTAATACCAACCTGCTGATGCTGATGCTGATGCTGATGCT 1003
QY 1004 GCGCTGCGGAATGTCATTAATACCAACCTGCTGATGCTGATGCTGATGCTGAT 1063
DB 1004 ATGCTGCGGAATGTCATTAATACCAACCTGCTGATGCTGATGCTGATGCTGAT 1063
QY 1064 CCAATGATGTCATTAATACCAACCTGCTGATGCTGATGCTGATGCTGATGCTGAT 1123
DB 1064 TCACTTGTGCTTTCATTAATACCAACCTGCTGATGCTGATGCTGATGCTGATGCT 1123
QY 1124 ATGCTGCGGAATGTCATTAATACCAACCTGCTGATGCTGATGCTGATGCTGAT 1183
DB 1124 TTAGGATGATGTCATTAATACCAACCTGCTGATGCTGATGCTGATGCTGATGCT 1183
QY 1184 CCAATGATGTCATTAATACCAACCTGCTGATGCTGATGCTGATGCTGATGCTGAT 1243
DB 1184 CCAATGATGTCATTAATACCAACCTGCTGATGCTGATGCTGATGCTGATGCTGAT 1243
QY 1244 TTAGGATGATGTCATTAATACCAACCTGCTGATGCTGATGCTGATGCTGATGCT 1303
DB 1244 TTAGGATGATGTCATTAATACCAACCTGCTGATGCTGATGCTGATGCTGATGCT 1303
QY 1304 ACACAGCTGCGACTCCATTAATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 1363
DB 1304 ACACAGCTGCGACTCCATTAATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 1363
QY 1364 ACCCTATGCTGATTAATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 1423
DB 1364 ACCCTATGCTGATTAATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 1423
QY 1424 TTAACCTATGCTGATTAATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 1483
DB 1424 TTAACCTATGCTGATTAATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 1483
QY 1484 AATGATGATGTCATTAATACCAACCTGCTGATGCTGATGCTGATGCTGATGCTGAT 1543
DB 1484 AATGATGATGTCATTAATACCAACCTGCTGATGCTGATGCTGATGCTGATGCTGAT 1543
QY 1544 GCAATGATGTCATTAATACCAACCTGCTGATGCTGATGCTGATGCTGATGCTGATGCT 1603
DB 1544 GCAATGATGTCATTAATACCAACCTGCTGATGCTGATGCTGATGCTGATGCTGATGCT 1603
QY 1604 TCTATTAATGTCATTAATACCAACCTGCTGATGCTGATGCTGATGCTGATGCTGAT 1663
DB 1604 TCTATTAATGTCATTAATACCAACCTGCTGATGCTGATGCTGATGCTGATGCTGAT 1663
QY 1664 AATGATGATGTCATTAATACCAACCTGCTGATGCTGATGCTGATGCTGATGCTGAT 1710
DB 1664 AATGATGATGTCATTAATACCAACCTGCTGATGCTGATGCTGATGCTGATGCTGAT 1710

RESULT 7
ID AA091564 standard; cDNA. 1713 BP.

XX AA091564;
XX 22-DEC-1995 (first entry)

DE OP-resistant esterase LC7L103C allele.

KW Esterase; E3; bioremediation; organophosphate; carbamate;
KW insecticide; pesticide; water decontamination; meat decontamination;
OS ss.

XX Lucilia cuprina.

QY 1664 AATTAACAAGTGGCAAGTATTCGATTAAGAAAGAGGATTTT 1710
 Db 1664 AGATTAAACAATGGAATGATGTTTGAAGAAACATGAGATTATTT 1710
 RESULT 8
 ID AA091563 standard; cDNA: 1713 BP.
 AC AA091563;
 XX
 XX 22-DEC-1995 (first entry)
 DE OP-resistant esterase Lc7L103B allele.
 XX
 XX Esterase; E3; bioremediation; organophosphate; carbamate;
 KM insecticide; pesticide; water decontamination; meat decontamination;
 KW ss.
 XX
 OS Lucilia cuprina.
 FH
 FH Key Location/Qualifiers
 FT CDS 1..1713
 FT /*tag= a
 XX
 XX MO9519440-A1.
 XX
 XX 20-JUL-1995.
 XX
 XX 13-JAN-1995; 95MO-AU00016.
 XX
 XX 13-JAN-1994; 94AU-0003347.
 XX
 XX (CSTR) COMMONWEALTH SCI & IND RES ORG.
 PA
 PI Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;
 PI Parker AG, Robin GC, Russell RJ, Smyth K;
 XX
 XX WPI: 1995-263870/34.
 DR
 XX Pure E3 esterase from *Lucilia cuprina* and related DNA - used to
 PT eliminate residues of Organophosphate and carbamate pesticides from
 PT water, meat etc.
 PS
 XX Example 4: Page 12-17; 38pp; English.
 CC RT-PCR was used to clone a cDNA allele of Lc-alpha-E7 (encoding
 CC OP-susceptible esterase E3 of L. cuprina) from a diazinon
 CC resistant strain, Llandillo 103. 4 isolated clones were
 CC sequenced (Lc7L103 A-D, AA091562-65) that encoded diazinon-resistant
 CC esterases. The esterases, or cells expressing them, are used
 CC in bioremediation.
 XX
 XX Sequence 1713 BP; 513 A; 308 C; 368 G; 524 T; 0 other;
 SO
 Query Match 55.6%; Score 950.2; DB 16; Length 1713;
 Best Local Similarity 73.1%; Pred. No. 1.9e-283;
 Matches 1219; Conservative 0; Mismatches 448; Indels 0; Gaps 0;

Db 224 CACCCACGACCAACACCTGGATGGTGGTGAATTTGTGCATCATTAAGATAGT 283
 QY 284 CGGTACACAGATTTTCAATAGTGGCAACCCACAGTTGGAGATTTCTATACCTGA 343
 Db 284 CAGTGCAGATTTTATTTACAGCAAAAGTGTGTGCTCAGAGGATTTCTATACCTAA 343
 QY 344 ATGTGTATACCATGACCTTGAAACCCAGCAAAAGCGCTGTTATGTTTATTCATCC 403
 Db 344 GCGTCTATACCAATATCTAATCCGAACTAAACGCTCCGTTTATGTTATACATCATG 403
 QY 404 GCGAGATTTTATTTTGGCGGAGCAAAATCGTAACGTGTTGTCGCCACTTATTA 463
 Db 404 GTGGGATTTTATTTATCGTGAATAATCATCGTGTATGTTGCTGATTTATTTCA 463
 QY 464 AGAAACCGTGTGCTGTGTAACCGTGAATAATCGTGTGTTGTTGTTGTTCTTATCC 523
 Db 464 AAAAGATGTGTGTTGTTATTTACATTAATATCTTTGGAGGCTCTAGGTTTCTA 523
 QY 524 TGAATCGGAATAATCTCATATGTCCTCCGCAACGCTGCTCAAGATCAATAGTGGCT 583
 Db 524 TAAATTCAGAAAGACCTTAATGTGCCAGTAATGCCCTTAAGATCAAGTATGACCT 583
 QY 584 TGAGATGGGTCAAGATTAATTTGCCATTTTGGTGGCGATGTAGACATATTAACCTCT 643
 Db 584 TGGGTGGATTTAAATAAATTAATGCGCAACTTGGTGGCAATCCCGATTAATTAACAGTCT 643
 QY 644 TCGGCGAAAGTGTGTGGGCGCTCAACCCATTACATGATGATACCGAACAAGCCGTG 703
 Db 644 TTGTTGAAAGTGGCGGCGGTGCTCTACCCCATCATGATGTTTACCGAACAACCTCGG 703
 QY 704 GTTTATTTCCATGTTGATCATGATGTCCGTAATTCATGCTCATGCGCTCTACAG 763
 Db 704 GTCTTTCCATCGTGTATCATTAATGTCCGTAATTCATGCTCATGCGCTCTACAG 763
 QY 764 AATGCCAAAGTCGCGCTGCTACCATGSCCAACGTTGCTTAAGGAGAGAGACAATG 823
 Db 764 AATGTCAACATCGTGGCTTACCTTAAGCCAAATTTGGTGGCTTAAGGAGAGAGACAATG 823
 QY 824 AAAAGATATCTCGGAATTCCTAATGAAAGCCAAATCCCTATGATTTGATCAAAAGAGAGC 883
 Db 824 ATAGGATATTTGAGATTTCTTTTGAAGCCAAAGCAGATTTAATTAATTAACCTTGAG 883
 QY 884 CACAGATTTTGACACCCGGAAGATGCAAAATTAAGTCAATGTTCTTTTGGACCCACTG 943
 Db 884 AAAAGTTTAACTTACGTAGAAGACGTAACAATTAAGTCAATGTTCTTTTGGACCCACTG 943
 QY 944 TAGAACCATACCAAGACGCGAGTGTGTGTAACCAACCAATCAAGAAATGTTGAGAA 1003
 Db 944 TTGAGCCATATCAAGACCGCTGATTTGTCTTACCCAAACATCTCGGGAATATGTTAAG 1003
 QY 1004 GCGCTGGGGAATTTGATACCCCAATGATAGTAAGCAATACCTCTACGAAGTTTGCCTT 1063
 Db 1004 ATGCTTGGGGTAAATTTGATACCCCAATGATAGTAAGCAATACCTCTATTTATTT 1063
 QY 1064 CCAATCAATTTGCCAAACATATCGGAGTGTGTAAGATTTGAAATTCCTGTGCAAT 1123
 Db 1064 TCACTTCTGTTTCAAGCAAAATGCTATGCTTTTAAGAAATTTGAAATTTGCTCAAT 1123
 QY 1124 ATGTGCTTGGAGTGTGCTGACAGTGAACGCAAGTGCCTCCGGAACCTCGAGAGGGCTG 1183
 Db 1124 TTGTGCAAGTGAATTTGGCTGATGCTGAACGCAAGTGCCTCCGGAACCTCGAGAGGGG 1183
 QY 1184 CCAATTTGAAAGAGCCCATGTGATGGGGAACACCACTACTGTGATTAATTTATGAGAC 1243
 Db 1184 CTAATAATTTAAAGAGCTCATGTTACAGGAGAAACACCAACCCCGATTAATTTATGAGAC 1243
 QY 1244 TTGTCTCATTTTCTAATTTCTCTTCCCATGATGCTTCTTCAATATGCTTCAAC 1303
 Db 1244 TTGTCTCATCATTAATTTCTGTTCCCATGATGCTTCTTCAATATGCTTCAATC 1303
 QY 1304 ACACAGCTGGCACTCCATTTAATTTGATGTTTGAATTTGATTTCCGAGAAATTAATA 1363
 Db 1304 ACACCTCGGCTACACCCGCTACTGTTATGCTTGCATTTGATTTGGAATTTCTTAATA 1363

Db 1082 CCAAGGAGATGATGAAAGCCGCGGAGTAACTCCATCCCATGTTTATGGAACACT 1141
 1045 TCCTACGAAAGTTTCTTCCAAATGCAATGCGCAACATATCCGAGGTGTAAAGAG 1104
 1142 TCGTACGAGGCGCTGCTGCGGTCCAGAGTAAAGCTTATGCCAGAGTGTGACAG 1201
 1105 TTGGAATCCTGTGTGATATGATGCTTGGAGTGGCTGACAGTGAACGAGTCCCG 1164
 1202 CTGTAGTGTGACACCTTCAATCCCAAGATTTGTGGCCACGAGGCCAGTAAAGA 1261
 1165 GAAACCCGTGAGAGGCTCCCATTTGTGAAAAAGCCCATGTGAGTGGGAAACACTCT 1224
 1262 AACTGAGATTCTGTGAGTGCACAGATGAGATGTTCAATGCACTGCTCAGAAAGC 1321
 1225 CTGATATATTTTATGAGCTTGTCTCTATTTCTATTTCTCTCCATGCTGCTTC 1284
 1322 CCAGATATATATGATGATCTGTCTGATTTCTACTTCTGTCTTCCGCTTGGAGT 1381
 1285 CTACATTTGCTGCTTCAACACACAGCTGGCACTCCATTTATTTGATGTTGATTC 1344
 1382 GTCCATTTCCGACACGCGTACGCGGCTGGAGCTCCAGTATATTTCTATGATATG 1441
 1345 GATTCGGAAGATATTTAATACCCATGATATGCTTATGCGTTTGGCCGTGCTTAACT 1404
 1442 GACTCCGAGAGCTCATTTTTCGACGCAATTAATGCGGTGGAGCGGCTCAAGGG 1501
 1405 GTAGCCATGCGCGATGAGCTAATCTATCTTCTGAAACATTTTGTCAAAAGCCTG 1464
 1502 GTACGCGATCGCGAGATTTGAGTACCAATTCACGACGCTGCTGCGCGGTGCG 1561
 1465 AAGGAAAGCCGCAATACAAACCTTGAAGCATGTTGGCATTTGACGGAATTCGCC 1524
 1562 AAGGAAAGCTGAGTACGAAATCAACGACGACGCGGTGAGTCTGAGCCAGTTTCT 1621
 1525 ACCACCGCAACCATACGCAATGATATAGCCGCGATGGAACCTGACCTGAGATCC 1584
 1622 GCCAGGGAATTCCTACAGCGAAGATCAAGGTATGAGCACTCTACCACTTATCA 1681
 1585 ATAAAAAATCCGATGATGCTATTAATGTTTAAATATCGCGATGAATGAAGTTATG 1644
 1682 GTTCGCAATCCGAGAGGTATCAAGTGCCTCAACATCAGTATGAGCTGAAAGTTATC 1741
 1645 GATTGCCGAAATGATTAATTAACATGAGGCAAGTATTTGATTAAGAAAGAGAA 1704
 1742 GATTCGCTGAGTGCCTCAAAATTAAGGCTGTGGAGAGCTCTATGACGAAACAAAGAT 1801
 1705 TTGTT 1709
 1802 TTATT 1806
 Db 1802 TTATT 1806
 RESULT 10
 ABL02099
 ID ABL02099 standard; cDNA; 1665 BP.
 XX
 AC ABL02099;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 779.
 XX
 KM Drosophila; developmental biology; cell signalling; insecticide;
 XX
 OS Pharmaceutical; gene; ss.
 XX
 PN Drosophila melanogaster.
 XX
 FN WO2001/1042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US09231.
 XX

PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PMD, Myers EM;
 XX
 DR WPI; 2001-65860/75.
 XX
 PT P-PSDB; ABB57996.
 PT
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 PS
 PS Claim 1; SEQ ID NO 779; 21pp + Sequence Listing; English.
 CC
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
 CC sequences (AB101840-AB16175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.
 CC
 SO Sequence 1665 BP; 397 A; 446 C; 468 G; 354 T; 0 other;
 Query Match 23.3%; Score 399.2; DB 23; Length 1665;
 Best Local Similarity 53.6%; Pred. No. 1.1e-112;
 Matches 880; Conservative 0; Mismatches 753; Indels 9; Gaps 2;
 53 TGCTCAATTAATACCAACTACCGTCTGATCAATATGAACCAATATGATCTG 112
 5 TCGACTTTAAGTCCAAACAGACGATACGACGCAAGAAAGATGCTGATGACCA 64
 113 AATATGCAAAATTAAGGTTTAAAGCAATGACCGTCTACGATGATCTTACTACGTT 172
 65 CTTACGACCATCAACAGAGGTGTAAGAGCAATGCTATCGGCGCATCTTCTACGCT 124
 173 TCGAGATATACCTTATGCTTAAGCTTCCAGTGGGTGATGATGATTCAGACGACCCGAC 232
 125 TCGAGCGGATCCCTTCCCAACCAACCGGTGGGCAAGCTACCTCAAGGCTCCCGAC 184
 233 GGCCTTACCATGAGAGGTGATGATGATGCTGTGGGCGAGCAACATCGGTACAGA 292
 185 CCGCGAGGCTGTGAGCGAGGTGAGAGCTGACCTCCAGGCTCCCAAGCCACTGACA 244
 293 CAGATTTCAATAGTGGCAACCCACAGGTTGAGAGGATGCTATACCTGAATGTATATA 352
 245 AGCACTTCTGTGATGAGATGACGAGATGCTCCAGAGACGCTCTACCTCAATGCTTACA 304
 353 CCAATGACTTGAACCCAGCAAAAGGCGTCTTATGTTGATTCATCCATGCGGAGATT 412
 305 CAAAGAAATTTGTATCCCAACCAACCAATGCCCTGATGCTGATGATGAGGCTGCT 364
 413 TTATTTGCGGCAAGCAAAATCTAAGTGTGTTGCTCCGCTCTTATTAAGAAACCGG 472
 365 TCCAGTTTGGCGAGGCTCTCAGGGAATGTACAGTCCGATTTATTTGCTGCGGAGATG 424
 473 TGTCTTGTGTAACCGTCAATATGTTGGGTGCTGTTGGGTTTCTTACCTGAATTCGG 532
 425 TGTGTGCTATTTCTATCACTACAGGTGGAGCACTGGGATTTCTGTGCTGAGATGC 484
 533 AAATCTCAATGTCCCGGCAACGCTGCGCTCAAGATCAAGTATGCGCTTGAATGGG 592
 485 CCGAATCGATGTGCCCGCAATGCGGACTCAAGATCAAGTGTGGCTTGGCGTGGG 544
 593 TCAAGAGTATATGCAATTTGCGGTGGGATGATAGCAATATTAACGCTTCCGGGAA 652
 545 TCAAGGCCAATCTGTGCGCTTGGAGGCGATTCGCGAATATTAACATTTTGGGGACA 604
 Db


```

QY 653 GTGCTGGTGGGCGCTCAACCATTCATGATGATACCGAACAGACCCGTTTATTC 712
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 605 GTGCGGGAAGTGCCTCGTTCATCTAGATGATGATACAGAGACGACGATTTTCC 664
QY 713 ATGCTGATTCATATGTCGGGTAATTCATGTCCTCATGGGCTCTACAGAAATCCAAA 772
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 665 ACAAGGCACTCTGCTGGGTAATACGCTTCCCTGGGAGTACTCTCAGAGAA 724
QY 773 GTGCTGGCTCACCATGGCCAAACGTTGGCTATAGGAGAGACATGAAGAAAGATA 832
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 725 ACTGGCCATATCGGTGGCTGTCCAGCGGGTTACGAGTGTAACACACCCCGCATG 784
QY 833 TCTGGAATTCCTAATGAAGAACCAATCCCTATGATTTGATCAAGAGAGCCACATTT 892
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 785 TCTGGAGTCTCTGAGAACCCCAAGGATCCGAATATCATCAAGCCCAATGGAACCTCT 844
QY 893 TGACACCCGAAAGAAATGCAAAATAGGTCATGTTCCCTTTGGACCCGCTAGAACCAT 952
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 845 GCATTGACGAGAGAGAGAGAGCGGATTTGATTTCTTTTGGCCCGTAAATGCAACCT 904
QY 953 ACCAGACAGCCGACTGTGTGTACCCAAACCAATCAGAGAAATGATGAAGAGCGCTGGG 1012
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 905 ATGTACACGACGACTGTGTGTGCGAGAGAAACCATGGAATGATGAGAACCCCTGGA 964
QY 1013 GAAATTCATACCCCATTTGATAGGCAATACCTCCTACGAAGTTTGTTCCTCAATCAA 1072
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 965 GCATTAATATCCCATTTATCATGCGAGGCGTTTCCACAGAGGGGCTTCTGTGACTAG 1024
QY 1073 TTGCAACAATATATCCGAGATTTGTAAGAGTTGAAATCCCTGTGTAATATGTCCTT 1132
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1025 AGACCAAGACCAATCCGAAGTGTCTAAGAGATTTGAGAGACTGCGGGTTGTGGGCTTA 1084
QY 1133 GGGATGTGGCTGACAGTAGAAGAGCTGCCCGGAAACCTTGAGAGGGCTGCCATTGGA 1192
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1085 TCGAATTAATATGAGACAGAGGAAAGTGCCTGTGCGGAGATGACGATAGCTGAGGC 1144
QY 1193 AAAAGGCCCATGTGATGGGAGAAACACCT-----ACTCGAATATTTATGAGCTTT 1246
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1145 AGCTGCTACTACGCGATTAAGACGCCCATCTGACACCTCTGATGATTAATCTTCAGATGG 1204
QY 1247 GCTCTATTTCTATTTCTCTTCCCATGATGCTGCTTCTCAATTTGGCTTCAACACA 1306
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1205 TTCCACAGAGTACTTGTGTTCCCAATATACCGCAGATATTTGCCGCTGCAAGTTCG 1264
QY 1307 CAGCTGGACATCCCATTTATTTGATGCTGCTGATTTGATTTCCGAAGAAATTTATACC 1366
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1265 CTCGAGATGCGCGACGATTTGTACCGCTTGTGACTTGTGACTCCAGACA---CTTCAACC 1321
QY 1367 CCTATCGTATATAGCGTTTGGCGCTGAGCTTAAGGTGTAAAGCTGATGCGCATGAGCTAA 1426
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1322 ACCTGGCGATCTGTAGTTGCGGCAAAAAGTGAAGGAGCGATGCGCACGCGCATCTGT 1381
QY 1427 CCTATCTCTTGGAAATTTTGTGAAAAGCTCTGCCAAAGAAACCGCGCAATCAAAA 1486
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1382 CCTACTTGTCTTACAACTGCTGGGAGAGAACCTCAAGAACACACGCGGGAGTGTACAGT 1441
QY 1487 CCATTGAAGCAATGGTTGGCATTTGGAGAGAAATTCGCCACACCGCAACCATCAACA 1546
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1442 GCATCGAGGCGCTGTGGAGACTGTGAGCACTTTGGGCAATGTGGAACCCCACTTCG 1501
QY 1547 ATGATATAGCCGCGCATGAAAACTTCACCTGGGATCCCATTAATAAATTCGATGTCT 1606
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1502 ATCCGGAACAGAGAGACCTGTGGACGCGCTGATCTCTGCGCGCTGAGAAACACAGC 1561
QY 1607 ATTAATGTTAAATATCGCGCATGATTAAGATTAATGATTTGCGAGAAATGGAATAAA 1666
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1562 TGAAGTCCCTTACATATCCGAGAGACTGAAGGTATGACGTGCCGACCTCAAGAGT 1621
QY 1667 TTAACAATGAGCAATATATT 1688
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1622 TGATGTCTGGGAGATTTCTT 1643

```

```

RESULT 11
ABL02103
ID ABL02103 standard; cDNA; 1593 BP.
XX
XX
AC ABL02103;
XX
DT 26-MAR-2002 (first entry)
XX
XX DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 791.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
XX
XX pharmacological; gene; ss.
XX
XX Drosophila melanogaster.
XX
XX WO200171042-A2.
XX
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001MO-US09231.
XX
XX 23-MAR-2000; 2000US-191637P.
XX
XX 11-JUL-2000; 2000US-0614150.
XX
XX (PEKE ) PE CORP NY.
XX
XX Venter JC, Adams M, Li FMD, Myers EM;
XX
XX WPI; 2001-656860/75.
XX
XX P-PSDB; ABB58000.
XX
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signalling and cell-cell
XX interactions -
XX
XX Claim 1; SEQ ID NO 791; 21pp + Sequence Listing; English.
XX
XX
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (AB116176-AB130511), expressed DNA
XX sequences (AB101840-AB116175) and the encoded proteins
XX (ABB57737-ABB72072).
XX
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct-sequences.
XX
XX
XX Sequence 1593 BP; 417 A; 394 C; 405 G; 377 T; 0 other;
XX
XX
XX Query Match 23.3%; Score 398.8; DB 23; Length 1593;
XX Best Local Similarity 55.4%; Pred. No. 1.4e-112;
XX Matches 888; Conservative 0; Mismatches 692; Indels 24; Gaps 5;
XX
XX
XX 111 TGAATGAGCAAAATTAAAGGTGTTAAGCGAATACCTCTACGATATTTCTACTACAG 170
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 6 TGACTGCGCTCTGTGGCGGAGTGAAGAAACACATCTGGGAGAGAACTACTCTAG 65
QY 171 TTTCGAGGTATTAACCTATGCTAAGCCCTCCAGTGGAGTGTGATTCAGATTCACGCCCA 230
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 66 TTTCGAGAGATTAACCTCTTCCCAAGCCCTCCGTTGGAGATCTGGCTTCAAGGCCCGGA 125
QY 231 GCGGCTGTACCATGAGAGGAGTGAAGTGTGCTGGGCCACCAACAGATCGTTACA 290
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 126 AGCATGTGAGCGCATGAGGATTCAGAAATTTGATTCGCTCCGCGACAGCAAGCCCTTCA 185
QY 291 GACGATTTCAATAGTGCACAAACCCACAGGTTTCGAGAGATGTGTATACCGAATGTGTA 350
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 186 GACACACATGTTTTCAGAAAATACGGGCTCAGAGAGACTGCTCTACTTAATATGTGTA 245
QY 351 TACCAATGACTTGAACCCAGACAAAGGCTCTGTTATGTTGATTCATTCATGCGGAGGA 410

```


OY	27	TCGCCTGAAACATATCCTTTTAATGCGATAGCTCAATAAATPACACAAACATACCGCTGAGATAC	86
Db	132	TCCTGCTGAAAATGGGCAACCAAGCTCATTTGGCCACAAAGATCGTCCAGTATGCGCTTGGCAC	251
OY	87	AAATGAAACCCAAATATCGATCTGAAATATGACAAATTAAGGGTTTAAGCGAATGAC	146
Db	252	AAAGCGACGAAAGGCGCTCCACCGAGGATGGCGCAGGTGCGCGCATGCGCGAAGGAC	311
OY	147	CGCTC --- ACGATGATTCCTTACTACAGTTTGTGAGAGTATACCCATATCCTTAAGCTCCAGT	203
Db	312	ACTCTACGACGAGGAGATGTACTTGGCTTGAAGGAAATCCCTTTTGACAGCGCCGCGT	371
OY	204	GGGTAGTTGGAATTCAAAGGCACCCAGCGGCTGTACATGGAGGGGTGTAGTGATTTG	263
Db	372	GGGGAGAGCTGGCGTTCCGAGCCCCCAGCCACATCCCTGGTTGGGGGTGGGGGATTG	421
OY	264	CTGTGGGCGACCAACAGATGGGTACAGACAGATTTATAAGTGGCAACCCAGAGTTG	323
Db	432	CACCTATCCGCGGGCAAGCCGATGCAAAAGCACTTGTGCTCAGCATCGTGCAGAGCAG	491
OY	324	GGAGAGATGTCTATACCGATGTGTATACCAATGACTGTGAACCCACACAAAGAGCGCTC	383
Db	492	CGAGGATGTGCTGTACCTGGAACGTATATTCGAACGCGCTGAGATCGGACAGCGCGCTGCC	551
OY	384	TGTTATGTTTTATTCATCCATGGCGGAGATTTTATTTGCGCGAAGCAATCGTAACTGTT	443
Db	552	CGTGATCTGTGGAATCTATATGCGGTGTGATTCACAGTTGCGGAGGCTGTGAGAAATTTCTA	611
OY	444	TGGTCCCACTACTTTATGAAAGAAACCGGTGCTGTGTAACGTCGAATATGTTTTGG	503
Db	612	CAGTCCAGACTACTTTATGCAAGCAAGATATGTGTGTTGTCATTAATTAATTAAGGGGG	671
OY	504	TGTGTTGGGTTTTCTTACCTGAAATCGGAAATCTCAATGTCCCGCGCAACGCTGGCCT	563
Db	672	CGCATTTGGGCTTCTTCAACCTCGCGGATCGGACTTGATGTGATGTGCGCGGAATGTGGTCT	721
OY	564	CAAGGATCAACTAATGGCGCTGATAGATGGGTCAABAGTATATTTGCCATTTTGGTGCGCA	623
Db	732	CAAGGACCAAGATGATGGCGCTTCTGCTGATAGTCAAGACACTAATCCAAATTCATGAGGA	791
OY	624	TGTAGCAATATTTACCGTCTTTCGGCGAAAGTGTGTTGGGGCGTCAACCCATTACATGAT	683
Db	792	TCCCCAAATATTAACCGTATGGGCGAGAGTGGCGGAGACGCTTCGCTCACCGTTGAT	851
OY	684	GATAACCGAACAAGACCGGTGTTATTCACATCGTGTGATCATGATGTGCGGTAAITTCAT	743
Db	852	GACCAACCGAGAAACCCGAGGGCGTTTCCAAAGGCCATCATGCAATCCGGGATTCATGTT	911
OY	744	GTGCTCATGTGGGCTCTTACAGAAATCCCAAAAGTCGTGGCCTGACCATGSCCAAAAGCTGTGG	803
Db	912	CTGCGAGTGGGCGCAATAGGCCAATGGCAGGTGGGCAATACGACTGGCTCGCCAATTTGGG	971
OY	804	CTATTAAGGAGAGCAATGAAAAAGATATTCCTGGAAATCTTATGAAAGCCATCCCTA	863
Db	972	ATACTCGGGCGATGAGAAAGGAAGATGTTTTCGATTACTTTCAGAAACACCCGCGCTC	103
OY	864	TGATTTGATTCAAAAGAGGCGCACAAAGTTTTTGACACCCGAAAGAAATGCAAAATTAAGTCA	923
Db	1032	CGAAATGGCCCAACGAGGTATTACTCTGTCTCTCCAAAGAGAAACGGGCGGAGTACGTCT	109
OY	924	GTTCCTCTTTGGACCACTGTAGAACCATATCCAGACAGCGGACTGTGTGTATCCCAAAAC	983
Db	1092	GTTCCTCTTTACTCTCGGTGTGTGAAACCATATATCACAGGAGATTTGCCCTTTGGCCCCGTG	115
OY	984	AATCAGAGAAATGCTGAAGAGCGCTGGGAAATTCGATACCCACATGATAGGCAATAC	104
Db	1152	CCACAGGAGAGTGTCTGCCGGAAGCTTGGGTAATGACCTCCGCTGATCTCTGGCGGCA	121
OY	1044	CTCCACAGAGGTTTGGTTTTCCAAATCAATTTGCCAAACATATTCGGAAGTTTAAATA	110
Db	1212	CTCCTTTGAAAGTCTGTTTCTCTTACCAAGATACCTTCGACAGAGAGGAACACATGCTGAG	127

QY	1104	GTTCGAATCCCTGTGTGAATTAATGTGCTTGGAGTTGGCTGACAGTGAACGCAAGTGGCCCC	1163
Db	1272	TGCTTTTGAGGTCTCAATTAATCTCTCGGAGATCAGAGGAAAGATACCACTCCGATCTTAA	1331
QY	1154	GGAACCCCTGGAGAGGGCTGCCATTGTGAAAAAAGGCCCATGTGGATGGGAAACACTTAC	1223
Db	1332	GGATCTGCTACGTCATTTTAAAGGTGGTAACCTTCGATGATGCGCACTCGAGGGCGAATGGA	1391
QY	1224	TCGTGATTAATTTTAATGAGAGCTTTCCTCCATTTTCTATTTTCTCTTCCCATGCAATCGCTT	1283
Db	1392	GTTCAATAGAGTCCCTGCACATACGTCTCCGTTAAACACTTTTGGCATAGCATTCATCGCAC	1451
QY	1284	CTTACATTTTGGCTTTCACACGACACAGCTGGCACTCCCATTTATTTTATTCGTTTGATTT	1343
Db	1452	TGTATTGGCCGCGCTCAGCACAGCCCCCGCAACGCCCCACTACTACTGATCCGCTCGATGT	1511
QY	1344	CGATTTCCGAAATAATTTTAACCCCTTATGATTAATGCGTTTGGCCGCGGTTAAAG	1403
Db	1512	GGACTCGCCCCA---TTTCAATCACTTCGCGGAGGTGATGTGGGAAACACGTTGCGGG	1568
QY	1404	TGTAAAGCCATCCCGATAGCTAACTATTCCTTCTGGAACATTTTTCGAAACGCGCTGCC	1463
Db	1569	AGTTAGTCAATCGCAGCATCTCTCTCTACCTTTTCTATACATTTTGGCAACAGAAGTGA	1628
QY	1454	AAAGAAAGCCGCAATTCACAAACCATTTGAACGATGGTTGGCATTTGGACGGAATTCGC	1523
Db	1629	TAAAGTCCTGATGGAGTACCAAAACCAATACAGACACTGTGGGCGATGTGGTGGCATTCGC	1688
QY	1524	CACACCGGCAACCATACAGCATATGATTAAGCGCGGATGGAAACCTACCGTGGGATCC	1583
Db	1689	CCGAAAGCACATTCCTCAATTTGTCCACAGATCGGCCCCA-----CCACATGGGAGGC	1739
QY	1584	CATAAAAAATCCGATGATGTCATAAATGTTTAAATATCGCGGATGGAATTTGAAAGTTAT	1643
Db	1740	ACTGATGATGA--GAAGGTCGCGAGATGTCTCATATTTGGAAAAACAACGTGATCAT	1796
QY	1644	GGATTTGGCAGAAATGATTAATAATTAAACAATGGCGAGATATTGCAATTAATAAA	1697
Db	1797	TGTGCTGCCGAGTGCAGAACGATCGGATTTGGATGACCTATACGATTAATAAA	1850
RESULT 13			
ID	ABA90480		
AC	ABA90480	standard; DNA; 1809 BP.	
DT	12-FEB-2002	(first entry)	
DE	Drosophila cell cycle progression protein coding sequence #115.		
KM	Antiproliferative; cyrostatic; cardiant; immunosuppressive; meiosis;		
KM	antitumoriacatory; antiproliferic; dermatological; antitungal; mtosis;		
KM	antiproliferic; antitumoriac; antitumoriac; antitumoriac; cell division;		
KM	cell cycle progression protein; tumour; proliferative disorder;		
KM	cardiovascular; autoimmune; dermatological disorder; ds.		
OS	Drosophila sp.		
PN	MO200172774-A2.		
PD	04-OCT-2001.		
PF	23-MAR-2001; 2001MO-GB01297.		
PR	24-MAR-2000; 2000GB-0007268.		
PA	(CYCL-) CYCLACEL LTD.		
PI	Deak P, Glover DM, Midgley C;		
PR	WPI; 2002-055132/07.		

OY 1343 TCGATTCCGAGAAATTTATTAACCCCTATCGATTATGCTTTGGCCGCTTAAG 1402
 DB 4614 TCGACTCCGAGAGCTCATTTTTCGTCATCCCATTAATGCGGTGAGCGGCTGTCAAG 4673
 OY 1403 GTGTAGCCATCCCATGAGCTAACCTATCTCTGTCGACATTTGTCGAAGCGCTGC 1462
 DB 4674 GGGTAGCCATGCGCAGCATTTGAGCTACCAATTCAGAGCGCTGCTGCGCGGTTC 4733
 OY 1463 CAAAGAAAGCCGCAATTAACCAACCATTAAGCATGTTGGCATTTGACGGAATTCG 1522
 DB 4734 CCAAGAAAGTCGCGAGTACAGAACATCGAACACCGTGGCATCTGGAACCAAGTTTG 4793
 OY 1523 CCACACCGCGCAACCATACAGCAATGATATGCGGCGCATGGAACCTGCGGATC 1582
 DB 4794 CTGCGCGGATATCCCTACAGCAGAAATCAACGATATGACACTCTGACCATTTGATC 4853
 OY 1583 CCATTAATAATCCGATGATCTATTAATGTTTAATATGCGCATTAATTAAGTTA 1642
 DB 4854 CAGTTCGCAATTCGACGAGTCTCAAGTGCCTCAATCATGATGACCTGTAAGTTCA 4913
 OY 1643 TGGATTTGCCAGAAATGATTAATAACATATGCGCATTAATTAAGAAAG 1702
 DB 4914 TCGATCTGCTGAGTGGCCCAAAATGTAAGTCTGGGAGACCTCTATGACGACAAAG 4973
 OY 1703 AATTGTT 1709
 DB 4974 ATTATTT 4980
 RESULT 15
 ABL10333 standard; cdna; 1791 BP.
 ID ABL10333 standard; cdna; 1791 BP.
 XX ABL10333;
 AC
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 25481.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KM pharmaceutical; gene; ss.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO2001/1042-A2.
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US09231.
 XX
 PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 DR WPI, 2001-656860/75.
 DR P-PSDB; ABB66230.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 PS
 PS Claim 1; SEQ ID NO 25481; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
 CC sequences (AB101840-AB16175) and the encoded proteins

CC (AB57737-AB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pc_sequences.
 XX
 SQ Sequence 1791 BP; 434 A; 471 C; 493 G; 393 T; 0 other;

Query Match 20.3%; Score 347.8; DB 23; Length 1791;
 Best Local Similarity 53.9%; Pred. No. 9.8e-97;
 Matches 828; Conservative 0; Mismatches 692; Indels 15; Gaps 5;

OY 31 CTGAACATATCTTTAATGATGCTATTAATTAACAAATACCTGCTGATCAAT 90
 DB 121 CTGAACATGCGCGCAAGATTAATGATGCTGATTAAGGTTTACGATGACCGG 180
 OY 91 GAAACCCAAATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 150
 DB 181 CAGACCAAGAGAGCTGGCCACCAATATGCTGATGATGATGATGATGATGATGATG 240
 OY 151 TAGCAT---GATTTCTACATGATGATGATGATGATGATGATGATGATGATG 207
 DB 241 TAGCATGCGCAACCTCTACTCTCTGAGGAGATTCCTTTGCCAGCGCGCTGGGT 300
 OY 208 GAGTTGATTTCAAGGACCGCGGCTGATGATGATGATGATGATGATGATGATGAT 267
 DB 301 GAGCTGCGTTTGGCGACCGCCACCAACGAGCTGATGATGATGATGATGATGATG 360
 OY 268 GGGCCAGCCCAAGATGCTGATGATGATGATGATGATGATGATGATGATGATG 327
 DB 361 TAGTCAGAGAGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 420
 OY 328 GATTTGCTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 387
 DB 421 GATTTGCTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
 OY 388 ATGTTTATCATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 447
 DB 481 ATGTTTATCATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
 OY 448 CCCGATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 507
 DB 541 CCGGATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
 OY 508 TTGGTTTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 567
 DB 601 TTGGTTTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
 OY 568 GATCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 627
 DB 661 GATCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
 OY 628 GACCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 687
 DB 721 GAGAGCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
 OY 688 ACCGACAGACCGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 747
 DB 781 ACCGACAGACCGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
 OY 748 TCATGAGGCTCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 807
 DB 841 GCTTGGGAGAGCAACCGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
 OY 808 AAGGAGAG---GACCAATGATGATGATGATGATGATGATGATGATGATGATGAT 864
 DB 901 GCCGCAATTTGAGAGCGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
 OY 865 GATTTGATCAAG 924
 DB 961 AAGTTGCGCAG 1020
 OY 925 TTTCCTTTGAGACCACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 984

Db 1021 TTGGCCCTTGCCCGGTTATCGAGCCATATGTTGGCGATGATGCGTGATCCCAAAATCG 1080
OY 985 ATCAGAGAAATGCTGAGAGAGGCGCTGGGAAATTCGATACCCACATGATAGCAATAC 1044
Db 1081 CAGCAAGAGCAGCTGTCCAGGCGCTGGGGTAATTCATTCCTCATGATCATAGCGGAAT 1140
OY 1045 TCCTACGAAAGGTTGCTTCCAAATCAATGCGCAAAACAATATCCG--GAGGTGTAA 1101
Db 1141 TCGTTGGAAGGACTCTCTCTATTCGACACCGCTGATGATCCGCTTTACATGCTGAGT 1200
OY 1102 GAGTTGGAATCCTGTGTAATTAATGCTTGGGAGTTGGCTGACAGTGAACGAGTCC 1161
Db 1201 GCTTTCGAGGCGCATTAATTCACAAACAGGTTGCGATGCCATCGACAGAGAGAGCTG-- 1258
OY 1162 CCGGAACCTGAGAGAGGCGTGCCTATGTGAAAAAGGCCATGTGATGGGAAACACCT 1221
Db 1259 -CGGAGATGTTGAGAGAGCTGAGAGATCTCTACTTTGACGATCCGACGGGCGCAGCATG 1317
OY 1222 ACTCTGATTAATTTATGAGGCTTGCCTATTTCTATTTCTCTTCCCATGCAATGC 1281
Db 1318 GAGCTCTACGAGTGCCTTCACATTCGTGAGCAATCAAGAACTCTGCGACGATATCCATGC 1377
OY 1282 TTCTACATTTGCGCTTCAACACAGAGCTGGCAGTCCCATTTATTTGATGTTGAT 1341
Db 1378 ACCTTGCTGCTGCGCTGCGCTATGCGACCAACTTGGCCAGTATCTCTATCGATTCGAT 1437
OY 1342 TTCGATTCGAGAAATTAATTAACCCCTATGCTATGCTTTGGCCGTGGGCTTAA 1401
Db 1438 ATGATTTGCCACA---CTTTAATCTACTATGCAATCTTGAAGTGGGCAAAAAGTGAAG 1494
OY 1402 GGTGTAGCCATGCGATGAGCTTAACCTATCTCTGTGAAACATTTTGTGAAAGGCTG 1461
Db 1495 GGTGTGTCGATGCGGATGACATTTCTACATGTTCTACGGCATATCTCCAGTAACTG 1554
OY 1462 CCAAGGAAAGCCGAGATACAAAACATTTGAAGCATGTTGGCATTTGACGGAATTC 1521
Db 1555 GACAAGAAATTCGCGCGAATACCGCATCGAGGAGCTGTGGGCAATGTGACATCTTTC 1614
OY 1522 GCGACCAACCGGAAACCATACAGCAATGATATAGC 1556
Db 1615 GCGACCAACCGGAGATCCCACTGTGAGATAATCCG 1649

Search completed: April 11, 2003, 01:07:10
Job time : 263.473 secs

GenCore version 5.1.4-p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 11, 2003, 00:24:12 ; Search time 1660.57 Seconds
(without alignments)
16677.553 Million cell updates/sec

Title: US-09-776-910-14

Sequence: 1 atgacttctgaagcaatt.....ataaagaagaattgttt 1710

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_estbm:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vtl:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	293	17.1	778	9	AI062034 GH01076.5
2	277.4	16.2	648	9	AI388926 GH19977.5
3	247.8	14.5	688	9	AI403569 GH23036.5
4	246.6	14.4	526	9	AI108080 GH06811.5
5	241.4	14.1	516	9	AI108156 GH06911.5
6	240.2	14.0	569	13	BI609541 RH14337.5

7	239.4	14.0	660	13	BI639486 SD22067.5
8	236	13.8	671	9	AI517692 GH28740.5
9	226.2	13.2	630	9	AI403830 GH23353.5
10	225.6	13.2	674	13	BI628316 RH56682.5
11	225.6	13.2	676	13	BI635372 SD16705.5
12	224.6	13.1	673	13	BI614181 RH43493.5
13	223	13.0	672	13	BI614443 RH43812.5
14	222.6	13.0	670	13	BI233202 RH29491.5
15	222.2	13.0	648	9	AI113763 GH10213.5
16	220.6	12.9	648	9	AI403098 GH22464.5
17	219	12.8	646	9	AI109901 GH09292.5
18	219	12.8	646	9	AI293416 LP06524.5
19	218.2	12.8	670	9	AI389766 RH1022.5
20	215.4	12.6	658	13	BI564586 RH6188.5
21	215.2	12.6	804	9	AA264069 LD07724.5
22	213	12.5	656	13	BI614821 RH44296.5
23	213	12.5	656	13	BI619037 RH44995.5
24	211.2	12.4	669	13	BI588370 RH29561.5
25	210.8	12.3	656	13	BI621302 RH2624.5
26	209.4	12.2	628	9	AI109573 GH0808.5
27	209.2	12.2	619	9	AI516869 GH27454.5
28	208.8	12.2	638	13	BI564361 RH32195.5
29	208.8	12.2	647	13	BI575862 RH32195.5
30	208.6	12.2	622	9	AI134524 GH12012.5
31	208.6	12.2	628	9	AI513346 GH26524.5
32	207.8	12.2	614	12	BG641228 SD12519.5
33	207.4	12.1	614	9	AI107729 GH05557.5
34	207.4	12.1	614	9	AI134360 GH11805.5
35	205.8	12.0	633	13	BI370683 RH57396.5
36	202.8	11.9	612	9	AA950522 LD30351.5
37	200.8	11.7	618	9	AI517217 GH27880.3
38	200	11.7	596	9	AI108346 GH07161.3
39	199.2	11.6	614	13	BI617897 RH48369.5
40	198.6	11.6	615	13	BI588504 RH2849.5
41	198.6	11.6	788	9	AA391794 LD11561.5
42	198	11.6	587	9	AI517539 GH28541.5
43	198	11.6	588	13	BI638519 SD20822.5
44	198	11.6	607	13	BI624437 RH63994.5
45	198	11.6	609	13	BI567399 RH37771.5

ALIGNMENTS

RESULT 1
LOCUS AI062034 778 bp mRNA linear EST 19-APR-2001
DEFINITION GH01076.5prime GH Drosophila melanogaster head P072 Drosophila melanogaster cDNA clone GH01076 5prime similar to U51050:

Drosophila melanogaster alpha esterase (aet7) gene, partial cds,
mRNA sequence.

ACCESSION AI062034
VERSION AI062034.1 GI:3337873

KEYWORDS
SOURCE EST.

ORGANISM fruit fly.

Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 778)

AUTHORS Harvey D., Brokstein P., Hong L., Evans-Holm M., Su C., Tsang G.,
Lewis S., and Rubin G. M.

BDGP/HMMI Drosophila EST project

Unpublished (2001)

Contact: Stapleton, M.

BDGP

Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA

Fax: 510 486 6798

Email: <http://www.fruitfly.org/EST>, est@fruitfly.berkeley.edu

Plate: 10 row: G column: 4

High quality sequence stop: 363.

Location/Qualifiers

FEATURES

Matches 351; Conservative 0; Mismatches 174; Indels 0; Gaps 0;

QY 202 GTGGGTGATTTGATTAAGCAGCCAGGCGCTGACCATGGAGGCTGACGAT 261
 Db 1 GTGGGGAGCTTGGCTTTAAGCCCTCAGAGGCCATCCCTGGGAGCGAGTTCGGAC 60
 QY 262 TGTGTGGGAGCCAGCAGATCGGTACAGACATTTCAATAGTGGCAACCCAGAGT 321
 Db 61 TGCAGCCAGCCGAGGATTAAGCGCTCCAGGTGCGTTCGTTCCGATTAAGTGAAGCC 120
 QY 322 TCGGAGGATTTGATTAACCTGAATGTATACCAATGACCTTGAACCCAGCAAAAGCGT 381
 Db 121 TCCAGAGAGCTGCTCTATCTCAATGTATACCAACATGTGAAGCCGAGCGAGTTCGC 180
 QY 382 CCGTATGATTTGATTCATCATGCGGAGATTTATTTTCGCGAGCAAAATTCGTAATGG 441
 Db 181 CCGGTATGATTTGATTTACAGGAGAGGCTTCATTTCCGCGAGGCAATTCGGAATGG 240
 QY 442 TTTGTCCGAGCTACTTTATGAAGAAACCGGTGCTTGTGTAACCGTCAATATCGTTTG 501
 Db 241 TATGGCCCGGATTTGATTAAGAAAGATGTGTCTCTACAGATACAGTACCGACTT 300
 QY 502 GGTGTGTTGGGTTTCTTACCTGTAATCGGAAATCTCATGTCCCGGCAACGCTGGC 561
 Db 301 GGGGCTTTGGGATTTATGAGCTTAATGCTCCCGAGCTAATGTACAGGAAATGCTGGC 360
 QY 562 CTCAGAGATCAAGTAATGCGCTTGAATGGTCAAGATATATTCGATTTTCGGTGGC 621
 Db 361 CTCAGAGATCAAGTGTGCGCTTCAAGTGTATCAAGAAATGCTGCTAGTTTCGGCGGA 420
 QY 622 GATGTAGACATATTAACCGCTTCCGGGAGAAAGTGTGGGCGCTCAACCCATTTATCATG 681
 Db 421 GATCCACAGCTGATCTGCTTTGAGAGAGATGCTGGAGGCGCTTCACTACTATCATG 480
 QY 682 ATGATTAACCGAGACACCGCGTTTATTCATCTGTGATCATG 726
 Db 481 ATGCTAACCGATCAGACCAAGGCGCTTTTCATCGCGGATCTTG 525

RESULT 5
 A1108156 516 bp mRNA linear EST 19-APR-2001
 LOCUS GH06911.5prime GH Drosophila melanogaster head pot2 Drosophila
 DEFINITION melanogaster cDNA clone GH06911 Splice similar to U51050.
 Drosophila melanogaster alpha esterase (aE) gene, partial cds,
 mRNA sequence.
 A1108156
 VERSION A1108156.1 GI:3476435
 KEYWORDS EST.
 SOURCE fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 516)
 Harvey, D., Brokslein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
 Lewis, S., and Rubin, G.M.
 BDGP/HIMI Drosophila EST Project
 Unpublished (2001)
 COMMENT Contact: Stapleton, M.
 BDGP
 Lawrence Berkeley National Lab
 One Cyclotron Rd, Berkeley, CA 94720, USA
 Fax: 510 486 6798
 Email: http://www.fruitfly.org/EST_est@fruitfly.berkeley.edu
 Plate: 69 row: A column: 11
 High quality sequence stop: 425.
 Location/Qualifiers
 1..516
 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /clone="GH06911"
 /clone_1lb="GH Drosophila melanogaster head pot2"

/sex="male and female"
 /dev-stage="adult"
 /lab_host="DH5 - alpha"
 /note="Organ: head; Vector: pot2; Site:1: EcoRI; Site:2:
 XhoI; Sized fractionated cDNAs were directly ligated into
 POT2. Plasmid cDNA library."
 BASE COUNT 119 a 125 c 150 g 122 t
 ORIGIN

Query Match 14.1% Score 241.4; DB 9; Length 516;
 Best Local Similarity 66.8%; Pred. No. 1.3e-61;
 Matches 344; Conservative 0; Mismatches 171; Indels 0; Gaps 0;

QY 202 GTGGGTGATTTGATTAAGCAGCCAGGCGCTGACCATGGAGGCTGATGAT 261
 Db 1 GTGGGGAGCTTGGCTTTAAGCCCTCAGAGGCCATCCCTGGGAGCGAGTTCGGAC 60
 QY 262 TGTGTGGGAGCCAGCAGATCGGTACAGACATTTCAATAGTGGCAACCCAGAGT 321
 Db 61 TGCAGCCAGCCGAGGATTAAGCGCTCCAGGTGCGTTCGATTAAGTGAAGGCGC 120
 QY 322 TCGGAGATTTGCTATACCTGAATGTATACCAATGACCTTGAACCCAGCAAAAGCGT 381
 Db 121 TCCAGAGAGCTGCTCTATCTCAATGTATACCAACATGTGAAGCCGAGCAAGGCTGC 180
 QY 382 CCGTATGATTTGATTCATCATGCGGAGATTTATTTTCGCGAGCAAAATTCGTAATGG 441
 Db 181 CCGGTATGATTTGATTTACAGGAGAGGCTTCATTAATGCGGAGCCAAATCGGGAATG 240
 QY 442 TTTGTCCGAGCTACTTTATGAAGAAACCGGTGCTTGTGAACCGGTCAATATCGTTTG 501
 Db 241 TATGGCCCGGATTTGATTAAGAAAGATGTGTCTCTGACAGATATACGATACCGACTT 300
 QY 502 GGTGTGTTGGGTTTCTTACCTGTAATCGGAAATCTCATGTCCCGGCAACGCTGGC 561
 Db 301 GGGGCTTTGGGATTTATGAGCTTAATGCTCCCGAGCTAATGTACAGGAAATGCTGGC 360
 QY 562 CTCAGAGATCAAGTAATGAGCTTGAGATGGGTCAAGATATATATGCTATTTTCGGTGGC 621
 Db 361 CTCAGAGATCAAGTGTGCTGCTCCCTCAAGTGTATCAAGAAATGCTGATTTGGCGGA 420
 QY 622 GATGTAGACATATTAACCGCTTTCGCGAAAGTGTGCGGCGCTCAACCCATTTATCATG 681
 Db 421 GATCCACAGCTGATCTGCTTTTGGAGAGAGTGTGAGGCGCTACACTACTACATG 480
 QY 682 ATGATTAACCGAGACACCGCGTTTATTCATCTGTGATCATG 716
 Db 481 ATGCTAACCGATCAGACCAAGGCGCTTTTCATCTG 515

RESULT 6
 B1609541 569 bp mRNA linear EST 07-SEP-2001
 LOCUS RH14337.5prime RH Drosophila melanogaster normalized Head p1C-1
 DEFINITION Drosophila melanogaster cDNA clone RH14337 5 similar to alpha-Est7:
 FBan001112 GO: [carboxylesterase (GO:0004911); carboxylesterase
 (GO:0004911)] located on: 3R 84D5-84D5; 08/17/2001, mRNA sequence.
 B1609541
 VERSION B1609541.1 GI:15505066
 KEYWORDS EST.
 SOURCE fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 569)
 Champe, M., Chavez, C., Dorsett, V., Farrant, D., Frise, E., Carlson
 R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., George
 Munhall, C.J., Nunoo, J., Pacleb, J., Parasas, V., Park, S.,
 Phouanavong, S., Wan, K., Yu, C., Lewis, S.E., Celniker, S. and Rubin
 G.M.
 BDGP/HIMI RH Drosophila EST Project

Db	302	GAGTTGCGGTTAAAGGCCCTCAGAGGCCCATTCCTCCGTGGAGCGAGTTCCGGATGTGCACG	361
Qy	268	GGGGCAGCAGCAACAGATCGGTACACACAGATTTCATTAAGTGGCAAAACCACAGTTGCGAG	327
Db	362	CAGCCGGAAGATTAAGGCCGCTCCAGGTGCAGTTCGTCTTCGTAAGGTAGAGGGCGTCCGAG	421
Qy	328	GATTGCTATACCTGAATGTGTATACCAATGACTTGAACCCAGACAAAGGCCGTCGTT	387
Db	422	GACTGCGCTCTATCTCATATGTGTACACCAACATGTGAAGCCCGACAGAGCGTCCGCGTT	481
Qy	388	ATGTTTTTCATCCATGCGCGAGATTTTATTTTGGCGCAACAAATCGTAATGTTTGT	447
Db	482	ATGTTTGGATTTACGAGAGAGCGGCTTATATCGCGACGCAATCGGAATGTATAGT	541
Qy	448	CCCACACTATTATGAGAAGAAACCGCTGCTGTGGTACCGTGAATTCGTTTGGGTG	507
Db	542	CCGATTACTATTATGAAGAAGATGTTGTTCTGTCACGATACAGTACGACTTGGGGCT	601
Qy	508	TTGGGTTTCTTACCTTACCTGAAATCGAAATCGAATGTCCCGCAACGCTGCGCTCAAG	567
Db	602	TTGGGATTATATGAGCTTAAAGTCCCGAGCTAAATGTATACAGGAATGTGGCTTCAG	661
Qy	568	GATCACT 575	
Db	662	GATCAGST 669	
RESULT 9			
LOCUS	A1403830	630 bp	mRNA
DEFINITION	A1403830	GH23353_5prime GH Drosophila melanogaster head port2 Drosophila melanogaster cDNA clone GH23353 5prime similar to U51052: Drosophila melanogaster alpha esterase (aE8) gene, partial cds, mRNA sequence.	
ACCESSION	A1403830	GI:4246917	
VERSION	A1403830		
KEYWORDS		EST.	
SOURCE		fruit fly.	
ORGANISM		Drosophila melanogaster	
		Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.	
REFERENCE		1 (bases 1 to 630)	
AUTHORS		Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G., Lewis,S., and Rubin,G.M.	
TITLE		BDGP/HMT Drosophila EST Project	
JOURNAL		Unpublished (2001)	
COMMENT		Contact: Stapleton, M.	
		BDGP	
		Lawrence Berkeley National Lab	
		One Cyclotron Rd, Berkeley, CA 94720, USA	
		Fax: 510 486 6798	
		Email: http://www.fruitfly.org/EST_estefruitfly.berkeley.edu	
		Plate: 233 row: E column: 5	
		High quality sequence stop: 548.	
FEATURES			
source		location/Qualifiers	
		1..630	
		/organism="Drosophila melanogaster"	
		/db_xref="taxon:7227"	
		/clone_id="GH23353"	
		/clone_lib="GH Drosophila melanogaster head port2"	
		/sex="male and female"	
		/dev_stage="adult"	
		/lab_host="DHS - alpha"	
		/note="Organ: head; Vector: port2, site_1: EcoRI; site_2: XhoI; Sized fractionated cDNAs were directly ligated into port2. Plasmid cDNA library."	
BASE COUNT	150 a	162 c	173 g
ORIGIN			144 t 1 others
Query Match	13.2%	Score 226.2;	DB 9; Length 630;
Best Local Similarity	60.1%	Pred. No. 6;	le-57;

JOURNAL
unpublished (2001)
COMMENT
Contact: Stapleton, M.
BDGP

BI635372 , mRNA sequence.

VERSION B1635372.1 GI:15537582
 KEYWORDS EST.
 SOURCE fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 REFERENCE 1 (bases 1 to 676)
 AUTHORS Harvey, D., Broksstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S. and Rubin, G.M.
 TITLE BDGP/HHMI Drosophila EST project
 JOURNAL Unpublished (2001)
 COMMENT Contact: Stapleton, M.
 BDGP

Lawrence Berkeley National Lab
 One Cyclotron Rd, Berkeley, CA 94720, USA
 Fax: 510 486 6798
 Email: http://www.fruitfly.org/EST_est@fruitfly.berkeley.edu
 Plate: SD.167 row: A column: 5
 High quality sequence stop: 641.
 FEATURES
 Source Location/Qualifiers
 1..676
 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /clone="SD16705"
 /clone.lib="SD Drosophila melanogaster Schneider L2 cell culture pot2"
 /lab_host="DHS-alpha"
 /note="Vector: pot2; Site: 1: EcorI; Site: 2: XhoI; Sized fractionated cDNAs were directly ligated into pot2. Plasmid cDNA library."
 BASE COUNT 155 a 173 c 194 g 154 t
 ORIGIN

Query Match 13.2%; Score 225.6; DB 13; Length 676;
 Best Local Similarity 63.8%; Pred. No. 9,6e-57;
 Matches 342; Conservative 0; Mismatches 194; Indels 0; Gaps 0;
 QY 28 CGCGTGAACCTAGCTTAAATGATGCAATTAATACACAACACCTGCTGATGACA 87
 DB 141 CGCTGGGCGGGCCGCTCAAAACATCGACATTAAGTCCAGCATGCGCGACGACC 200
 QY 88 AATGAACCAATTAATGATGCAATTAATGCAAAATTAAGGCTGTTAAGCATGACC 147
 DB 201 AATGAACCAATTAATGATGCAATTAATGCAAAATTAAGGCTGTTAAGCATGACC 147
 QY 148 GTCTAGATGATCTTACTAGAGTTTCGAGATTAACCTATGCTTAAGCTTCAGTGGT 207
 DB 261 CTCTAGATGATCTTACTAGAGTTTCGAGATTAACCTATGCTTAAGCTTCAGTGGT 207
 QY 208 GAGTTGATGATCAAGGACCCGAGGCTGTACCATGGAGGATGATGATGCTGT 267
 DB 321 GAGTTGATGATCAAGGACCCGAGGCTGTACCATGGAGGATGATGATGCTGT 267
 QY 268 GGGCCAGCAAGATCGGTACAGACATTTCAATGTCGCAACCCACAGGTTGGAG 327
 DB 381 CAGCCCAAGATCGGTACAGACATTTCAATGTCGCAACCCACAGGTTGGAG 327
 QY 328 GATTTGATGATCAAGGACCCGAGGCTGTACCATGGAGGATGATGATGCTGT 387
 DB 441 GACTGCTCTATCTCAATGTTACCAACAATGTTGAAGGCTGCGGCTGCGGTT 500
 QY 388 ATGCTTTTCAATGATGAGGAGATTTATTTTGGGCAAGCAATTCGTAATGTTGGT 447
 DB 501 ATGCTTTTCAATGATGAGGAGATTTATTTTGGGCAAGCAATTCGTAATGTTGGT 447
 QY 448 CCGGACTATTATGAACCAACCGGCTGTGTTGTAACCGTGAATTCGTTGGGTG 507
 DB 561 CCGGACTATTATGAACCAACCGGCTGTGTTGTAACCGTGAATTCGTTGGGTG 507
 QY 508 TTGGGTTCTTACGCTGAATTCGAAATTCATGCTCCCGGCAACGCTGGGCT 563
 DB 621 TTGGGTTCTTACGCTGAATTCGAAATTCATGCTCCCGGCAACGCTGGGCT 563

RESULT 12
 B1614181
 LOCUS
 DEFINITION
 B1614181 673 bp mRNA linear EST 07-SEP-2001
 RH43493: Sprime RH Drosophila melanogaster normalized Head pR1c-1
 Fban0001112 GO: (carboxyesterase (GO:0004091); carboxyesterase (GO:0004091)) located on 3R 84D5-84D5; 08/18/2001, mRNA sequence.
 B1614181
 ACCESSION
 B1614181 GI:15509706
 VERSION
 B1614181
 KEYWORDS
 SOURCE
 ORGANISM
 Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 REFERENCE 1 (bases 1 to 673)
 AUTHORS Stapleton, M., Broksstein, P., Hong, L., Tyler, D., Berman, B., Carlson, J., Champagne, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Mista, S., Mungall, C.J., Nuno, J., Pacle, J., Paragas, V., Park, S., Phouanavong, S., Wan, K., Yu, C., Lewis, S.E., Celinker, S. and Rubin, G.M.
 BDGP/HHMI RH Drosophila EST project
 Unpublished (2001)
 COMMENT Contact: Stapleton, M.
 BDGP

Lawrence Berkeley National Lab
 One Cyclotron Rd, Berkeley, CA 94720, USA
 Fax: 510 486 6798
 Email: http://www.fruitfly.org/EST_est@fruitfly.berkeley.edu
 Plate: RH 434 row: H column: 9
 High quality sequence stop: 553.
 FEATURES
 Source Location/Qualifiers
 1..673
 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /clone="RH43493"
 /clone.lib="RH Drosophila melanogaster normalized Head pR1c-1"
 /sex="male and female"
 /dev_stage="Adult"
 /lab_host="DHS-alpha Tona"
 /note="Organ: head; Vector: pR1c1; Site: 1: XhoI; Site: 2: BamHI; Library was kindly generated by Piero Carninci at the RIKEN. The library was normalized and excised using Cre recombinase. Plasmid cDNA library."
 BASE COUNT 153 a 169 c 195 g 155 t
 ORIGIN

Query Match 13.1%; Score 224.6; DB 13; Length 673;
 Best Local Similarity 63.6%; Pred. No. 1,9e-56;
 Matches 341; Conservative 0; Mismatches 195; Indels 0; Gaps 0;
 QY 28 CGCGTGAACCTAGCTTAAATGATGCAATTAATACACAACCTGCTGATGACA 87
 DB 138 CGCTGGGCGGGCCGCTCAAAACATCGACATTAAGTCCAGCATGCGCGACGACC 197
 QY 88 AATGAACCAATTAATGATGCAATTAATGCAAAATTAAGGCTGTTAAGCATGACC 147
 DB 198 AATGAACCAATTAATGATGCAATTAATGCAAAATTAAGGCTGTTAAGCATGACC 147
 QY 148 GTCTAGATGATCTTACTAGAGTTTCGAGATTAACCTATGCTTAAGCTTCAGTGGT 207
 DB 258 GTCTAGATGATCTTACTAGAGTTTCGAGATTAACCTATGCTTAAGCTTCAGTGGT 207
 QY 208 GAGTTGATGATCAAGGACCCGAGGCTGTACCATGGAGGATGATGATGCTGT 267
 DB 318 GAGTTGATGATCAAGGACCCGAGGCTGTACCATGGAGGATGATGATGCTGT 267
 QY 268 GGGCCAGCAAGATCGGTACAGACATTTCAATGTCGCAACCCACAGGTTGGAG 327
 DB 381 CAGCCCAAGATCGGTACAGACATTTCAATGTCGCAACCCACAGGTTGGAG 327

Db 378 CAGCCGAAGATTAAGCCGCTCAGTGTCTCTGATGAAGTAGAGGCTCCGAG 437
 QY 328 GATTGCTATACCTGAATGTATATACCAATGACTTGAACCCAGCAAAAGGCGTCTGT 387
 Db 438 GACTGCTCTATCTCATGTGTACACCAATGTGAAGCCGCAAGGCTCGCCGCTT 497
 QY 388 ATGCTTTTCATCATGCGGAGATTTATTTTCGGCAGCAAAATCTTAATCTTTGGT 447
 Db 498 ATGCTTTGATTCACGAGAGGAGCTTATTCGCGAGGCAATCGGAATGATGGC 557
 QY 448 CCGCAGCTATTAGCAAAACCGGTGTCTGTGTACCGGCAATATCGTTGGGTGTG 507
 Db 558 CCGATTAATCTTATGAAGAAGATGTGTCCTGACGATACGATCCGATCTGGGCT 617
 QY 508 TTGGGTTTCTTACCTGAATTCGAAATCTCAATGTCTCCCGCAGCGCTGGCT 563
 Db 618 TTGGGATTATGATCTTAACTGCTCCCGAGGTAATATGACGAATGCTGGCT 673

RESULT 13
 Bi614443
 LOCUS 672 bp mRNA linear EST 07-SEP-2001
 DEFINITION RH43812.5prime RH Drosophila melanogaster normalized Head pfic-1
 Drosophila melanogaster cDNA clone RH43812.5 similar to alpha-Est7:
 Fban000112 Go:|carboxylesterase (Go:0004091); carboxylesterase
 (Go:0004091) located on: 3R 84D5-84D5; 08/18/2001, mRNA sequence.
 Bi614443
 ACCESSION Bi614443.1 GI:15509968
 VERSION EST
 KEYWORDS fruit fly.
 SOURCE Drosophila melanogaster
 ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 REFERENCE 1 (bases 1 to 672)
 AUTHORS Stapleton,M., Broksstein,P., Hong,L., Tyler,D., Berman,B., Carlson
 J., Champe,M., Chavez,C., Dorsett,V., Farfan,D., Frise,E., George
 R., Gonzalez,M., Guarin,H., Harris,N., Li,P., Liao,G., Mista,S.,
 Mungall,C.J., Nunoo,J., Pacleb,J., Paragas,V., Park,S.,
 Phouanavong,S., Wan,K., Yu,C., Lewis,S.E., Celnikier,S. and Rubin
 G.M.
 BDGP/HMI RH Drosophila EST Project
 JOURNAL Unpublished (2001)
 COMMENT Contact: Stapleton, M.

TITLE Lawrence Berkeley National Lab
 JOURNAL One Cyclotron Rd, Berkeley, CA 94720, USA
 COMMENT Fax: 510 486 6798
 Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
 Plate: RH.438 row: A column: 12
 High quality sequence stop: 554.
 FEATURES
 source
 1. 672
 location/Qualifiers
 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /clone="RH43812"
 /clone_lib="RH Drosophila melanogaster normalized Head
 pfic-1"
 /sex="male and female"
 /dev_stage="adult"
 /lab_host="DH5-alpha Tona"
 /note="Organ: Head; Vector: pfic1; Site:1; XhoI; Site:2;
 BamHI; Library was kindly generated by Piero Carlini at
 the RIKEN. The library was normalized and excised using
 Cre recombinase. Plasmid cDNA library."

BASE COUNT 154 a 169 c 194 g 155 t
 ORIGIN

Query Match 13.0%; Score 223; DB 13; Length 672;
 Best Local Similarity 63.6%; Pred. No. 5.9e-56;
 Matches 340; Conservative 0; Mismatches 195; Indels 0; Gaps 0;

QY 28 CGCCTGAACCTATGCTTAATGATGATCAATATACACAACTACGCTGTGAGTACA 87

Db 138 CGCTTCGGGTGGGCGCTCAAAACCATGAGCATAAAGTCACAGAGATGCGCAGTAC 197
 QY 88 AATGAACCCCAATATATGATGATGATGATGATGATGATGATGATGATGATGATG 147
 Db 198 AATGAACCCAGTTGTCGCGCAGGAGTACGAGGAGTACGAGGAGTACGAGGAGTAC 257
 QY 148 GTCTAGATGATTTCTACTACAGTTCGAGAGATATCCATGATGATGATGATGATGAT 207
 Db 258 CTCTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 317
 QY 208 GAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 267
 Db 318 GAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 377
 QY 268 GGGCAGCCAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 327
 Db 378 CAGCCGAAGATTAAGCCGCTCAGTGTCTCTGATGAAGTAGAGGCTCCGAG 437
 QY 328 GATTGCTATACCTGAATGTATATACCAATGACTTGAACCCAGCAAAAGGCGTCTGT 387
 Db 438 GACTGCTCTATCTCATGTGTACACCAATGTGAAGCCGCAAGGCTCGCCGCTT 497
 QY 388 ATGCTTTTCATCATGCGGAGATTTATTTTCGGCAGCAAAATCTTAATCTTTGGT 447
 Db 498 ATGCTTTGATTCACGAGAGGAGCTTATTCGCGAGGCAATCGGAATGATGGC 557
 QY 448 CCGCAGCTATTAGCAAAACCGGTGTCTGTGTACCGGCAATATCGTTGGGTGTG 507
 Db 558 CCGATTAATCTTATGAAGAAGATGTGTCCTGACGATACGATCCGATCTGGGCT 617
 QY 508 TTGGGTTTCTTACCTGAATTCGAAATCTCAATGTCTCCCGCAGCGCTGGCT 562
 Db 618 TTGGGATTATGATCTTAACTGCTCCCGAGGTAATATGACGAATGCTGGCT 672

RESULT 14
 Bi233202
 LOCUS 670 bp mRNA linear EST 11-JUL-2001
 DEFINITION RE29491.5prime RE Drosophila melanogaster normalized Embryo pfic-1
 Drosophila melanogaster cDNA clone RE29491.5 similar to alpha-Est7:
 Fban000112 located on: 3R 84D5-84D5; 04/12/2001, mRNA sequence.
 Bi233202
 ACCESSION Bi233202.1 GI:14700784
 VERSION EST
 KEYWORDS fruit fly.
 SOURCE Drosophila melanogaster
 ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 REFERENCE 1 (bases 1 to 670)
 AUTHORS Stapleton,M., Broksstein,P., Hong,L., Tyler,D., Berman,B., Carlson
 J., Champe,M., Chavez,C., Dorsett,V., Farfan,D., Frise,E., George
 R., Gonzalez,M., Guarin,H., Harris,N., Li,P., Liao,G., Mista,S.,
 Mungall,C.J., Nunoo,J., Pacleb,J., Paragas,V., Park,S.,
 Phouanavong,S., Wan,K., Yu,C., Lewis,S.E., Celnikier,S. and Rubin
 G.M.
 BDGP/HMI RE Drosophila EST Project
 JOURNAL Unpublished (2001)
 COMMENT Contact: Stapleton, M.

TITLE Lawrence Berkeley National Lab
 JOURNAL One Cyclotron Rd, Berkeley, CA 94720, USA
 COMMENT Fax: 510 486 6798
 Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
 Plate: RE.294 row: H column: 7
 High quality sequence stop: 534.
 FEATURES
 source
 1. 670
 location/Qualifiers
 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /clone="RE29491"
 /clone_lib="RE Drosophila melanogaster normalized Embryo

QY 28 CGCCTGAACCTATGCTTAATGATGATCAATATACACAACTACGCTGTGAGTACA 87

GenCore version 5.1.4-p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 11, 2003, 00:41:37 ; Search time 40.4409 seconds
(without alignments)
12967.505 Million cell updates/sec

Title: US-09-776-910-14

Perfect score: 1710
Sequence: 1 atgactttctgaagcaatt.....ataaagaaggaattgttt 1710

Scoring table: IDENTITY_NDC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_MA:*
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCMB.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfileseq1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1710	100.0	1710	4	US-09-068-960-14
2	956.6	55.9	1713	2	US-08-669-524-1
3	956.6	55.9	1713	4	US-09-068-960-1
4	956.6	55.9	1713	4	US-09-068-960-7
5	956.6	55.9	1713	4	US-09-068-960-9
6	955	55.8	1713	4	US-09-068-960-3
7	952.2	55.7	1713	2	US-08-669-524-2
8	951.8	55.7	1713	4	US-09-068-960-5
9	162.6	9.5	1584	3	US-08-747-221B-51
10	162.6	9.5	1584	3	US-08-747-221B-52
11	162.6	9.5	1584	4	US-09-005-051-51
12	162.6	9.5	1584	4	US-09-005-051-52
13	162.6	9.5	2007	3	US-08-747-221B-36
14	162.6	9.5	2007	3	US-08-747-221B-38
15	162.6	9.5	2007	3	US-09-005-051-36
16	162.6	9.5	2007	4	US-09-005-051-38
17	127	7.4	1590	4	US-08-747-221B-23
18	127	7.4	1590	4	US-09-005-051-23
19	127	7.4	1650	3	US-08-747-221B-21
20	127	7.4	1650	3	US-08-747-221B-22
21	127	7.4	1650	4	US-09-005-051-21
22	127	7.4	1650	4	US-09-005-051-22
23	127	7.4	1792	3	US-08-747-221B-18
24	127	7.4	1792	3	US-08-747-221B-20
25	127	7.4	1792	4	US-09-005-051-18
26	127	7.4	1792	4	US-09-005-051-20
27	117	6.8	1650	3	US-08-747-221B-60

C	28	117	6.8	1650	3	US-08-747-221B-61	Sequence 61, Appl
C	29	117	6.8	1650	4	US-09-005-051-60	Sequence 60, Appl
C	30	117	6.8	1650	4	US-09-005-051-61	Sequence 61, Appl
C	31	117	6.8	2144	3	US-08-747-221B-57	Sequence 57, Appl
C	32	117	6.8	2144	3	US-08-747-221B-59	Sequence 59, Appl
C	33	117	6.8	2144	4	US-09-005-051-57	Sequence 57, Appl
C	34	117	6.8	2144	4	US-09-005-051-59	Sequence 59, Appl
C	35	115.8	6.8	1982	3	US-08-747-221B-13	Sequence 13, Appl
C	36	115.8	6.8	1982	3	US-08-747-221B-15	Sequence 15, Appl
C	37	115.8	6.8	1982	4	US-09-005-051-13	Sequence 13, Appl
C	38	115.8	6.8	1982	4	US-09-005-051-15	Sequence 15, Appl
C	39	115.6	6.8	1515	3	US-08-747-221B-16	Sequence 16, Appl
C	40	115.6	6.8	1515	3	US-08-747-221B-17	Sequence 17, Appl
C	41	115.6	6.8	1515	4	US-09-005-051-16	Sequence 16, Appl
C	42	115.6	6.8	1515	4	US-09-005-051-17	Sequence 17, Appl
C	43	90.4	5.3	3047	1	US-07-927-851-2	Sequence 2, Appl
C	44	90.4	5.3	3047	1	US-08-453-323-2	Sequence 2, Appl
C	45	90.4	5.3	3047	1	US-08-440-520-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-068-960-14
Sequence 14, Application US/09068960A
Patent No. 6235515
GENERAL INFORMATION:
APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.
TITLE OF INVENTION: MALATHION CARBOXYESTERASE
FILE REFERENCE: Attorney Docket No. 6235515 50179-051
CURRENT FILING DATE: 1998-05-20
CURRENT APPLICATION NUMBER: PCT/AU96/00746
EARLIER FILING DATE: 1996-11-22
EARLIER APPLICATION NUMBER: AU 6751
EARLIER FILING DATE: 1995-11-23
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 1710
TYPE: DNA
ORGANISM: Musca domestica
US-09-068-960-14

Query Match	100.0%	Score 1710;	DB 4;	Length 1710;
Best local Similarity	100.0%	Pred. No. 0;	Mismatches 0;	Indels 0;
Matches 1710;	Conservative	0;		
QY	1	ATGACTTTCTGAGCAATTCATATTCGCTGAACACTATGCTTAAATGATGTCAT	60	
DB	1	ATGACTTTCTGAGCAATTCATATTCGCTGAACACTATGCTTAAATGATGTCAT	60	
QY	61	AAATACCAACACTACGCTGCTGACTACAAATGAACCCAAATATGATACATATGGA	120	
DB	61	AAATACCAACACTACGCTGCTGACTACAAATGAACCCAAATATGATACATATGGA	120	
QY	121	CAATTTAAGGTGTTAAGCAATGACCGCTACGATGATTTCTTACTACAGTTTGAGAGT	180	
DB	121	CAATTTAAGGTGTTAAGCAATGACCGCTACGATGATTTCTTACTACAGTTTGAGAGT	180	
QY	181	ATACCTATGCTAGACCTCCAGTGGGTGAGTTAGATTCAGATCAAGCCACCCAGGCGCTGA	240	
DB	181	ATACCTATGCTAGACCTCCAGTGGGTGAGTTAGATTCAGATCAAGCCACCCAGGCGCTGA	240	
QY	241	CCATGGGAGGTGATGATGATGCTGGGCGACCAACAGATGGGTACAGACATTTTC	300	
DB	241	CCATGGGAGGTGATGATGATGCTGGGCGACCAACAGATGGGTACAGACATTTTC	300	
QY	301	ATAAGTGCAACACCCAGAGTTGCGAGATTTCTATACCTGATGTATACATATGAC	360	
DB	301	ATAAGTGCAACACCCAGAGTTGCGAGATTTCTATACCTGATGTATACATATGAC	360	

Db	1441	AACATTTTGTGAAACGCTCGGCCAAGGAAGCCCGGAAATACAAAACCATTTGAACGATG	1500
Qy	1501	GTTGGCATTTTGGAGCGAATTGGCCACACCGGCAACCTACAGCAATGATTTAGCGGC	1560
Db	1501	GTTGGCATTTTGGAGCGAATTGGCCACACCGGCAACCTACAGCAATGATTTAGCGGC	1560
Qy	1561	ATGGAAACCCGACCCCTGGAGATGCCATAAAAAATCCGATGATGTCTATAAATGTTTAAAT	1620
Db	1561	ATGGAAACCCGACCCCTGGAGATGCCATAAAAAATCCGATGATGTCTATAAATGTTTAAAT	1620
Qy	1621	ATCGCGCATGAATTTGAAAGTTATGATTTTGCAGAAATGGAATTAATTAACATGSGCA	1680
Db	1621	ATCGCGCATGAATTTGAAAGTTATGATTTTGCAGAAATGGAATTAATTAACATGSGCA	1680
Qy	1681	AGTATTTCGATAAAGAAGGAAATTTGTT	1710
Db	1681	AGTATTTCGATAAAGAAGGAAATTTGTT	1710

```

RESULT 2 --
US-08-669-524-1
: Sequence 1, Application US/08669524
: Patent No. 5843758
:
: GENERAL INFORMATION:
: APPLICANT: RUSSELL, Robyn J.
: APPLICANT: NEWCOMB, Richard D.
: APPLICANT: ROBIN, Geoffrey C.
: APPLICANT: BOYCE, Thomas M.
: APPLICANT: CAMPBELL, Peter M.
: APPLICANT: PARKER, Anthony G.
: APPLICANT: OAKESHOTT, John G.
: APPLICANT: SMYTH, Kerrie A.
: TITLE OF INVENTION: ENZYME BASED BIOREMEDIATION
: NUMBER OF SEQUENCES: 22
:
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Lowe Price Leblanc & Becker
: STREET: 99 Canal Center Plaza, Suite 300
: CITY: Alexandria
: STATE: Virginia
: COUNTRY: USA
: ZIP: 22314
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/669,524
: FILING DATE:
:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Price, Robert L.
: REGISTRATION NUMBER: 22,685
: REFERENCE/DOCKET NUMBER: 1451-021
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 703-684-1111
: TELEFAX: 703-684-1124
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1713 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: US-08-669-524-1
:
: Query Match 55.9%; Score 956.6; DB 2; Length 1713;
: Best Local Similarity 73.4%; Pred. No. 2,4e-304;
: Matches 123; Conservative 0; Mismatches 444; Indels 0; Gaps 0;
:
: 44 TTAATGCGATGGCGAATAATACAAACTACCGTCGATGACAAATGAAACCAATAA 103
: ||||||||| | ||||| | ||||| ||| | ||| |||||||
: ||

```



```

Db 164 ACTACAGTTTGGAGGTATACCTAGCCCAACCCGAGTGGGTGAGTGAATTTAAAG 223
OY 224 CACCCAGGCGCTGATACATGGGAGGTGATGATTCGTGTGGCCACCAACAGAT 283
Db 224 CACCCAGGCGCTGATACATGGGAGGTGATGATTCGTGTGGCCACCAACAGAT 283
OY 284 CCGTACAGACAGATTCATAGTGGCAACCCACAGGTTCCGAGAGTTGTCTATACCGA 343
Db 284 CAGTGCAGATGATTTTATACGGGCAAGTGTGGCTCAGAGATTTGTCTATACCGA 343
OY 344 ATGTGATACCAATGACTTGAACCCAGCAAAAGGCGCTGTATGTTTCATCATG 403
Db 344 GTGTCTATCAGATATCTAAATCCCAAACTAAAGTCCGCTTTAGATACATACATG 403
OY 404 GCGAGATTTTATTTTGGGCAAGCAATGCTAGTGGTTGGTCCGACTATTANGA 463
Db 404 GTGGTGTGTTTATTCGTGTAATCATCGATATGATGTCCTATTTATTTCAATTA 463
OY 464 AGAAACCCGTGTGTGTGTAACCGTCAATATGTTGGGTGTGGTTCCTTACCC 523
Db 464 AAAAGAGATGTGTGTGATTAACATACATATCGTTGGAGCTGTAGTTTCTAAGTT 523
OY 524 TGAATTCGCAAAATCTCATATGTCGCGCAACCGTGGCTCAAGATCAAGTGGCT 583
Db 524 TAAATTCAGAAAGACTTATATGTCGCGCAACCGTGGCTCAAGATCAAGTGGCT 583
OY 584 TGAGATGGGTCAAGATATATTTGCCATTTTCGATGCGATGAGACATATTTCCGCT 643
Db 584 TGCGTGGATTAATAATTAATGCGCAACTTTGGTGGCAATCCGATATATTTACAGCT 643
OY 644 TCGGGAAGTGTGGTGGGCTTCAACCATATCATATATATACCAACAGACCGCTG 703
Db 644 TTGGTGAAGTGTGGTGGGCTTCAACCATATCATATATATACCAACAGACCGCTG 703
OY 704 GTTATTCATCTGATGATCATGATGTCGCTGATTCATGCTGCTGCTTACAG 763
Db 704 GTTATTCATCTGATGATCATGATGTCGCTGATTCATGCTGCTGCTTACAG 763
OY 764 AATGCCAAGTGTGGCTGCTCAACCATGCGCAACGTTGGCTATTAAGGAGAGACATG 823
Db 764 AATGCCAAGTGTGGCTGCTCAACCATGCGCAACGTTGGCTATTAAGGAGAGATG 823
OY 824 AAAAGATATCTGGAATCTTATGAAAGCCATGCTTATGATTTGATTAAGAGAGAG 883
Db 824 AATGAGATGTTTGAATTTCTTATGAAAGCCAGGAGATTAATTAAGAGAGAG 883
OY 884 CACAAGTTTGAACCCGCAAGAAATGCAATATGATGTTCTTGTGAACCCAGT 943
Db 884 AAAAGATTTAACTCTAGAAAGAGGCTAAATAAGTATGTTCTTGTGAACCCAGT 943
OY 944 TAGAACCATACCAAGACGCGAGTGTGTAACCAACCAATCAGAAATGATGAGA 1003
Db 944 TTGAGCCATATCAGACGCGTGTGTTGTTTACCAACCAATCCTCGGGAATGTTAAA 1003
OY 1004 GCGCCTGGGGAATTCGATACCCATTTGATAGCAATATCTCTCAAGAGTTGGTT 1063
Db 1004 CTGCTTGGGGAATTCGATACCCATTTGATAGCAATATCTCTCAAGAGTTGGTT 1063
OY 1064 CCAATGCAATTTGCCAATATCCGAGTGTGTAAGAGGTTGAATCTGTGTGAAT 1123
Db 1064 TCACTTCAATTTTGAACCAATGCTTATGTTTAAAGGATTAAGAACTGTGTGAAT 1123
OY 1124 ATGTGCTGGAGTGTGGTGAAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAG 1183
Db 1124 TTGAGCAAGTGAATGGTGTGATGTAAGAGAGAGAGAGAGAGAGAGAGAGAG 1183
OY 1184 CCAATTTGAAAAAGCCATGTTGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 1243
Db 1184 CTAATAATTAAAGGCTCATGTTACAGAGAGAGAGAGAGAGAGAGAGAGAG 1243
OY 1244 TTGCTCTATTTCTATTTCTTCCCATGATGCTTCCATCAATTTGCGCTTACCC 1303
Db 1244 TTGCTCTATTTCTATTTCTTCCCATGATGCTTCCATCAATTTGCGCTTACCC 1303

Db 1244 TTGCTCTCATATCTATTTCTGTTCCCATGATGCTTGTGTCATTTACGTTCAATC 1303
OY 1304 ACAGAGTGGACATCCCATTTATTTGATGCTTGTGATTCGATTCGAGAAATTTA 1363
Db 1304 ACAGTGGGATGACAGCCGTTACTGTATGCTTGTGATTCGATTCGAGAAATTTA 1363
OY 1364 ACCCTATGATTTATGCTGTTTGGCCGTGAGGCTTAAAGGTGTAAGCATGCGATGAGC 1423
Db 1364 ATCCCTATGATTTATGCTGATGAGGAGGCTGTTTAAAGGTGTAAGCATGATGAT 1423
OY 1424 TAACCTATCTTGTGAAACATTTGTGAAAGCCGCTGCAAGAGAAAGCCGAGATAC 1483
Db 1424 TAACCTATCTTGTGAAACATTTGTGAAAGCCGCTGCAAGAGAAAGCCGAGATAC 1483
OY 1484 AAACATTTGAAGCAGTGTGGAATTTGAGAGAGATTTGCGACACCGGCAACCATAC 1543
Db 1484 AAACATTTGAAGCAGTGTGGAATTTGAGAGAGATTTGCGACACCGGCAACCATAC 1543
OY 1544 GCAATGATATAGCGGAGTGAAGAAACCTCAGCTGGATCCATTAATAAATCCGATGATG 1603
Db 1544 GCAATGATATAGCGGAGTGAAGAAAGTTCCTGGATCCATTAATAAATCCGATGATG 1603
OY 1604 TCTATAATGTTTAAATATGCGGATGATTAAGTATGATTTGCGAGAAATGATGATA 1663
Db 1604 TATACAGTGTGTAATATGATGATGATTAAGTATGATTTGCTGAGAAATGATGATA 1663
OY 1664 AATTTAAACATGCGCAGATATTCGATTAATAAAGAGATTTGTT 1710
Db 1664 AGATTTAAACATGAGGATGATGTTGAAAAACATGAGATTTATTT 1710

RESULT 4
US-09-68-960-7
; Sequence 7, Application US/09068960A
; Patent No. 6235515
; GENERAL INFORMATION:
; APPLICANT: Commonwealth Scientific and Industrial Resrch. Org.
; TITLE OF INVENTION: MALATHION CARBOXYLESTERASE
; FILE REFERENCE: Attorney Docket No. 6235515 50179-051
; CURRENT APPLICATION NUMBER: US/09/068,960A
; EARLIER APPLICATION NUMBER: PCT/AU96/00746
; EARLIER FILING DATE: 1996-11-22
; EARLIER APPLICATION NUMBER: AU 6751
; EARLIER FILING DATE: 1995-11-23
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1713
; TYPE: DNA
; ORGANISM: Lucilia cuprina
US-09-68-960-7

Query Match 55.9%; Score 956.6; DB 4; Length 1713;
Best Local Similarity 73.4%; Pred. No. 2.4e-304;
Matches 1223; Conservative 0; Mismatches 444; Indels 0; Gaps 0;

OY 44 TTAATGATGTCATTAATTAATACCAAACTACCGTGTGATGTAACCAATGAACCAATAA 103
Db 44 TTAATGATGTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 103
OY 104 TCGATACGATATGAGCAATTAAGGTTTAAAGGATTAAGCAATGACCGTCTACGATATCTT 163
Db 104 CTGAAATGATATGAGCAATTAAGGTTTAAAGGATTAAGCAATGACCGTCTACGATATCTT 163
OY 164 ACTACAGTTTGGAGGTATACCTATGCTAAGCCTCCAGTGGGTGAGTGAAGTTCAAGG 223
Db 164 ACTACAGTTTGGAGGTATACCTATGCTAAGCCTCCAGTGGGTGAGTGAAGTTCAAGG 223
OY 224 CACCCAGGCGCTGTACCATGAGAGGTTGATGTTGCTGTGGCCACCAACAGAT 283
Db 224 CACCCAGGCGCGTGTACCATGAGAGGTTGATGTTGCTGTGGCCACCAACAGAT 283

```

QY 284 CCGTACAGACAGTTCATTAAGTGGCAACCCAGAGTTGGAGATTTGTCTATACCTTA 343
 DB 284 CAGTGCAGAGTGTGTTTAAATACGGGCAAGGTGTGGCTCAGAGGATTTGTCTATACCTTA 343
 QY 344 ATGTGATACCAATGACTGGAACCCAGACAAAAGGCGCTGTTATGTTGTTTATCATCAG 403
 DB 344 GTGTCTATACGAATTAATCTTAATCCGGAACCTTAACGTCCGTTTATGATACATCAG 403
 QY 404 GCGAGATTTTATTTTGGGGAAGCAAAATGTAATGTTTGGTCCGACTACTTTATGA 463
 DB 404 GTGTGTTTATTTATTCGGGGAATATCATGATATGATGTTGCTGATTTATTTATTA 463
 QY 464 AGAAGCCCGGTGTGTGTACCGGTGCAATATGTTGGTGTGTGGTGTGGTTCCTTAC 523
 DB 464 AAAAGATGTGTGTGTGATTAACATCAATATGTTGGAGCTTAAGTTTCTAAGTT 523
 QY 524 TGAATGCGAATATCAATATGTCCTCCGCAACGCTGCTCAAGATCAATATGAGCT 583
 DB 524 TAAATTCAGAAAGACTTAATGTCCCGGTATCCGCGCTTAAAGATCAATGATGAGCT 583
 QY 584 TGAGATGGGTCAAGATTAATTTGCAATTTTGGTGGGCAATGTAACATATTTACCTCT 643
 DB 584 TGGGTGATTAATAAATATTTGGCCAACTTTGGTGGCAATCCGATTAATATTTACAGTCT 643
 QY 644 TCGGCGAAATGCTGTGGGGGCGCTCAACCATTAATGATGATACCGAGACAGCCGCTG 703
 DB 644 TTGGTGAAGTGGCGGTGTGGCTCTTACCACTACATGATGATTAACCGAACAACCTGCG 703
 QY 704 GTTATTTCCATGCTGATCATGATGTCGCTTAATTCATATGCTCATGAGCCCTTAAC 763
 DB 704 GTCTTTCCATGCTGATCATGATGTCGCTTAATTCATATGCTCATGAGCCCTTAAT 763
 QY 764 AATGCAAGTGTGTGGCTCAACCTTACGCAACGCTGTGGCTTAAGGAGAGACATG 823
 DB 764 AATGCAAGTGTGTGGCTCAACCTTACGCAACGCTGTGGCTTAAGGAGAGACATG 823
 QY 824 AAAAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 883
 DB 824 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 883
 QY 884 CACAAGTTTGGACACCCGGAAGAAATGCAAAATTAAGTCAATGTTCTTTGGACCCACTG 943
 DB 884 AAAAGTTTAACTCTGAAGAGAGGCTACAAATTAAGTCAATGTTCTTTGGACCCACTG 943
 QY 944 TAGAATCATACACAGACCCAGCTGTGTGTACCCAAACCAATAGAGAAATGTTGAGA 1003
 DB 944 TTGAGCCATATACAGACCCAGCTGTGTGTGTACCCAAACCAATGTTGAGAATGTTGAGA 1003
 QY 1004 GCGGCTGGGAAATTCGATACCATGATGATGATGATGATGATGATGATGATGATGATG 1063
 DB 1004 CTGCTTGGGAAATTCGATACCATGATGATGATGATGATGATGATGATGATGATGATG 1063
 QY 1064 CCAATATCAATTCGCAAAATATCCGAGGTTGTAAGAGTTGGAATCTGTGTGATTT 1123
 DB 1064 TCATCTCAATTCGCAAAATATCCGAGGTTGTAAGAGTTGGAATCTGTGTGATTT 1123
 QY 1124 ATGTGCTTGGAGTG 1183
 DB 1124 TTGTGCTTGGAGTG 1183
 QY 1184 CCAATGTAAGAAAGGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1243
 DB 1184 CTAATATTAAGAAAGGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1243
 QY 1244 TTTGCTCTATTTCTATTTCT 1303
 DB 1244 TTTGCTCTATTTCTATTTCT 1303
 QY 1304 ACAGAGTGGAGCTGATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTA 1363
 DB 1304 ACAGAGTGGAGCTGATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTA 1363
 QY 1364 ACCCTATCTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTA 1423

DB 1364 ATCCCTATCTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTA 1423
 QY 1424 TAACCTATCT 1483
 DB 1424 TAACCTATCT 1483
 QY 1484 AAACATTTGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1543
 DB 1484 AAACATTTGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1543
 QY 1544 GCAATGATATACCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1603
 DB 1544 GCAATGATATACCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1603
 QY 1604 TCTATTAATGTTTAAATTTTGGGCAATGATGATGATGATGATGATGATGATGATGATG 1663
 DB 1604 TATACAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1663
 QY 1664 AATTAACATGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1710
 DB 1664 AGATTTAACAATGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1710

RESULT 5
 US-09-068-960-9
 ; Sequence 9, Application us/09068960A
 ; Patent No. 6235515
 ; GENERAL INFORMATION:
 ; APPLICANT: Commonwealth Scientific and Industrial Resch. Org.
 ; TITLE OF INVENTION: MALATION CARBOXYL ESTERASE
 ; FILE REFERENCE: Attorney Docket No. 6235515 50179-051
 ; CURRENT APPLICATION NUMBER: US/09/068, 960A
 ; EARLIER FILING DATE: 1998-05-20
 ; EARLIER APPLICATION NUMBER: PCT/AU96/00746
 ; EARLIER FILING DATE: 1996-11-22
 ; EARLIER APPLICATION NUMBER: AU 6751
 ; EARLIER FILING DATE: 1995-11-23
 ; NUMBER OF SEQ ID NOS: 43
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 9
 ; LENGTH: 1713
 ; TYPE: DNA
 ; ORGANISM: Lucilia cuprina
 ; US-09-068-960-9

Query Match 55.9%; Score 956.6; DB 4; Length 1713;
 Best Local Similarity 73.4%; Pred. No. 2.4e-304;
 Matches 1223; Conservative 0; Mismatches 444; Indels 0; Gaps 0;

QY 44 TTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 103
 DB 44 TTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 103
 QY 104 TCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 163
 DB 104 TCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 163
 QY 164 ACTAAGTGTGAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 223
 DB 164 ACTAAGTGTGAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 223
 QY 224 CACCCGAGGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 283
 DB 224 CACCCGAGGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 283
 QY 284 CCGTACAGACAGTTCATTAAGTGGCAACCCAGAGTTGGAGATTTGATGATGATGATGATG 343
 DB 284 CAGTGCAGAGTGTGTTTAAATACGGGCAAGGTGTGGCTCAGAGGATTTGATGATGATGATG 343
 QY 344 ATGTGATACCAATGACTGGAACCCAGACAAAAGGCGCTGTTATGTTTATGTTTATGATCATG 403
 DB 344 GTGTCTATACGAATTAATCTTAATCCGGAACCTTAAGTGTCCGTTTATGATACATCATG 403

QY 404 GCGAGATTTTATTTTCGCGAAGCAAACTGTAAGTGGTTGGTCCGCACTACTTTATGA 463
 DB 404 GTGGTGGTTTATATCGGTGAATAATCATGATATGATGATGCTTATTTATTTATTA 463
 QY 464 AAAAAACCGTGGTCTGGTGAACCGTGCATATCTGTTGGGGTGTGGGTTTCTTAAACC 523
 DB 464 AAAAAAGATGGTGGTGAATTAACATACATATCGTTGGGGGCTCTAGTTTCTTAAGT 523
 QY 524 TGAATTCGGAATAATCTCATATGTCGCCGCAACGCTGGGCTCAAGGATGCAATATGGCT 583
 DB 524 TAAATTCAGAAAGACTTATATGTCGCCGTAATGCGGCTTAAGATCAAGTCAATGGCT 583
 QY 584 TGAGATGGGTCAAGATATATGTCATTTGCGTGGGATGAGACAAATTAATCCGCT 643
 DB 584 TGCGTTGGATTAATAATTAATGCGGCAACTTGGGCAATCCGATTAATTTACAGCT 643
 QY 644 TCGGGAAGTGGTGGTGGGCTCAACCACTATCATATGATATACCAAGACACCGCTG 703
 DB 644 TTGGTGAAGTGGCGGTGCTGCTCTACCTACATATGATATTAACCAACCACTGCG 703
 QY 704 GTTATTCATCGTGGTATCATATGATGTCGGTAATTCATGTCGTCATGCGCTCTACAG 763
 DB 704 GTCTTTCATCGTGGTATCATATGATGTCGGTAATGTCATGTCATGTCATGTCATATACC 763
 QY 764 AATGCCAAGTGGTGGTCTACCATGCGCAACGTTGGCTATTAAGGAGAGACATG 823
 DB 764 AATGCCAAGTGGTGGTCTACCATGCGCAACGTTGGCTATTAAGGAGAGATGATG 823
 QY 824 AAAAAATATCTGTAATTTCTTAATGAAGCAATCCATGATGTCATGTCATGTCATGTCATG 883
 DB 824 AATAGATGTTTGGATTTTGAATTTTGAAGCAAGCAAGCAAGATTTAATAAATTTAGG 883
 QY 884 CACAAGTTTACACCCGAAAGAAATGAAGTCAATGTTCCCTTTGGACCACTG 943
 DB 884 AAAAAATTTAATCTGTAATTTCTTAATGAAGCAATCCATGATGTCATGTCATGTCATGTCATG 943
 QY 944 TAGAATCATACCAAGCAAGCAAGTGTGGTGAACCAACCAATGAGAAATGTTAGAGA 1003
 DB 944 TTGAGCCATATCAAGCGGTGATGTTGTTTACCAACCAATCTCGGGAATGTTTAA 1003
 QY 1004 GCGCCTGGGGAATTTGATACCAATGATAGGCAATACCTCTCAAGAGTTGCTT 1063
 DB 1004 CTGCTGGGGAATTTGATACCAATGATAGGCAATACCTCTCAAGAGTTGCTT 1063
 QY 1064 CCAATCAATTTGCAACATATGCGAGTGTGAAGAGTTGGAATCTGTGTGAT 1123
 DB 1064 TCACTCAATTTTAAAGCAATGCTTGTGTTAAGGAATGGAATTTGTGCAAT 1123
 QY 1124 ATGTGCTTGGGATGCTGACAGTGAAGCAAGTGGCGGAAACCTTGAGAGGGCTG 1183
 DB 1124 TTGTGCAAGTGAATGCTGATGCTGATGACGACCGCCAGAGACTTGGAAATGGGTG 1183
 QY 1184 CCAATTTGAAAAAGCCCAATGAGAGGGAACACCTACTCTGATTAATTTTAAAGAG 1243
 DB 1184 CTAATAATTAAGAGCTGATTAAGAGAGAAACACCAAGCTGATTAATTTTAAAGAG 1243
 QY 1244 TTGCTCTGATTTCTATTTCTCTTCCCAATGATGCTTCTCAATTTGCGTTAACC 1303
 DB 1244 TTGCTCTGATTTCTATTTCTCTTCCCAATGATGCTTCTCAATTTGCGTTAACC 1303
 QY 1304 ACACAGTGGCACTCCATTTATTTGATGCTTCAATTTGATTTGCGAAGAAATTA 1363
 DB 1304 ACACAGTGGCACTCCATTTATTTGATGCTTCAATTTGATTTGCGAAGAAATTA 1363
 QY 1364 ACCCTATGATTTATGCTTTGGCGTGGCTTAAGGTGTAAGCAATGCGGATGAGC 1423
 DB 1364 ATCCCTATGATTTATGCTTTGGCGTGGCTTAAGGTGTAAGCAATGCGGATGAGC 1423
 QY 1424 TAACCAATCTCTTGGGAATTTTGTCAAGAGCTGCCAAGAGAAAGCCGCAATTA 1483
 DB 1424 TAACCAATCTCTTGGGAATTTTGTCAAGAGCTGCCAAGAGAAATGCGTGAATTA 1483

QY 1484 AAACATTTGAAGCAGTGGTGGATTTGACAGGAATTTGCGCACACCGCAACCATTA 1543
 DB 1484 AAACATTTGAAGCAGTGGTGGATTTGACAGGAATTTGCGCACACCGCAACCATTA 1543
 QY 1544 GCAATGATATAGCCGCGCATGGAAGAAACCTCACTGGGATCCATTAAGAAATTCGATGATG 1603
 DB 1544 GCAATGATATAGCCGCGCATGGAAGAAATTCCTGGGATCCATTAAGAAATTCGATGATG 1603
 QY 1604 TCTATTAATGTTTAAATATGCGGATGATTAAGTATGATTTGCGAAGAAATGATTA 1663
 DB 1604 TATCAAGTGTGTAATTAATGATGATTAAGTATGATTTGCGTGAAGAAATGATTA 1663
 QY 1664 AAATTAACATAGGCAAGTATGATTAAGTATTAAGAAAGAAATGATTT 1710
 DB 1664 AGATTAACATAGGCAAGTATGATTTGAAAGAAATGATTAATTT 1710

RESULT 6
 US-09-068-960-3
 ; Sequence 3, Application US/09068960A
 ; Patent No. 6235515
 ; GENERAL INFORMATION:
 ; APPLICANT: Commonwealth Scientific and Industrial Resrch. Org.
 ; TITLE OF INVENTION: MALATHION CARBOXYL ESTERASE
 ; FILE REFERENCE: Attorney Docket No. 6235515 50179-051
 ; CURRENT APPLICATION NUMBER: US/09/068,960A
 ; EARLIER FILING DATE: 1998-05-20
 ; EARLIER APPLICATION NUMBER: PCT/AU96/00746
 ; EARLIER FILING DATE: 1996-11-22
 ; EARLIER APPLICATION NUMBER: AU 6751
 ; EARLIER FILING DATE: 1995-11-23
 ; NUMBER OF SEQ ID NOS: 43
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 3
 ; LENGTH: 1713
 ; TYPE: DNA
 ; ORGANISM: Lucilia cuprina
 US-09-068-960-3

Query Match 55.8%; Score 955; DB 4; Length 1713;
 Best Local Similarity 73.3%; Pred. No. 8.2e-304;
 Matches 1222; Conservative 0; Mismatches 445; Indels 0; Gaps 0;

QY 44 TTAATGCAATGCTAATAATAACACAACTACCGTCTGATGATCAATAATGAACCAATA 103
 DB 44 TTAATGCAATGCTAATAATAACACAACTACCGTCTGATGATCAATAATGAACCAATA 103
 QY 104 TCGATACGTAATATGGAACAAATTAAGGTTAAGCAATGACCGTCTACATGATTTCT 163
 DB 104 TCGATACGTAATATGGAACAAATTAAGGTTAAGCAATGACCGTCTACATGATTTCT 163
 QY 164 ACTACAGTTTGCAGATATACCTATGCTAAGCCCTCAGTGGTGAATGATTTCAAG 223
 DB 164 ACTACAGTTTGCAGATATACCTATGCTAAGCCCTCAGTGGTGAATGATTTCAAG 223
 QY 224 CACCCAGGCGCTTACCATGGAAGGTGTACGTGATGCTGTGGGCCACCAAGAT 283
 DB 224 CACCCAGGCGCTTACCATGGAAGGTGTACGTGATGCTGTGGGCCACCAAGAT 283
 QY 284 CAGTCAAGATGATTTTAAACGGCAAGAGTGTGCTCAGAGATGCTATACCTGA 343
 DB 284 CAGTCAAGATGATTTTAAACGGCAAGAGTGTGCTCAGAGATGCTATACCTGA 343
 QY 344 ATGTATATACCAATGACTTGAACCCAGCAAGAGCGCTGTATGATGTTTCAATCATG 403
 DB 344 ATGTATATACCAATGACTTGAACCCAGCAAGAGCGCTGTATGATGTTTCAATCATG 403
 QY 404 GCGGAGATTTATTTTGGCGAGCAATGCTAATGCTGTTGCTGCCGACTACTTATGA 463
 DB 404 GTGGTGGTTTATTAATGCTGAATAATCATGATGATGATGCTGATTAATTTATTA 463
 QY 464 AGAAACCGGTGCTGTGTAACCGTCAATGATGCTTTGGGTGTGGTTTCTTATGCC 523
 DB 464 AGAAACCGGTGCTGTGTAACCGTCAATGATGCTTTGGGTGTGGTTTCTTATGCC 523

Db 464 AAAAGATGATGTTGATTACATCAATATCTGTTGGAGCTCAGCTTTCTAAGT 523
 QY 524 TGAATATGGAATATCTCAATGTCCTGGGCAACGCTGGCTTCAAGATCAATGATGCTT 583
 Db 524 TAAATATGAGACCTTAATATGTCGGGTAAATGTCGCGCTTAAAGATCAAGATGCTT 583
 QY 584 TGAGATGGGTCAAGATATATGTCATTTGCGGTGCGCATATGACATATATACCTCT 643
 Db 584 TGGCTGATTAATAATATGTCGCACTTGGGCAATCCGATATATATACAGTCT 643
 QY 644 TCGCGGAAGTCTGGTGGGCTCAACCATATGATATGATTAACGCAAGACCGCTG 703
 Db 644 TTGGTGAAGTGGCGGTGCTCTTACCATGATGATTAACGCAAGACCGCTG 703
 QY 704 GTTATTCATCTGATATCATGATGTCGGTATTCATATGCTCATTTGGGCTCTACAG 763
 Db 704 GTCTTTCCATCTGATATCATGATGTCGGTATTCATATGCTCATTTGGGCTCTACAG 763
 QY 764 AATGCCAAGTGTGCGCTCAACCATGTCGCAACGCTGCTATTAAGGAGACATG 823
 Db 764 AATGTCATCATGTCGCTCAACCATGTCGCAACGCTGCTATTAAGGAGATATG 823
 QY 824 AAAAGATATCTGGAATCTTATGAAAGCCATTCCTATGATTTGATCAAGAGAGC 883
 Db 824 ATTAAGATGTTTGAATTTCTTATGAAAGCCATTCCTATGATTTGATCAAGAGAGC 883
 QY 884 CACAGTTTGCACCCGCAAGATGCAAAATATGATGTTCTTTGGACCCACTG 943
 Db 884 AAAAGTATTAATCTTAAGAGAGCTTCAAAATATGATGTTCTTTGGACCCACTG 943
 QY 944 TAGACCATACAGAGAGAGCTGCTGATCCCAACCAATCAAGAAATGATGAAGA 1003
 Db 944 TTGAGCATATCAGAGAGAGCTGCTGATCCCAACCAATCAAGAAATGATGAAGA 1003
 QY 1004 GCGCTGGGAAATGATATCCCAATGATAGCAATATCTGCAAGAGGTTGCTT 1063
 Db 1004 CTGCTGGGAAATGATATCCCAATGATAGCAATATCTGCAAGAGGTTGCTT 1063
 QY 1064 CCAATATGATGCAAAATATCCGAGGTTGTAAGAGTTGGAATCTGCTGATTT 1123
 Db 1064 TCACTTCAATCTTAAGCAAAATGCTTCTTGAAGATGGAATCTGCTGATTT 1123
 QY 1124 ATGTCCTGGAGTGGCTGACAGAGAGTGGCGGAAACCTGGAAGAGGCTG 1183
 Db 1124 TTGTGCAAGTGAATGGCTGATGCTGACAGAGAGTGGCGGAAACCTGGAAGAGGCTG 1183
 QY 1184 CCATGTAAGAAAGCCATGATGAGGGAACACCTACTCTGATATATTTATGAGC 1243
 Db 1184 CTAAATTAAGAAAGCCATGATGAGGGAACACCTACTCTGATATATTTATGAGC 1243
 QY 1244 TTTGCTCTATTTCTTCT 1303
 Db 1244 TTTGCT 1303
 QY 1304 ACACAGCTGGACCTCCATTTATTTGATCGTTTGGATTTGATTTGCAAGAAATTTT 1363
 Db 1304 ACACAGCTGGACCTCCATTTATTTGATCGTTTGGATTTGATTTGCAAGAAATTTT 1363
 QY 1364 ACCCTATGATATGAGCTTTTGGCGGTAAAGGTATGAGCCTGATGAGC 1423
 Db 1364 ATCCCTATGATATGAGCTTTTGGCGGTAAAGGTATGAGCCTGATGAGC 1423
 QY 1424 TAACTATCTCTCTGGAACATTTTGTGCAAGAGCTGCAAGAGAAAGCCGCAATCA 1483
 Db 1424 TAACTATCTCTCTGGAACATTTTGTGCAAGAGCTGCAAGAGAAAGCCGCAATCA 1483
 QY 1484 AAACATTTGAACGATTTGAGCAATTTGCAAGAGCTGCAAGAGAAAGCCGCAATCA 1543
 Db 1484 AAACATTTGAACGATTTGAGCAATTTGCAAGAGCTGCAAGAGAAAGCCGCAATCA 1543
 QY 1544 GCAATGATATAGCGGATGGAAGAAACCTCACTGAGATCCATATAAAATCCGATGATG 1603
 Db 1544 GCAATGATATAGCGGATGGAAGAAACCTCACTGAGATCCATATAAAATCCGATGATG 1603

QY 1604 TCTATTAATGTTTAAATATCGCGGATGAATGAAATGATGATTTGCCAGAAATGATA 1663
 Db 1604 TATCAAGTGTGGAATATGATGATGAAATGAAATGATGATGCTGAAATGAGATA 1663
 QY 1664 AAATTAACATGCGCAAGATATGATTAAGAAAGAAAGAAATGTTT 1710
 Db 1664 AGATTAACATGCGAGTGTGTTGAAAAACATAGATGATTTATTT 1710

RESULT 7

US-08-669-524-2

Sequence 2, Application US/08669524

Patent No. 5843758

GENERAL INFORMATION:

APPLICANT: RUSSELL, Robyn J.

APPLICANT: NEWCOMB, Richard D.

APPLICANT: BOYCE, Geoffrey C.

APPLICANT: CAMPBELL, Peter M.

APPLICANT: PARKER, Anthony G.

APPLICANT: OAKESHOT, John G.

APPLICANT: SMYTH, Kerrie A.

TITLE OF INVENTION: ENZYME BASED BIOREMEDIATION

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Lowe Price Leblanc & Becker

STREET: 99 Canal Center Plaza, Suite 300

CITY: Alexandria

STATE: Virginia

COUNTRY: USA

ZIP: 22314

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/669,524

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Price, Robert L.

REGISTRATION NUMBER: 22,685

REFERENCE/DOCKET NUMBER: 1451-021

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-684-1111

TELEFAX: 703-684-1124

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1713 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-669-524-2

Query Match

Best Local Similarity

Matches 1209; Conservative

55.7%; Score 952.2; DB 2; Length 1713;

72.5%; Pred. No. 6.8e-303;

0; Mismatches 458; Indels 0; Gaps 0;

QY 44 TTAATGCTATGCTATTAATACAACTACCTGATGATCAAAATGAAGAAATCAATA 103
 Db 44 TTAATGCTATGCTATTAATGCTATTAATGCTATTAATGCTATTAATGCTATTAAT 103
 QY 104 TCGATATGATATGCAAAATTAAGGCTTAAAGCAATGACGCTCAAGATGATCTT 163
 Db 104 CTGAATCTGAATATGCAAAATTAAGGCTTAAAGCAATGACGCTCAAGATGATCTT 163
 QY 164 ACTACATTTGAGAGATATACCTATGCTAAAGCTTCAAGTGGATGATGATCAAG 223
 Db 164 ACTACATTTGAGAGATATACCTATGCTAAAGCTTCAAGTGGATGATGATGATTAAG 223

QY	224	CACCCCGGGGGCTGTACCATGGAAGGGTGTACGTATGTTCTGTGGGCCAGCCACGAT	28
Db	224	CACCCCGGGCACCAACACCCCTGGATGGTGTGGCTGATTTGTGCATCTAATAAGTAACT	28
QY	284	CGGTACGACAGATTTTCATTAAGTGGCAACCCACAGTTTCGGAGCATTTGTCTATCTGA	34
Db	284	CAGTGCAGAGTGAATTTTANMONGCAAGGTGTGGCTCGAGAGATGTCTATACCTAA	34
QY	344	ATGTGATTCACATGACTTTGAACCCAGACAAAGGGGCTCTGTATAGTTTTCATCCATG	40
Db	344	GNTCTATACGATATATCTAAATCCCAAACTAAAGCTCCGTTTATATACATACATG	40
QY	404	GGGAGATTTTATTTTCGGCAACGAATATGTAAGTGGTTGGTCCGACTACTTATGA	46
Db	404	GTGGTGNATTTTATATCGGTGAAATATGCTGNTATGATGGTCTGATTAATTTCAATA	46
QY	464	AGAAACCCGGTCTGTGTAAACCGTGCATATATGTTGGGTGTGTGGTTTCCCTTGGCC	52
Db	464	AAAGAGATGTGGTGTGTATACATACAAATATCTGTTGGAGCTCTAGTTTCTAAAGTT	52
QY	524	TGAAATCGAAATATCTAATGTCCCGGACAGCTGGGCTCAAGATCAAGTATAGCCT	58
Db	524	TAAATTCAGAAAGACTTAATGTGCCNGTAAATGCCGGCTTAAAGATCAAGTATAGCCT	58
QY	584	TGAGATGGGTCAAGATTAATATGCAATTTTGCTGGCGATGAGACAAATATACCGTCT	64
Db	584	TGCGTGGATTTAAATAATATATGGCCCAATTTGGTGGCAATCCGATATATTAACGCT	64
QY	644	TGGCGAAAGTGTGTGTGGGGCTCAACCATATCATATGATATACCGAAGACCCGTG	70
Db	644	TTGGTGAAGCTGGCGGTGCTGCCTCAACCACTATGATGTTTACCGAACAACCTCGG	70
QY	704	GTTATTTCCATGCTGATACATGATGCTCCGTAATTCATGTCTCATGGGCTCTACAG	76
Db	704	GCTTTTCCATGCTGATATACAAATGTTGGGTAAATGCTATTTNCCATGGGCTTAATACC	76
QY	764	AATGCCAAAGTGTGTGGCTCACATGAGCCAAACCTGTTGGCTTAAGGAGAGGCATAATG	82
Db	764	AATGTCAACATGCTGCTTCACCTTAGCCAAATTTGGCCGCTTAAGGGTGGAGTAATG	82
QY	824	AAAAAGTATCCGGAATTTCTAATGAAGCCATCCCTATGTTGATCAAGAGGAGC	88
Db	824	ATAGGATGTTTGGANATTTCTTTGAAGCCAAAGCCACAGATTTAATAAACTGAGC	88
QY	884	CACAGTTTTCACCCGAAGAATGCAAAATAGCATATGTTCTTTTGACCCACTG	94
Db	884	AAAAATTTTAACTCTAGAAAGGCTACAAATTAAGTCAATGTTCTTTTGCTCCACTG	94
QY	944	TAAACATACACAGACGCGACTGTGTGTCACCAACCAATCAGAAATAGGTGAAGA	100
Db	944	TTBANCATATACGCGGTATGTGTCTTACCCAAACATCTCGGSAATGTTTAAN	100
QY	1004	GGCGTGGGAATTCGATACCCACATGTAATGTAAGGCAATACCTCCACGAAAGTTGCTT	106
Db	1004	NTGCTTGGGGTAATTCGATACCCACATATAGGTGTAACCTTCATATAGAGGCTATTTT	106
QY	1064	CCAAATCAATGCCAAACATATCCGGAAGTGTAAAGAGTGGAAATCCTGTGTAATT	112
Db	1064	TCACCTCANNITCTTAACCAATCCCTATCTGTTAAGGAATGGAACTTGTGTCAAT	112
QY	1124	ATGTGCTTGGAGATTTGGCTGACAGAGTAAGGAGTGGCCCGGAACCTGTGAGAGGGCTG	118
Db	1124	TTTGCCCAAGTAATTTGGCTGACTGTAAGACGACCGGCCACGAAACCTTTGGAAATGGGTG	118
QY	1184	CCATTTGAAAAAAGGCCCATGTGTGATGGGGAACACCTACTCTGGATAATTTATGAGAC	124
Db	1184	CTTAAATTTAAAAAGGCTCATGTTACAGAGAAACCAACGACGNGATATTTTATGAGATC	124
QY	1244	TTTGCTCTATTTTCTATTTTCCCTCCGCAATGCACTGCTTCTACATATGCGCTTCAAC	130
Db	1244	TTTGCTCTGACATCTATTTCTGTGTGCCCAAGCAATGCTTTNTTGCATATACCTTCAATC	130
QY	1304	ACACAGCTGGCACTCCCAATTAATTTGATGCTTTCGATTCGGAAGAAATATATA	136

Db	1304	ACMCCGCGGATACACCCGCTCTCTGATCGCTTGAGATTNGATTCGGAAAGATCTTATTA	136
Qy	1364	ACCCCTATGCTATATATGCGTTTGGCCGTGCGCTTAAAGCTGTAAAGCATGCGGATGAGC	142
Db	1364	ATCCCTATGTAATATGCGTATGATGACGTGCTGTTTAAAGGCTGTAGTCATGCTGATGAAT	142
Qy	1424	TAACTTATCTCTTCGGAACATTTTGTGTGAAGCCCTGCCAAAGAAAGCCGGAATACA	148
Db	1424	TAACTTATCTCTTCGGAATCAATTTGCCCAACGTAATCCCTAAAGATCNCGTGAATACA	148
Qy	1484	AAACCATGGAACGCATGCTGTGGCAATTTGGACGGAATTCGCCACACCGGCAATACATA	154
Db	1484	AAACCATTTGAACGTAATGCTGCTGTATGATGATACAAATTTGCCACACCTGCTATCCTTATA	154
Qy	1544	GCAATGATATAGCCGGCATGGAAACCTCACCTCGGGATCCCATMAAAATATCCGATGTG	160
Db	1544	GCAATGAATATGAAGGTAATGGAATAATGTTCTCTGGGATCMAATTTAAGAAATCCGANGAAG	160
Qy	1604	TCTATTAATGTTTAAATATGCGCGGATGAATGAAAGTTATGGAATTTGCAGAAATATGATA	166
Db	1604	TATTAAGTGTGTAATATTTAAGGANGAATGTGAAATGATGATNGCCTGAANAATGATA	166
Qy	1664	AAATTAACAATGGCGAAGTATATTGAGTATMAAAAGAAGAAATTTGTT	172
Db	1664	AGATTAACAATGGGAATGCATGTTTGAANAACCATAGAGATTATTT	172

RESULT 8
 US-09-068-960-5
 Sequence 5' A235515
 Patent No. 6235515
 GENERAL INFORMATION:
 APPLICANT: Commonwealth Scientific and Industrial Resrch. Org
 TITLE OF INVENTION: MALATHION CARBOXYL ESTERASE
 FILE REFERENCE: Attorney Docket No. 6235515 50179-051
 CURRENT APPLICATION NUMBER: US/09/068,960A
 CURRENT FILING DATE: 1998-05-20
 EARLIER APPLICATION NUMBER: PCT/AU96/00746
 EARLIER FILING DATE: 1996-11-22
 EARLIER APPLICATION NUMBER: AU 6751
 EARLIER FILING DATE: 1995-11-23
 NUMBER OF SEQ ID NOS: 43
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 5
 LENGTH: 1713
 TYPE: DNA
 ORGANISM: *Lucilia cuprina*
 US-09-068-960-5

Query Match	55.78;	Score 951.8;	DB 4;	Length 1713;
Best Local Similarity	73.28;	Pred. No. 9.3e-303;		
Matches 1220; Conservative	0;	Mismatches 447;	Indels 0;	Gaps 0

QY	44	TTAAATGCATGTCATTAATATACAAACCTACCGTCGTAGTACCAATGAACCAACCAATAA	10
Db	44	TTAAATGCATTAAGAAATAATTTTAAATACGTCTTAACCAATGAACCAACGTGTG	10
QY	104	TCGATCTGAATATGACAAATTAAGGGGTGTTAACCGAATGACCGCTCATGATCTTCT	16
Db	104	CTGAACCTGATATGCGCAAGTGAAGGGGTAAACGTTTAACTGTGTGATGATCTCT	16
QY	164	ACTACAGTTTCGAGATATACCTTATGCTAAGCTTCCAGTGGGTGATTTGATTTCAAG	22
Db	164	ACTACATTTTGGAGGTATACCGTACGCGCCACGCGCAAGGGGTGAGCTGATTTAAG	22
QY	224	CACCCACGCGCCTGTACCATGGAGGGTGTACCTGATTTCTGTGGCCAGCCACACAT	28
Db	224	CACCCACGCGCCACACACCCCTGGGTGCTGTGCTGATTTGTCATCATCTAAGATTAAGT	28
QY	284	CGGTACAGACAGATTTTCATTAATGTGCACAACCCACAGGTTCGAGAGATTTCTATTCCTGA	34
Db	284	CAGTGCAGGTGATTTTATTAAGGGCAAAAGTGTGTGCTCTAAGAGATTTCTATTAACCTAA	34

```

OY 344 ATGTATACCAATGACTTGAACCCAGACAAAGGCGCTGTTATGGTTTCAATCCATG 403
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 344 GTGTATACCAATGACTTGAACCCAGACAAAGGCGCTGTTATGGTTTCAATCCATG 403
OY 404 GCGGAGATTTTATTTTTCGCGGAGCAATGTAACGTGTTTGTCCGACTACTTATGA 463
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 404 GTGTGTTTATTTATTCGTAATTAACATGATATGATGATGATGATGATGATGATG 463
OY 464 AGAAACCGGTGTCTGTGTATACCGTGAATATCGTTGGGTGTGTGGTTTCCCTAGCC 523
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 464 AAAAGATGTGTGTGTATTAACATTAATATCGTTGGGAGTCTAGGTTTCTAGGTT 523
OY 524 TGAATTCGGAATATCTCAATGTCGCCGAGCGCTGAGGCTGAAGGTAAGTAATGGCT 583
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 524 TAAATTCAGAAAGACTTATATGTCGCCGTAATGCCGCTTAAGATCAATGATGCT 583
OY 584 TGAGATGGGTGAGATATATTTGCCATTTTGGTGGGATGATGATGATGATGATGATG 643
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 584 TGCAATGGATTAATAATATATGCGCAACTTGGTGGCAATCCGATTAATTAAGAGCT 643
OY 644 TCGGGAAGATGTGTGTGGGCGCTCAACCCATTAATATATATATATATATATATATG 703
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 644 TTGGTGAAGTGTGGGCGCTGCTGCTACCACTACATGATGATGATGATGATGATGATG 703
OY 704 GTTATTCATGTCGTATCAATGATGTCGGTAATTCATGTCGTCATGTCGTCATGAG 763
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 704 GTCTTTTCATGTCGTATCAATGATGTCGGTAATTCATGTCGTCATGTCGTCATGAG 763
OY 764 AATGCCAAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 823
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 764 AATGCCAAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 823
OY 824 AAAAAGATATCTGGAATTTCTAATGAAGGCAATCCATGATGATGATGATGATGATG 883
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 824 ATAGGATGATTTTGAATTTCTTATGAAGGCAAGCAAGATTTAGTAATGATGATG 883
OY 884 CACAAGTTTGAACACCCGAAAGAAATGCAAAATAGATGATGATGATGATGATGATG 943
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 884 AAAAAGTTTGAACACCCGAAAGAAATGCAAAATAGATGATGATGATGATGATGATG 943
OY 944 TAGAAGCATACAGACAGCGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1003
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 944 TTGAGCCATATACAGACCGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1003
OY 1004 GCGCTGGGAAATTCATACCCATGATGATGATGATGATGATGATGATGATGATG 1063
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1004 CTGCTGGGAAATTCATACCCATGATGATGATGATGATGATGATGATGATGATG 1063
OY 1064 CCAATATCAATTCGCAAAATATCCGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1123
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1064 TCACATCAATTCGCAAAATATCCGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1123
OY 1124 ATGTGCTTGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1183
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1124 TTGTGTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1183
OY 1184 CCATTTGAAAAAGGCGATGATGATGATGATGATGATGATGATGATGATGATGATG 1243
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1184 CTAATATTAAGGCGATGATGATGATGATGATGATGATGATGATGATGATGATG 1243
OY 1244 TTGTGCTATTTCTATTTCTTCCCATGATGATGATGATGATGATGATGATGATG 1303
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1244 TTGTGCTATTTCTATTTCTTCCCATGATGATGATGATGATGATGATGATGATG 1303
OY 1304 ACACAGCTGGACATCCATTTATTTGATGATGATGATGATGATGATGATGATGAT 1363
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1304 ACACAGCTGGACATCCATTTATTTGATGATGATGATGATGATGATGATGATGAT 1363
OY 1364 ACCCTATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1423
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1364 ATCCCTATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1423

```

```

OY 1424 TAACCTATCTCTCTGTGACATTTTGTGGAAGCGCTGCCAAAGAAAGCGGATATGA 1483
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1424 TAACCTATCTCTCTGTGGAATTAATGCGCAAGGATGATGCTTAAGAAATGCGGATATGA 1483
OY 1484 AAACCATTTGAAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1543
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1484 AAACCATTTGAAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1543
OY 1544 GCAATGATATAGCGCATGGAAGAACTCACTGGGATGATGATGATGATGATGATG 1603
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1544 GCAATGATATTTGAAGGATGATGATGATGATGATGATGATGATGATGATGATG 1603
OY 1604 TCTATTAATGTTTAAATATGCGGATGATGATGATGATGATGATGATGATGATG 1663
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1604 TATTAAGATGTTTGAATATTTAGATGATGATGATGATGATGATGATGATGATG 1663
OY 1664 AAATTAACATGCGCAAGATATTTGATGATGATGATGATGATGATGATGATG 1710
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1664 AGATTAACATGCGCAAGATGATGATGATGATGATGATGATGATGATGATGATG 1710

```

RESULT 9

US-08-747-221B-51

; Sequence 51, Application US/08747221B

; Patent No. 6063610

; GENERAL INFORMATION:

; APPLICANT: Silver, Gary W.

; TITLE OF INVENTION: No. 6063610e1 Carboxylesterase Nucleic Acid

; NUMBER OF SEQUENCES: 66

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Carol Talkington Verser, Ph.D.

; ADDRESS: Hesk Corporation

; STREET: 1825 Sharp Point Drive

; CITY: Fort Collins

; STATE: Colorado

; COUNTRY: USA

; ZIP: 80525

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: Windows 95

; SOFTWARE: Wordperfect for Windows, Version 7.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/747,221B

; FILING DATE: No. 6063610e1 December 12, 1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Verser, Carol Talkington

; REGISTRATION NUMBER: 37,459

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 970/493-7272

; TELEFAX: 970/484-9505

; INFORMATION FOR SEQ. ID NO: 51:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1584 nucleotides

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..1584

; US-08-747-221B-51

Query Match 9.5%; Score 162.6; DB 3; Length 1584;
 Best Local Similarity 55.8%; Pred. No. 4.5e-43;
 Matches 334; Conservative 0; Mismatches 259; Indels 6; Gaps 1;
 OY 125 TTAAAGGTGTAAAGCAATGACCGCTACGATGATCTTACTACAGTTTCGAGAGTATATAC 184
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

Db      38 TAAAGGAAAGAGCAAAATTAGTGAAGAAAGAAATGTGTTCCATAGTATTTCGTGAATTC 97
QY      185 CCTATGTAAGCCTCCAGGAGGTGAGTGAATTCAGGACCCAGCGGCTGTACCAT 244
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      98 CATATGCCAAACCTCCTAGTGTATCTTAAGATTTAAGCCACCTCACTGAGAACTT 157
QY      245 GGGAGGGTGTACGTATGCTGTGGGCCAGCAACAGATCGGTACAGACATTTTCATA 304
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      158 GGTGAGGTGTTCTTATGCTAGTAAGAAAGGAAATAGTGTGATCAGTACATTTATTA 217
QY      305 GTGGCAAAACCCAGAGTTCGGAGATGTCTATACCTGATGTGTATACCATGACTTA 364
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      218 AAAAAATTAAAGTGGGCTGAAGATGTTTATACCTCAATGTCTATGACCAAAAAACAT 277
QY      365 ACCGAGCAAAAGGCGCTCTTATGTTTATCATCCATGCGAGATTTTATTTTCGGC 424
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      278 CAGAGAAATCACTTCTTCCAGTAATGTATGATACATGAGAGAGGCTTCTCATGAGAT 337
QY      425 AAGCAATCGTAACGTGTTGGTCCCGACTACTTATGAAGAAACCCGTGCTTGTAA 484
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      338 CTGAAATATGATATGATGTGCTCGAATATTGATGATTAAGAAATGTTCTGTGTA 397
QY      485 CCGTCAATATGTTGGGTGTGTTGGTCTTACCTGAATCGGAAATCTCAATG 544
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      398 CTTCAATATGATTAAGTGTGTTGGGATTTTGAACCTGGGAAATGAAGAA-----G 451
QY      545 TCCCGGAGAGCGTGGCCCAAGGATCAAGTAATGCGCTTGAGATGGGCAAGATATA 604
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      452 CCGCTGGCAATGTTGTTGATGAGCAGGTTGAAGCTTAAATGGTAAAAACAAATA 511
QY      605 TTGCAATTTCCGTGCGCATGTAGACAAATATTACCGTCTTCGCGGAAAGTGTGGGG 664
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      512 TTGCATCCTTTGGTGTGACCCCAACATGTGACTATTTTGGAGATCAGCAGGTGGTG 571
QY      665 CCTCAACCATTAACATGATGATACCGAAGACCGGTGTTTATTCATCGGTATC 723
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      572 CAAGTGTCTATTATTTGATGATTATCAGATCTTCCAAAGACTTTTTCATTAAGCGATC 630

```

RESULT 10

US-08-747-221B-52/c
Sequence 52, Application US/08747221B

Patent No. 6063610

GENERAL INFORMATION:

APPLICANT: Silver, Gary W.

APPLICANT: Wisniewski, Nancy

TITLE OF INVENTION: No. 6063610e1 Carboxylesterase Nucleic Acid

NUMBER OF SEQUENCES: 66

CORRESPONDENCE ADDRESS:

ADDRESSEE: Carol Talkington Verser, Ph.D.

ADDRESS: Heska Corporation

STREET: 1825 Sharp Point Drive

CITY: Fort Collins

STATE: Colorado

COUNTRY: USA

ZIP: 80525

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: Windows 95

SOFTWARE: Wordperfect for Windows, Version 7.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/747/221B

FILING DATE: No. 6063610e1ember 12, 1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Verser, Carol Talkington

REGISTRATION NUMBER: 37/459

REFERENCE/DOCKET NUMBER: FC-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 970/493-7272

TELEFAX: 970/484-9505

```

; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1584 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-747-221B-52

```

Query Match 9.5%; Score 162.6; DB 3; Length 1584;

Best Local Similarity 55.8%; Pred. No. 4.5e-43;

Matches 334; Conservative 0; Mismatches 259; Indels 6; Gaps 1;

```

QY      125 TTAAGGGTTAAGCGAATGACCGTCTACGATTTCTTACTACAGTTTCGAGATATAC 184
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1547 TAAAGGAAAGAGCAAAATTAGTGAAGAAAGAAATGTTCCATAGTATTTCGAAATTC 1488
QY      185 CCTATGCTAAGCCTCCAGTGGGTGAGTTGAGATTCAGAGCACCAGCGGCTGTACCAT 244
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1487 CATATGCCAAACCTCCTGTAGTGTATGATCTAAGATTTAAGCCACCTCACTGAGAACTT 1428
QY      245 GGGAGGGTGTACGTGATGTTCTGTGGGCCAGCAACAGATCGGTACAGACATTTTCATA 304
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1427 GGTACAGTGTCTTGTATGCTAGTAAGAAAGGAAATGTTGATACATGATACATTTATTA 1368
QY      305 GTGGCAAAACCAAGAGTGTGGAGGATGTCTATACCTGATGTGTATACCAATGACTTA 364
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1367 AAAAAATTAAAGTAGGCGCTGAAGATGTTTATACCTCAATGTCTATGACCAAAAAACAT 1308
QY      365 ACCGAGCAAAAGGCGTCTCTGTATGTTTATCATCCATGGCGAGATTTATTTTCGGGG 424
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1307 CAGAGAAATCACTTCTTCCAGTAATGTATGATACATGAGAGGCTTCTCATGAGAT 1248
QY      425 AAGCAATCGTAACGTGTTGGTCCCGACTACTTATGAAGAAACCCGTGCTTGTAA 484
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1247 CTGGAATATGATATGATGTATGCTCGAATATTGATGATTAAGAAATGTTCTGTGTTA 1188
QY      485 CCGTCAATATGTTGGGTGTGTTGGTTCCTTAGCCTGAATCGGAAATCTCAATG 544
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1187 CTTCAATATGATTAAGTATGATGTTTGGGATTTTGAACCTGGGAAATGAAGAA-----G 1134
QY      545 TCCCGGCAACGCTGGCCCAAGATCAAGTATGAGCCTTGAGATGGGCAAGATATA 604
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1133 CCGCTGGCAATGTTGGTGTGATGAGCAGATATTACCGTCTTCGCGGAAAGTGTGGGG 1074
QY      605 TTGCAATTTCCGTGCGCATGTAGACAAATATTACCGTCTTCGCGGAAAGTGTGGGG 664
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1073 TTGCATCCTTTGGTGTGTAACCCCAACATGTGACTATTTTGGAGATCAGCAGGTGGTG 1014
QY      665 CCTCAACCATTAACATGATGATACCGAAGACCGGTGTTTATTCATCGGTATC 723
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1013 CAAGTGTCTATTATTTGATGATTATCAGATCTTCCAAAGACTTTTTCATTAAGCGATC 955

```

RESULT 11

US-09-005-051-51
Sequence 51, Application US/09005051

Patent No. 6291222

GENERAL INFORMATION:

APPLICANT: Silver, Gary W.

APPLICANT: Wisniewski, Nancy

TITLE OF INVENTION: No. 6291222e1 Carboxylesterase Nucleic Acid

NUMBER OF SEQUENCES: 66

CORRESPONDENCE ADDRESS:

ADDRESSEE: Carol Talkington Verser, Ph.D.

ADDRESS: Heska Corporation

STREET: 1825 Sharp Point Drive

CITY: Fort Collins

STATE: Colorado

COUNTRY: USA

ZIP: 80525

COMPUTER READABLE FORM:

```

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordperfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,051
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/747,221
FILING DATE: No. 6291222member 12, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: PC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 1584 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1584
US-09-005-051-51

```

```

Query Match          9.5%; Score 162.6; DB 4; Length 1584;
Best Local Similarity 55.8%; Pred No. 4.5e-43;
Matches 334; Conservative 0; Mismatches 259; Indels 6; Gaps 1;

```

```

125 TTAAGGTTTAAAGCAATGACCGTCTACAGATGATTCTTACTACAGTTTCGAGATATAC 184
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
38 TAAAGGAAAAGAGCAAAATTAAGAAAAGAAATGTGTTCCATAGTTATTCGTGAAATTC 97
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
185 CCTATGTAAGCTCCAGTGGGTGAGTGTGATGATCAAGGACCCGAGGCGCTGTACAT 244
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
98 CATATGCAAAACCTCTGATGATCAATTAAGCACTCAACCTCAACCTGCAAAACCTT 157
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
245 GGGAGGTTAGCTGATTTGCTGGGCGACCAACAGATCGTACAGACAGATTTCTATA 304
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
158 GGTGAGTGTCTTGTAGCTAGTAAGAAAGGAAATGTTAGATCAGTACATTTATTA 217
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
305 GTGGCAAAACCCAGGTTGCGAGGATTTCTATACCTGATGTATACCAATGACTTGA 364
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
218 AAAAAATTAAAGTAGGGGCTGAAGATTTTATACCTCAATGTCTATGTAACCAAAACAT 277
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
365 ACCAGCAAAAGCGCTCCGTGATATGTTTTCATCCATGCGGAGATTTATTTTCGGCG 424
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
278 CAGAGAATCACTTCTCCAGTAATGATGATACATGAGAGGCTTCTTCATGGAT 337
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
425 AAGCAATGTAAGTCTGTTGGTCCGACTACTTTATGAAGAAACCCGTGCTTGTATA 484
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
338 CTGAAATAGATATGTATGATGCTGATATTTGATGATTAATGAAATGTTCTGTGTTA 397
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
485 CCGTCAATATCTGTTGGGTGTGTTGGTTCCTTACCTGGAATCGGAAATCTCATG 544
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
398 CTTTCAATTAATGATTAAGGCTGTTTGGATTTTGAACCTGGGAAATGAAGAA-----G 421
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
545 TCCCGGCAACGCTGGGCTCAGAGATCAAGTAATGGCTTGAGATGAGTAAGAGTATA 604
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
452 CGCTGGCAATGTTGTTGATGAGACAGGTGGAAGCTCTAATAATGGTAAAAACATA 511
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
605 TTGCCATTTTCGTTGGGATGACAAATATACCGTCTTCCGCGAAAGTCTGGTGGG 664
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
512 TTGATCCTTGTGGTGAACCCCAACAATGATGATTTTGGAGATCAAGAGGTGGTG 571
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
665 CCTCAACCATATGATGATTAACCAAGACAGACCCGCTGTTTATCCATCGTGTATC 723
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
572 CAAGTTCATTAATGATTAATCAAGATCTTTCAAAAGACCTTTTCAATAAACGATC 630
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

```

```

RESULT 12
US-09-005-051-52/c
; Sequence 52, Application US/09005051
; Patent No. 6291222
GENERAL INFORMATION:
APPLICANT: Silver, Gary W.
APPLICANT: Wisniewski, Nancy
TITLE OF INVENTION: No. 6291222el Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heka Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordperfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,051
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/747,221
FILING DATE: No. 6291222member 12, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: PC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 1584 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-005-051-52

```

```

Query Match          9.5%; Score 162.6; DB 4; Length 1584;
Best Local Similarity 55.8%; Pred No. 4.5e-43;
Matches 334; Conservative 0; Mismatches 259; Indels 6; Gaps 1;

```

```

125 TTAAGGTTTAAAGCAATGACCGTCTACAGATGATTCTTACTACAGTTTCGAGATATAC 184
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
1547 TAAAGGAAAAGAGCAAAATTAAGAAAAGAAATGTGTTCCATAGTTATTCGTGAAATTC 1488
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
185 CCTATGTAAGCTCCAGTGGGTGAGTGTGATGATCAAGGACCCGAGGCGCTGTACAT 244
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
1487 CATATGCAAAACCTCTGATGATCAATTAAGCACTCAACCTCAACCTGCAAAACCTT 1428
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
245 GGGAGGTTAGCTGATTTGCTGGGCGACCAACAGATCGGTACAGACAGATTTCTATA 304
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
1427 GGTGAGTGTCTTGTGATGCTAGTAAGAAAGGAAATGTTGATGATCAGTACATTTATTA 1368
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
305 GTGGCAAAACCCAGGTTGCGAGGATTTCTATACCTGATGTATACCAATGACTTGA 364
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
1367 AAAAAATTAAAGTAGGGGCTGAAGATTTTATACCTCAATGATGATTAACCAAAACAT 1308
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
365 ACCAGCAAAAGCGCTCTGTTATGTTTATCATCATGCGGAGATTTATTTTCGGG 424
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
1307 CAGAGAATCACTTCTCCAGTAATGATGATACATGAGAGGCTTCTTCATGAGGAT 1248
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
425 AAGCAATGTAAGTCTGTTGGTCCGACTACTTTATGAAGAAACCCGTGCTTGTATA 484
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

```


SEQUENCE CHARACTERISTICS:
LENGTH: 2007 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-747-221B-38

Query Match 9.5%; Score 162.6; DB 3; Length 2007;
Best Local Similarity 55.8%; Pred. No. 5.3e-43;
Matches 334; Conservative 0; Mismatches 259; Indels 6; Gaps 1;

125 TTAAGGGTGAATGAGTACGCTCTACATGATTTCTTACTACAGTTTCAGAGTATAC 184
1960 TAAAGGAAAGCAATATGTAAGAAAGAAATGTTCCATAGTTATCTCGAATTC 1901
185 CCTATGTAAGCCTTCAGTGGGTAGTGAATTCAGAGCCAGCCAGGCGCTTACCAT 244
1900 CATATGCCAAACCTCTGTAGTATCTTAAGATTTAAGCCCTCAACCTGACAGACCTT 1841
245 GGGAGGGTGTACGATGCTGTGGGCCAGCCACAGATCGTACAGACAGATTTCAATA 304
1840 GGTCAAGTGTCTTGATCTGTAGTAAGAGGAATAGTTAGATCACTATTTTATTA 1781
305 GTGGCAAAACCCAGGTTGAGGAGATTTCTATACCTGAATGTATACCAATGACTTGA 364
1780 AAAAATTAAGTAGGGGCTGAAGATTTGTATACCTCAATGCTATGACCAAAACAT 1721
365 ACCAGACAAAAGGCGCTCTGTATGTTTCACTACAGGCGGAGATTTTTCGGCG 424
1720 CAGAGAAATCACTTCTTCAGTATGATGATACATGAGGAGGCGCTTCTTCATGGAT 1661
425 AAGCAATGTAACGTTGGTCCGCTACTTATGTAAGAAACCCGCTGCTGTGTA 484
1660 CTGAAATAGTATGATGATGATGCTCTGAATTTGATGATGATGATGATGATGATGAT 1601
485 CCGTCAATATGCTTTGGGTGTTGGGTCTTCTTACCTGAAATCGGAAATCTCATG 544
1600 CTTCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1547
545 TCCCGGAGAGCGCTGCTCAAGATCAAGTATGAGCTTGAAGTGGTCAAGATTA 604
1546 CGCTGGAATGTTGTTGATGACAGGTTGAAGCTTAAGGTTGATGATGATGATGATGAT 1487
605 TTGCAATTTGCGGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 664
1486 TTGCACTCTTTGTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1427
665 CCTCAACCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 723
1426 CAAGTGTCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1368

RESULT 15
US-09-005-051-36
Sequence 36, Application US/09005051

GENERAL INFORMATION:
APPLICANT: Silver, Gary W.
APPLICANT: Wisniewski, Nancy
TITLE OF INVENTION: No. 6291222e1 Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordperfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,051
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/747,221
FILING DATE: No. 6291222e1, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505

INFORMATION FOR SEQ ID NO: 36:

SEQUENCE CHARACTERISTICS:

LENGTH: 2007 nucleotides

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 11..1594

Query Match 9.5%; Score 162.6; DB 4; Length 2007;
Best Local Similarity 55.8%; Pred. No. 5.3e-43;
Matches 334; Conservative 0; Mismatches 259; Indels 6; Gaps 1;

125 TTAAGGGTGAATGAGTACGCTCTACATGATTTCTTACTACAGTTTCAGAGTATAC 184
48 TAAAGGAAAGCAATATGTAAGAAAGAAATGTTCCATAGTTATCTCGAATTC 107
185 CTAATGCTAAGCCTCCAGTGGTGAATGATGATGATGATGATGATGATGATGATGAT 244
108 CATATGCCAAACCTCTGTAGTATGATGATGATGATGATGATGATGATGATGATGAT 167
245 GGGAGGGTGTACGATGCTGTGGGCCAGCCAGAGATCGGTACAGACAGATTTATATA 304
168 GGTGAGTGTCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 227
305 GTGGCAAAACCCAGGTTGAGGAGATTTCTATACCTGAATGTATACCAATGACTTGA 364
228 AAAAATTAAGTAGGGGCTGAAGATTTTATACCTCAATGCTATGATGATGATGATGAT 287
365 ACCAGACAAAAGGCGCTCTGTATGATGATGATGATGATGATGATGATGATGATGAT 424
288 CAGAGAAATCACTTCTTCAGTATGATGATGATGATGATGATGATGATGATGATGAT 347
425 AAGCAATGTAACGTTGGTCCGCTACTTATGTAAGAAACCCGCTGCTGTGTA 484
348 CTGAAATAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 407
485 CCGTCAATATGCTTTGGGTGTTGGGTCTTCTTACCTGAAATCGAATGCTCATG 544
408 CTTCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 461
545 TCCCGGAGAGCGCTGCTCAAGATCAAGTATGAGCTTGAAGTGGTCAAGATTA 604
462 CGCTGGAATGTTGTTGATGACAGGTTGAAGCTTAAGGTTGATGATGATGATGATGAT 521
605 TTGCAATTTGCGGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 664
522 TTGCACTCTTTGTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 561
665 CCTCAACCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 723
582 CAAGTGTCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 640

Mon Apr 14 10:18:11 2003

Search completed: April 11, 2003, 08:51:41
Job time : 46.4409 secs

us-09-776-910-14.rni

Page 14

[illegible]

```

OY 559 GGCCTCAAGATCAAGTATGAGCTTGGAGATGCTCAAGATATATATGCAATTTGGT 618
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 565 GGTCTCCGGATCAGGTAAACCTGTGGCTGGCTGCAAGAAAGCAAGAAATTTCCGA 624
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 619 GGGCATGTAGACATATATACCTCTTGGCGCAAGTCTGTGGGGCCTCAACCATTTAC 678
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 635 GAGAGCCCGACGACATACCATAGCGGGGAGAGCGCTGGTGCATCAGCTGGCATCTA 684
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 679 ATGATGATTAACGACAGACCGGTGTTTATTCATCGTGTATCATCATATGTCGGTAT 738
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 685 CTGACTCTTTTCAAGCTACGAGAGCTTTTCAAAAGAGCATTCATGATGAGCGAACA 744
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 739 TCCATGTCTCATGGGCGCTTAC 761
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 745 GGAATGAGCTACTTCTTACTAC 767
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 2

```

US-09-738-626-1254
: Sequence 1254, Application US/09738626
: Publication No. US20020197605A1
: GENERAL INFORMATION:
: APPLICANT: NAKAGAWA, SATOSHI
: APPLICANT: MIZOGUCHI, HIROSHI
: APPLICANT: ANDO, SEIKO
: APPLICANT: HAYASHI, MIKIRO
: APPLICANT: OCHIAI, KEIKO
: APPLICANT: YOKOI, HARUHIKO
: APPLICANT: TATEISHI, MOKO
: APPLICANT: SENOH, AKIHIRO
: APPLICANT: IKEDA, MASATO
: APPLICANT: OZAKI, AKIO
: TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
: FILE REFERENCE: 249-125
: CURRENT APPLICATION NUMBER: US/09/738,626
: CURRENT FILING DATE: 2000-12-18
: PRIOR APPLICATION NUMBER: JP 99/377484
: PRIOR FILING DATE: 1999-12-16
: PRIOR APPLICATION NUMBER: JP 00/159162
: PRIOR FILING DATE: 2000-04-07
: PRIOR APPLICATION NUMBER: JP 00/280988
: PRIOR FILING DATE: 2000-08-03
: NUMBER OF SEQ ID NOS: 7059
: SOFTWARE: Patentin ver. 3.0
: SEQ ID NO 1254
: LENGTH: 1611
: TYPE: DNA
: ORGANISM: Corynebacterium glutamicum
US-09-738-626-1254

```

```

Query Match      5.2%: Score 88.4; DB 9; Length 1611;
Best Local Similarity 49.7%: Pred. No. 1.4e-16;
Matches 314; Conservative 0; Mismatches 306; Indels 12; Gaps 3;

```

```

OY 177 GAGTATACCTATGTGTAAGCTCCAGTGGGTGAGTGTGAGATTCAGGACCCAGCGGC 236
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 78 GGGAAATTCCTACGGCCGCAACACAGTGGGGAAATATGCTTCCGGGCAACCCGCGCCG 137
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 237 TGTACACGAGGAGGTGATGATGCTGTGGCCAGCCCAACAGATGGTACAG--AC 293
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 138 CAAGAAATGGGAGCGGTGGCGGATGCTCAATGTTCCGTAAGAGCTTCTCAGGCCAAC 197
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 294 AGATTTCATTAAGTGGCAAAACCCACAGGTTGGAGATGTGTATACCTGATGTGTATAC 353
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 198 GTACCTCGTGAACAGATTAAGTTCGGGCTTCAAGAGACTGCTTAACCTCGATGTGTGCG 257
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 354 CATGACTTGAACCCAGCAAAAGCGCTGTATATGTTTCAATCCATGGCGAGATTT 413
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 258 GCGTGATTT-----CCGAAAGAAAGCTTCTGTGTGTGTATCTCCAGCGCGTTCCTT 311
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 414 TATTTGGGGAAGCAATCTGTAAGTGT---GTCGCCGACTACTTATGAAGAAACC 470
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

Db 312 CATCATGCGCTCATCAAGCAAAAGCGCTGCGGGATATATACCTGTCAAAACATGAA 371
OY 471 CGATGCTTGTGTAACCGTGCATATATGCTTGGGTGTGGTTCCTTACGCTGAATAC 530
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 372 TGTGTCTACGCTGTCCGTATATTTCCGCTCGGCGCTTGGGTATCTATGATCTGGCTTC 431
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 531 GGAATATCTAATGTCCCGGCAAGCTGAGCTCAAGATCAAGTAATGGCTTGAGATG 590
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 432 CGTGGGGAGAGATTTGGTATGCCCAACCCCGCTCCACGATCAGCTCTGGCCCTGAGAG 491
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 591 GGTCAAGAGTAATATATGATTCATTTGGTGGCGCATGTATGACATATATACCGTCTTGGCGA 650
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 492 GGTACGCGGTATATATGAAGCATTCGTTGGGATCTCTGACAAAGTCAACCTCATGAGGCGA 551
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 651 AAGTGTGTGGGGGCTCAACCATTTACATGATATACCAAGACAGACCGGTGTATTT 710
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 552 ATCCGGGGCGGCTGACGAGTGTGCTACATCATGTGTGTGCCCGTGAGAGGAGCTATT 611
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 711 CCATGCTGTGATCATATGTCGGGTATTCATGCTATGCTATGAGCTCTACAGAAATGCCA 770
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 612 CCACCGCGCATGCGCCCAATCCGCGCGGTCTGTGTGCACTCATCTATACCAAGCAAA 671
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 771 AAGTGTGGCTCACCATGCGCCCAACGTTTG 802
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 672 ATTCTGGCAGCGTGAACGTGATCTACCGCATG 703
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 3

```

US-09-917-800A-1511
: Sequence 1511, Application US/09917800A
: Patent No. US20020119462A1
: GENERAL INFORMATION:
: APPLICANT: Mendrick, Donna
: APPLICANT: Porter, Mark
: APPLICANT: Johnson, Kory
: APPLICANT: Castler, Arthur
: APPLICANT: Elashoff, Michael
: TITLE OF INVENTION: Molecular Toxicology Modeling
: FILE REFERENCE: 44921-5038-US
: CURRENT APPLICATION NUMBER: US/09/917,800A
: CURRENT FILING DATE: 2001-07-31
: PRIOR APPLICATION NUMBER: US 60/222,040
: PRIOR FILING DATE: 2000-07-31
: PRIOR APPLICATION NUMBER: US 60/222,880
: PRIOR FILING DATE: 2000-11-02
: PRIOR APPLICATION NUMBER: US 60/290,029
: PRIOR FILING DATE: 2001-05-11
: PRIOR APPLICATION NUMBER: US 60/290,645
: PRIOR FILING DATE: 2001-05-15
: PRIOR APPLICATION NUMBER: US 60/292,336
: PRIOR FILING DATE: 2001-05-22
: PRIOR APPLICATION NUMBER: US 60/295,798
: PRIOR FILING DATE: 2001-06-06
: PRIOR APPLICATION NUMBER: US 60/297,457
: PRIOR FILING DATE: 2001-06-13
: PRIOR APPLICATION NUMBER: US 60/298,884
: PRIOR FILING DATE: 2001-06-19
: PRIOR APPLICATION NUMBER: US 60/303,459
: PRIOR FILING DATE: 2001-07-09
: NUMBER OF SEQ ID NOS: 1740
: SOFTWARE: Patentin Ver. 2.1
: SEQ ID NO 1511
: LENGTH: 2141
: TYPE: DNA
: ORGANISM: Rattus norvegicus
: FEATURE:
: OTHER INFORMATION: Genbank Accession No. US20020119462A1 X65296
US-09-917-800A-1511

```

```

Query Match      4.3%: Score 74.2; DB 10; Length 2141;
Best Local Similarity 54.3%: Pred. No. 4.4e-12;
Matches 220; Conservative 0; Mismatches 173; Indels 12; Gaps 3;

```

QY	498	TTTGGGCGTGTGGGTTCTCTTAACTCGAAATCGGAAATCTCAATGTCCCGGAAACGC	557
Db	580	CTGGGGCATCTGGGGATCTTCTTACG-----ACAGGGGAGTAACAACAGCGCGGGGSAATCG	633
OY	558	TGCGCTTCAGAGATCAAGTATATGCGCTTGAGATGAGTGAATAGTAAATATATTCGCTATTTTCGG	617
Db	634	GGGTCACCTGAGACCAAGTGGCTGCTCCCTCGCTCGGTCTCCAGAGACACAACTTGGCAAGCTTTGG	692
OY	618	TGCGATGTAGCAATATTAATCCGTCTTTCGGGAAAGTGTGTGGGG	664
Db	654	AGGGAACCCACAGGCTCTGTGACCATCTTTGGAGAGATCAAGCGGGAGGAG	740

```

; ORGANISM: Homo sapiens
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (72)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (2098)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (2114)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (2117)
; OTHER INFORMATION: n equals a,t,g, or c
;
US-09-925-301-335

```

Qy	321	TTGCGAGCATGTGCTATTAAGTATGTA---TACCAATAGCTTGAACCAACAAAG	377
Db	506	TTCTGAACACAGCTTTTACCTCAATATTTTAACTCTGCTGACTTGAACCAAGAAAAACAG	565
Qy	378	GGGTCCTGTATGTGTTTTCATCCATGCGGAGATTTTATTTTCGGCGCAACCAATGCTAA	437
Db	566	GCTGCGCGGTGAATGGTGAATCCACGAGAGGGGGCTATGTTGGTCCGGATCA---AC	622
Qy	438	CTGGTTTGGTCCCACTACTTTATGAAGAAACCGCTGTGGTATACCTGCATATATCG	497
Db	623	CTATGATGGGCTGGGCCCTTGCTGCGCCATGAAACAGTGGTGGTGACATTCATATATCG	682
Qy	498	TTTGGGTGTGGTGGTTTCTTAAGCTGGAATGGAANAATCTCAATCTCCCGGGCAACGC	557
Db	683	CCTGGGCACTTGGGCAATCTTCAG-----ACAGGGGATGAACACAGCGGGGGAACTG	736
Qy	558	TGGCCCTCAAGGATCAAGTAAATGAGCCTTGAGATGGGTAAGAAGTAAATGGCATTTTGG	617
Db	737	GGGTACCTCGAGACAGGTGGCGCTCGCTCGGTGCTCCAGACAACATTTGCACACTTGG	796
Qy	618	TGGCAGTATGACAATATTACCGTCTTGGCGCAAAAGTCTGTGGGG	664

Db 797 AGGGAACCCAGGCTCTGTGACCATCTTTGGAGAGTACAGCGGAGAG 843

RESULT 6

US-09-894-991-1

; Sequence 1, Application US/09894991

; Patent No. US2002090619A1

; GENERAL INFORMATION:

; APPLICANT: Pfeiffer, Douglas R.

; APPLICANT: Murphy, Anne M.

; APPLICANT: Jung, Dennis W.

; APPLICANT: Bradshaw, Patrick C.

; TITLE OF INVENTION: METHODS FOR IDENTIFYING MITOCHONDRIAL

; TITLE OF INVENTION: DIVALENT CATION TRANSPORTERS

; FILE REFERENCE: 660088.430

; CURRENT APPLICATION NUMBER: US/09/894,991

; CURRENT FILING DATE: 2001-06-29

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 1470

; TYPE: DNA

; ORGANISM: Bacillus subtilis

US-09-894-991-1

Query Match 4.2%; Score 71.6; DB 10; Length 1470;
Best Local Similarity 52.6%; Pred. No. 2.2e-11;

Matches 265; Conservative 0; Mismatches 214; Indels 25; Gaps 4;

QY 179 GTATACCTTATGCTTAACCTCCAGTGGGTGAGTTGATTTCAAGGACCCCGCGCTG 238
Db 77 GCATCCCTTATGCCAAGCCCGCTGTGCAACATGCGCTTTTAAAGCACTGAGCGCGCTG 136
QY 239 TACCATGGAGGAGTACGATGATTTGGGCTG-----CAGCCACAG 281
Db 137 AAGTGGGGAAGATGCTTATGATCCACAGCGTACGCTTATTTGCCCGCAGCGCTG 196
QY 282 ATGGGTACAGAGATTTTCATATAGTGCAACCCAGGTTGGAGATTTGTATACCT 341
Db 197 ATTTGCTCTACGTGCTATACAGAGCTGCCCCGCGAG--TCCGAGATTTGCTGTATGT 254
QY 342 GAATGTATACCAATGACTTAACCAACAAAGGCGCTCTGTTAGGTTTCATCCA 401
Db 255 CAATGTATTTGGCGCTGAC--ACTCCAAGTCAAAATCTCTCTGTCATGCTGTGATTC 311
QY 402 TGCGGAGATTTTATTTTGGCGGAAGCAATGCTAATGCTTGTCCGACTACTTAT 461
Db 312 CGAGGCGCTTTTATCTTTGAGCGGCGAGTGAAGCATTTGATGACGATCAAAACTTGC 371
QY 462 GA--AGAAACCCGTGCTTGTGTAACCGTCAATATGCTTGGTGTGGTTGCT 518
Db 372 GGCACAGGAGAGATCATTTGCTTACANTGACATATGCGTGGCGCGCTTTTGGCTTTT 431
QY 519 TAGCCGAATGCGAAATCTAATGTCCTCCGCAACGCTGCGCTCAAGATCAATAT 578
Db 432 GCACCTTGTCTTGTGATGAGCGCTATTCGATTAACCTTGGCTTTTAAAGCAAGCGCG 491
QY 579 GGCCTTGAGATGCTCAAGATATATGCAATTTTGGTGGCATATGACAAATATAC 638
Db 492 CCGGCTGAATGCGTGGGGAAGATATCTCAGCGTTTGGCGGTATCCGATTAACGTAAC 551
QY 639 CCGTTCGCGCAAGTGTGCTG 662
Db 552 AGTATTTGAGAAATCCCGCGCGG 575

RESULT 7

US-09-894-991-7

; Sequence 7, Application US/09894991

; Patent No. US2002090619A1

; GENERAL INFORMATION:

; APPLICANT: Pfeiffer, Douglas R.

; APPLICANT: Murphy, Anne M.
; APPLICANT: Jung, Dennis W.
; APPLICANT: Bradshaw, Patrick C.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MITOCHONDRIAL
; TITLE OF INVENTION: DIVALENT CATION TRANSPORTERS
; FILE REFERENCE: 660088.430
; CURRENT APPLICATION NUMBER: US/09/894,991
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1470
; TYPE: DNA
; ORGANISM: Bacillus subtilis
US-09-894-991-7

Query Match 4.2%; Score 71.6; DB 10; Length 1470;
Best Local Similarity 52.6%; Pred. No. 2.2e-11;

Matches 265; Conservative 0; Mismatches 214; Indels 25; Gaps 4;

QY 179 GTATACCTTATGCTTAACCTCCAGTGGGTGAGTTGATTTCAAGGACCCCGCGCTG 238
Db 77 GCATCCCTTATGCCAAGCCCGCTGTGCAACATGCGCTTTTAAAGCACTGAGCGCGCTG 136
QY 239 TACCATGGAGGAGTACGATGATTTGGGCTG-----CAGCCACAG 281
Db 137 AAGTGGGGAAGATGCTTATGATCCACAGCGTACGCTTATTTGCCCGCAGCGCTG 196
QY 282 ATGGGTACAGAGATTTTCATATAGTGCAACCCAGGTTGGAGATTTGTATACCT 341
Db 197 ATTTGCTCTACGTGCTATACAGAGCTGCCCCGCGAG--TCCGAGATTTGCTGTATGT 254
QY 342 GAATGTATACCAATGACTTAACCAACAAAGGCGCTCTGTTAGGTTTCATCCA 401
Db 255 CAATGTATTTGGCGCTGAC--ACTCCAAGTCAAAATCTCTCTGTCATGCTGTGATTC 311
QY 402 TGCGGAGATTTTATTTTGGCGGAAGCAATGCTAATGCTTGTCCGACTACTTAT 461
Db 312 CGAGGCGCTTTTATCTTTGAGCGGCGAGTGAAGCATTTGATGACGATCAAAACTTGC 371
QY 462 GA--AGAAACCCGTGCTTGTGTAACCGTCAATATGCTTGGTGTGGTTGCT 518
Db 372 GGCACAGGAGAGATCATTTGCTTACANTGACATATGCGTGGCGCGCTTTTGGCTTTT 431
QY 519 TAGCCGAATGCGAAATCTAATGTCCTCCGCAACGCTGCGCTCAAGATCAATAT 578
Db 432 GCACCTTGTCTTGTGATGAGCGCTATTCGATTAACCTTGGCTTTTAAAGCAAGCGCG 491
QY 579 GGCCTTGAGATGCTCAAGATATATGCAATTTTGGTGGCATATGACAAATATAC 638
Db 492 CCGGCTGAATGCGTGGGGAAGATATCTCAGCGTTTGGCGGTATCCGATTAACGTAAC 551
QY 639 CCGTTCGCGCAAGTGTGCTG 662
Db 552 AGTATTTGAGAAATCCCGCGCGG 575

RESULT 8

US-09-917-800A-1450

; Sequence 1450, Application US/09917800A

; Patent No. US20020119462A1

; GENERAL INFORMATION:

; APPLICANT: Mendrick, Donna

; APPLICANT: Porter, Mark

; APPLICANT: Johnson, Kory

; APPLICANT: Castle, Arthur

; APPLICANT: Elashoff, Michael

; APPLICANT: Gene Logic, Inc.

; TITLE OF INVENTION: Molecular Toxicology Modeling

; FILE REFERENCE: 44921-5038-US

; CURRENT APPLICATION NUMBER: US/09/917,800A

; CURRENT FILING DATE: 2001-07-31

; PRIOR APPLICATION NUMBER: US 60/222,040

PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/222,880
PRIOR FILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/295,798
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,884
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/303,459
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 1740
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1450
LENGTH: 1885
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20020119462A1 U10697
US-09-917-800A-1450

Query Match 4.2%; Score 71; DB 10; Length 1885;
Best Local Similarity 53.8%; Pred. No. 3.9e-11;
Matches 218; Conservative 0; Mismatches 175; InDels 12; Gaps 3;

QY 321 TTGCGAGATTGTCTAATCGATGTATACCAAT--GACTTGAACCCAGACAAAG 377
DB 350 TTCTGAGATTGTCTCTAATTAATTTACCTCTGACAGACTTTACAAAGAAATAGCAG 409
QY 378 GCGTCTGTATGTTTCATGCGGAGATTTTATTTCCGCCAGCAAAATCGTAA 437
DB 410 GCTGCCAGTCACTGTGTGATTCATGAGGTGGAATGACACTGGGCGGATCA--AC 466
QY 438 CTGTTGGTCCGACCTATTATGAAAGAACCCGCTGCTTGTGTAACCGTCATATCG 497
DB 467 CTATGATGCGCGGCTCTCTGCTATGAAAGCGTGTGAGTGGCATTCAGTATCG 526
QY 498 TTTGGTGTGTTGGTTTCTTACGCTGAATCGGAATATCAATGTCCTCCCGGACGC 557
DB 527 CTTGGGCACTGGGGATTCTTCAGCACAGGGGANTGAAACACAGCAGG-----GGAACGTG 580
QY 558 TGGCCTCAAGGATCAAGTAATGAGCTTGATGAGATGGGTCAAGAGTAATATTGCAATTTGCG 617
DB 581 GGGTCATTGGAACCAAGTGGCTGCGCTCAGCTGGTCCAGACACATTCGCAACTTGG 640
QY 618 TGGCGATGTAGCAATATTACCGTTCGCGGAAAGTGCTGTGGGCGCTCAACCATTA 677
DB 641 GGGTGACCCAGCTCTGACCATCTTTGGAGAGTCAAGAGAGGAGTTTCATGCTCTCTGT 700
QY 678 CATGATGATTAACCAAGACACCGGTGTTTATTCATCGTGTAT 722
DB 701 TCTGTGTGTTGCCACCTGACCAAGAACCTCTCTCCACAGGGGCAAT 745

RESULT 9

US-09-418-176-1
Sequence 1, Application US/09418176
Publication No. US20030040040A1
GENERAL INFORMATION:
APPLICANT: Das, Goutam
TITLE OF INVENTION: DNA Molecules for Expression of
TITLE OF INVENTION: Polypeptides
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case
STREET: 1155 Avenue of the Americas
CITY: New York

STATE: New York
COUNTRY: United States
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/418,176
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/624,398
FILING DATE: 04-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/SE96/00318
FILING DATE: 12-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9501939-4
FILING DATE: 24-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Theima A. Chen Cleland
REGISTRATION NUMBER: 40,948
REFERENCE/DOCKET NUMBER: 1103326-0206
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8200
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2428 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: mammary gland
FEATURE:
NAME/KEY: CDS
LOCATION: 82..2319
OTHER INFORMATION: /product= "bile-salt-stimulated
OTHER INFORMATION: lipase"
FEATURE:
NAME/KEY: exon
LOCATION: 985..1173
FEATURE:
NAME/KEY: exon
LOCATION: 1174..1377
FEATURE:
NAME/KEY: exon
LOCATION: 1378..1575
FEATURE:
NAME/KEY: exon
LOCATION: 1576..2415
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 151..2316
FEATURE:
NAME/KEY: polyA_signal
LOCATION: 2397..2402
FEATURE:
NAME/KEY: repeat_region
LOCATION: 1756..2283
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..81
FEATURE:
NAME/KEY: repeat_unit
LOCATION: 1756..1788
FEATURE:

NAME/KEY: repeat_unit
LOCATION: 1789..1821
FEATURE: repeat_unit
NAME/KEY: repeat_unit
LOCATION: 1822..1854
FEATURE: repeat_unit
NAME/KEY: repeat_unit
LOCATION: 1855..1887
FEATURE: repeat_unit
NAME/KEY: repeat_unit
LOCATION: 1888..1920
FEATURE: repeat_unit
NAME/KEY: repeat_unit
LOCATION: 1921..1953
FEATURE: repeat_unit
NAME/KEY: repeat_unit
LOCATION: 1954..1986
FEATURE: repeat_unit
NAME/KEY: repeat_unit
LOCATION: 1987..2019
FEATURE: repeat_unit
NAME/KEY: repeat_unit
LOCATION: 2020..2052
FEATURE: repeat_unit
NAME/KEY: repeat_unit
LOCATION: 2053..2085
FEATURE: repeat_unit
NAME/KEY: repeat_unit
LOCATION: 2086..2118
FEATURE: repeat_unit
NAME/KEY: repeat_unit
LOCATION: 2119..2151
FEATURE: repeat_unit
NAME/KEY: repeat_unit
LOCATION: 2152..2184
FEATURE: repeat_unit
NAME/KEY: repeat_unit
LOCATION: 2185..2217
FEATURE: repeat_unit
NAME/KEY: repeat_unit
LOCATION: 2218..2250
FEATURE: repeat_unit
NAME/KEY: repeat_unit
LOCATION: 2251..2283
PUBLICATION INFORMATION:
AUTHORS: Nilsson, Jeanette
AUTHORS: Blackberg, Lars
AUTHORS: Carlsson, Peter
AUTHORS: Enerback, Sven
AUTHORS: Herneil, Olle
AUTHORS: Bjursell, Gunnar
TITLE: cDNA cloning of human-milk
TITLE: bile-salt-stimulated lipase and evidence for its
TITLE: Identity to pancreatic carboxylic ester hydrolase
JOURNAL: Eur. J. Biochem.
VOLUME: 192
PAGES: 543-550
DATE: Sept. -1990
US-09-418-176-1

Query Match 4.1%; Score 70.4; DB 9; Length 2428;
Best Local Similarity 55.6%; Pred. No. 7.2e-11;
Matches 159; Conservative 0; Mismatches 121; Indels 6; Gaps 1;

471 CGTGGCTGTGTAACCGGCAATATGCTTGGGTGTGTTGGTTCTTAGCCTGAATC 530
DB 555 CGTCACTGGTGACCTTAACTACCGGTTCGGCCCCCTTGGTTCTCAGC-----AC 608
QY 531 GGAATATCTCAATGTCCTCCGCAACGCTGCGCTCAAGATCAAGTAAGCCCTTGAGATG 590
DB 609 TGGGAGCGCAATCTGCGCAAGTAATGAGCTTGGGATACAGCATGCGCATTCCTTG 668
QY 591 GGTCAAGATTAATTTGCTTGGTGGCGATGTAGACAAATATACCGTCTTGGCGCA 650

DB 669 GGTGAAGAGAAATATCGGGGCTTCGGGGGGGAGACCCCAACAATCAAGCTCTTCGGGGA 728
QY 651 AAGTCTGTGGGCGCTCAACCCATTCATGATGATTAACCAACAGACCCGTGTTATT 710
DB 729 GTCTGTGAGAGTGCACAGCTCTCTGCAAGACCCCTCCCTCAACAAGAGGCTTCAT 788
QY 711 CCATCGTGTATCATGATGTCCGGTAATTCATGATGCTGATGGGCC 756
DB 789 CCGGAGGACATCAAGCCAGAGCGGCGTGGCCCTGAGTCTTGGGTC 834

RESULT 10
US-09-969-347-220
Sequence 220, Application US/09969347
Patent No. US20020115085A1
GENERAL INFORMATION:
APPLICANT: Ebner, Reinhard
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign
FILE REFERENCE: 689290-69
CURRENT APPLICATION NUMBER: US/09/969, 347
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US/60/237, 598
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: US/60/237, 604
NUMBER OF SEQ ID NOS: 318
SOFTWARE: PatentIn version 3.0
SEQ ID NO 220
LENGTH: 2428
TYPE: DNA
ORGANISM: Homo sapiens
US-09-969-347-220

Query Match 4.1%; Score 70.4; DB 10; Length 2428;
Best Local Similarity 55.6%; Pred. No. 7.2e-11;
Matches 159; Conservative 0; Mismatches 121; Indels 6; Gaps 1;

471 CGTGGCTGTGTAACCGGCAATATGCTTGGGTGTGTTGGTTCTTAGCCTGAATC 530
DB 555 CGTCACTGGTGACCTTAACTACCGGTTCGGCCCCCTTGGTTCTCAGC-----AC 608
QY 531 GGAATATCTCAATGTCCTCCGCAACGCTGCGCTCAAGATCAAGTAAGCCCTTGAGATG 590
DB 609 TGGGAGCGCAATCTGCGCAAGTAATGAGCTTGGGATACAGCATGCGCATTCCTTG 668
QY 591 GGTCAAGATTAATTTGCTTGGTGGCGATGTAGACAAATATACCGTCTTGGCGCA 650
DB 669 GGTGAAGAGAAATATCGGGGCTTCGGGGGGGAGACCCCAACAATCAAGAGGCTTCAT 728
QY 651 AAGTCTGTGGGCGCTCAACCCATTCATGATGATTAACCAACAGACCCGTGTTATT 710
DB 729 GTCTGTGAGAGTGCACAGCTCTCTGCAAGACCCCTCCCTCAACAAGAGGCTTCAT 788
QY 711 CCATCGTGTATCATGATGTCCGGTAATTCATGATGCTGATGGGCC 756
DB 789 CCGGAGGACATCAAGCCAGAGCGGCGTGGCCCTGAGTCTTGGGTC 834

RESULT 11
US-09-917-800A-480
Sequence 480, Application US/09917800A
Patent No. US20020119462A1
GENERAL INFORMATION:
APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Castle, Arthur
APPLICANT: Elashoff, Michael
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5038-US

```

CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/222,880
PRIOR FILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/295,798
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,884
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/303,459
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 1740
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 480
LENGTH: 1902
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20020119462A1 AB010635
US-09-917-800A-480

```

```

Query Match          4.1%; Score 69.6; DB 10; Length 1902;
Best Local Similarity 52.8%; Pred No. 1,le-10;
Matches 225; Conservative 0; Mismatches 189; Indels 12; Gaps 3;

322 TCGGAGATTGCTATACCTGATGTATACCAATGACTTGACCCAGCA--CAAAAG 378
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
389 TCTGAGAGACCTGCTATATCTCAACATCTATACCAAGCCCATGAGGCTCTAC 448
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
379 CGTCTGATATGTTTTCATCCATGCGGAGATTTTATTTGGGGAAGCAATGCTAC 438
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
449 CTGCTGATGATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 505
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
439 TGGTTGGTCCGACACTTATGAGAAACCGTGTGTTGTAACCGTGCATATGCT 498
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
506 TGTGATGATCTCTATTTGAGATCAATGAGACTTGTGTTGCTATTCAGATGCT 565
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
499 TTGGTGTGTTGGTTCCTTACCTGAAATCGAAATCTCATGTCCTCCGCAACGT 558
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
566 CTGGTGTCTCGGGCTTTTTCAGC-----ACTGAGATGAGCATCCAGAGCACTGG 619
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
559 GGCCTCAAGATCAAGTAATGCGCTGAGATGGTCAAGATTAATTTGCCATTTTCGGT 618
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
620 GGATACCTGAGCAAGGCTGCTGCTGAGATGGTCCAGAGCAATATCCGCCATTTTGA 679
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
619 GGCATGATGACCAATATTTACCGTCTTGGGGAAGTGTGCGGCTCAACCCATTCAC 678
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
680 GCGAACCTTACCGGGTCACTATTTTGGCGTGTGCTGCAAGTGTGCTTCA 739
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
679 ATGATGATACCGAAGACAGCCCGTGTGTTATTCATGCTGATGATGATGCTGTAAT 738
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
740 CATGTTATATCCCATGCTCAAGGCTCTTCATGATGCTCATGATGAGATGAGATG 799
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
739 TCCATG 744
    |||||
800 GGCCTG 805

```

```

RESULT 12
US-09-917-800A-1324
; Sequence 1324, Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna

```

```

APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Castle, Arthur
APPLICANT: Elashoff, Michael
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5038-US
CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/222,880
PRIOR FILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/295,798
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,884
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/303,459
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 1740
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1324
LENGTH: 1442
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20020119462A1 D00362
US-09-917-800A-1324

```

```

Query Match          4.1%; Score 69.4; DB 10; Length 1442;
Best Local Similarity 53.6%; Pred No. 1e-10;
Matches 217; Conservative 0; Mismatches 176; Indels 12; Gaps 3;

321 TCGGAGATTGCTATACCTGATGTATACTGATGATGATGATGATGATGATGATG 377
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
435 TTCGAGAGACTGCTCTACTGATGATGATGATGATGATGATGATGATGATGATG 494
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
378 GCGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 437
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
495 ATTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 554
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
438 CTGTTGTTGGTCCGACACTTATGAGAAACCGTGTGTTGTAACCGTGCATATG 497
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
555 TAG---TGGACTGATCTCTCTGCTGCCAGCAAAAGTGTGTTGTAACCATTCAC 611
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
498 TTTGGTGTGTTGGTTCCTTACCTGAAATCGAAATCTCAATGTCCTCCGCAACGC 557
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
612 CCGTGATATTTGGGATGTTTACG-----ACCGTGAAGAACACAGCGGGGAACTG 665
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
558 TGGCTCAAGATCAAGTAATGCGCTGAGATGGTCAAGATTAATTTGCCATTTTCGG 617
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
666 GCGTCACTTGGACCAAGCTGGCTGCTACTACCTGAGTCCAGAGATTAATTCGAACTTGG 725
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
618 TGGCGATGATGACCAATATTTACCGTCTTGGGGAAGTGTGTTGGGCTCAACCCATTA 677
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
726 AGGGAACCGGATTCAGTACCATCTTTGGAGATCAGCAGAGATGATGATGATGATG 785
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
678 CATGATGATTAACCAAGACAGCCGCTGTTTATTCATGCTGATGAT 722
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
786 TCTTGTCTTATCTCTCTGCGCAAGAACCTCTTCCACAGAGCCAT 830
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

```

RESULT 13
US-09-895-860-3
; Sequence 3, Application US/09895860

```

```

; Patent No. US20020076786A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A. J.
; APPLICANT: Logan, Thomas Joseph
; TITLE OF INVENTION: 25869, A NOVEL HUMAN CARBOXYL ESTERASE
; FILE REFERENCE: MNI-167
; CURRENT APPLICATION NUMBER: US/09/895,860
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/215,370
; PRIOR FILING DATE: 2000-06-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1641
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1641)
; US-09-895-860-3

```

```

Query Match      4.1%; Score 69.4; DB 10; Length 1641;
Best Local Similarity 53.3%; Pred. No. 1.1e-10;
Matches 220; Conservative 0; Mismatches 181; Indels 12; Gaps 3;

```

```

QY 315 CACAGTTCGAGAGATTGTCTATACCTGAATGTGTATA---CCAAATGACTTGAACCCAGA 371
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 262 CTCCTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 341
QY 372 CAAAGAGGCTCTGTATAGTTTTCATTCATGCGGAGATTTTATTTTGGCGCAACCAAA 431
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 342 GTCCGGTAGGCGCGGTATGATGAGGTCATGAGGAGGCGCTTATACAGGCGCTGCCA- 400
QY 432 TCGTACTGTTTGTGCTCCCACTACTTTATGAAGAAACCGTGTGTGTAAACCTGCA 491
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 401 --CTCTACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 458
QY 492 ATATCGTTGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 551
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 459 GTACCGGCTTGGGTGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 512
QY 552 CAACGCTGCGCTCAAGAGATCAAGTAATGAGCTTGAAGATGAGTCAAGAGATATATGCAAT 611
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 513 CAACCAAGGCTTCTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 572
QY 612 TTTCGTGGCGATGTAGACAATATTAACGCTTGGCGCAAGTGTGTGTGTGTGTGTGTGTGTGT 671
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 573 CTTCGGGGGTGACCTCACTGTCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 632
QY 672 CCAATTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 724
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 633 CTCTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 685

```

```

RESULT 14
US-09-895-860-1
; Sequence 1, Application US/09895860
; Patent No. US20020076786A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A. J.
; APPLICANT: Logan, Thomas Joseph
; TITLE OF INVENTION: 25869, A NOVEL HUMAN CARBOXYL ESTERASE
; FILE REFERENCE: MNI-167
; CURRENT APPLICATION NUMBER: US/09/895,860
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/215,370
; PRIOR FILING DATE: 2000-06-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2087

```

```

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (222)...(1862)
; US-09-895-860-1

```

```

Query Match      4.1%; Score 69.4; DB 10; Length 2087;
Best Local Similarity 53.3%; Pred. No. 1.3e-10;
Matches 220; Conservative 0; Mismatches 181; Indels 12; Gaps 3;

```

```

QY 315 CACAGTTCGAGAGATTGTCTATACCTGAATGTGTATA---CCAAATGACTTGAACCCAGA 371
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 503 CTCCTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 562
QY 372 CAAAGAGGCTCTGTATAGTTTTCATTCATGCGGAGATTTTATTTTGGCGCAACCAAA 431
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 563 GTCCGGTAGGCGCGGTATGATGAGGTCATGAGGAGGCGCTTATACAGGCGCTGCCA- 621
QY 432 TCGTACTGTTTGTGCTCCCACTACTTTATGAAGAAACCGTGTGTGTAAACCTGCA 491
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 622 --CTCTACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 679
QY 492 ATATCGTTGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 551
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 680 GTACCGGCTTGGGTGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 733
QY 552 CAACGCTGCGCTCAAGAGATCAAGTAATGAGCTTGAAGATGAGTCAAGAGATATATGCAAT 611
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 734 CAACCAAGGCTTCTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 793
QY 612 TTTCGTGGCGATGTAGACAATATTAACGCTTGGCGCAAGTGTGTGTGTGTGTGTGTGTGTGT 671
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 794 CTTCGGGGGTGACCTCACTGTCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 853
QY 672 CCAATTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 724
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 854 CTCTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 906

```

```

RESULT 15
US-10-036-041-22
; Sequence 22, Application US/10036041
; Publication No. US20020192751A1
; GENERAL INFORMATION:
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3030R1C8
; CURRENT APPLICATION NUMBER: US/10/036,041
; CURRENT FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/112514
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/113300
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/113430
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113605
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113621
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/114140

```

1	PRIOR FILING DATE: 1998-12-23	
2	PRIOR APPLICATION NUMBER: 60/115552	
3	PRIOR FILING DATE: 1999-01-12	
4	PRIOR APPLICATION NUMBER: 60/116843	
5	PRIOR FILING DATE: 1999-01-22	
6	PRIOR APPLICATION NUMBER: 60/125774	
7	PRIOR FILING DATE: 1999-03-23	
8	PRIOR APPLICATION NUMBER: 60/125778	
9	PRIOR FILING DATE: 1999-03-23	
10	PRIOR APPLICATION NUMBER: 60/125826	
11	PRIOR FILING DATE: 1999-03-24	
12	PRIOR APPLICATION NUMBER: 60/127035	
13	PRIOR FILING DATE: 1999-03-31	
14	PRIOR APPLICATION NUMBER: 60/127706	
15	PRIOR FILING DATE: 1999-04-05	
16	PRIOR APPLICATION NUMBER: 60/129122	
17	PRIOR FILING DATE: 1999-04-13	
18	PRIOR APPLICATION NUMBER: 60/130359	
19	PRIOR FILING DATE: 1999-04-21	
20	PRIOR APPLICATION NUMBER: 60/131270	
21	PRIOR FILING DATE: 1999-04-27	
22	PRIOR APPLICATION NUMBER: 60/131272	
23	PRIOR FILING DATE: 1999-04-27	
24	PRIOR APPLICATION NUMBER: 60/131291	
25	PRIOR FILING DATE: 1999-04-27	
26	PRIOR APPLICATION NUMBER: 60/132371	
27	PRIOR FILING DATE: 1999-05-04	
28	PRIOR APPLICATION NUMBER: 60/132379	
29	PRIOR FILING DATE: 1999-05-04	
30	PRIOR APPLICATION NUMBER: 60/132383	
31	PRIOR FILING DATE: 1999-05-04	
32	PRIOR APPLICATION NUMBER: 60/135750	
33	PRIOR FILING DATE: 1999-05-25	
34	PRIOR APPLICATION NUMBER: 60/138166	
35	PRIOR FILING DATE: 1999-06-08	
36	PRIOR APPLICATION NUMBER: 60/144791	
37	PRIOR FILING DATE: 1999-07-20	
38	PRIOR APPLICATION NUMBER: 60/146970	
39	PRIOR FILING DATE: 1999-08-03	
40	PRIOR APPLICATION NUMBER: 60/162506	
41	PRIOR FILING DATE: 1999-10-29	
42	PRIOR APPLICATION NUMBER: 60/311832	
43	PRIOR FILING DATE: 1999-05-14	
44	PRIOR APPLICATION NUMBER: 60/380142	
45	PRIOR FILING DATE: 1999-08-25	
46	PRIOR APPLICATION NUMBER: 60/644848	
47	PRIOR FILING DATE: 2000-08-22	
48	PRIOR APPLICATION NUMBER: 60/747259	
49	PRIOR FILING DATE: 2000-12-20	
50	PRIOR APPLICATION NUMBER: 60/816744	
51	PRIOR FILING DATE: 2001-03-22	
52	PRIOR APPLICATION NUMBER: 60/854208	
53	PRIOR FILING DATE: 2001-05-10	
54	PRIOR APPLICATION NUMBER: 60/854280	
55	PRIOR FILING DATE: 2001-05-10	
56	PRIOR APPLICATION NUMBER: 60/874503	
57	PRIOR FILING DATE: 2001-06-05	
58	PRIOR APPLICATION NUMBER: 60/869599	
59	PRIOR FILING DATE: 2001-06-29	
60	PRIOR APPLICATION NUMBER: 60/908, 827	
61	PRIOR FILING DATE: 2001-07-18	
62	PRIOR APPLICATION NUMBER: 60/US99/10733	
63	PRIOR FILING DATE: 1999-05-14	
64	PRIOR APPLICATION NUMBER: 60/US99/28551	
65	PRIOR FILING DATE: 1999-12-02	
66	PRIOR APPLICATION NUMBER: 60/US99/30720	
67	PRIOR FILING DATE: 1999-12-22	
68	PRIOR APPLICATION NUMBER: 60/US00/05601	
69	PRIOR FILING DATE: 2000-03-01	
70	PRIOR APPLICATION NUMBER: 60/US00/05841	
71	PRIOR FILING DATE: 2000-03-02	
72	PRIOR APPLICATION NUMBER: 60/US00/14042	
73	PRIOR FILING DATE: 2000-05-22	

```

; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23528
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US00/34956
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 22
; LENGTH: 3824
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-036-041-22

```

Search completed: April 11, 2003, 13:24:11
Job time : 101.362 secs

GenCore version 5.1.4.P5-4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2003, 09:08:22 ; Search time 15.9846 Seconds
(without alignments)
1725.596 Million cell updates/sec

Title: US-09-776-910-15

Perfect score: 1093

Sequence: 1 QTDFTSGKPRGSEDCLYLV.....KANPYDLKEPQVLTPEKN 207

Scoring table: BLOSUM62

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: /SID52/gcgdata/geneseq/emb1/AA1980.DAT:*
2: /SID52/gcgdata/geneseq/emb1/AA1981.DAT:*
3: /SID52/gcgdata/geneseq/emb1/AA1982.DAT:*
4: /SID52/gcgdata/geneseq/emb1/AA1983.DAT:*
5: /SID52/gcgdata/geneseq/emb1/AA1984.DAT:*
6: /SID52/gcgdata/geneseq/emb1/AA1985.DAT:*
7: /SID52/gcgdata/geneseq/emb1/AA1986.DAT:*
8: /SID52/gcgdata/geneseq/emb1/AA1987.DAT:*
9: /SID52/gcgdata/geneseq/emb1/AA1988.DAT:*
10: /SID52/gcgdata/geneseq/emb1/AA1989.DAT:*
11: /SID52/gcgdata/geneseq/emb1/AA1990.DAT:*
12: /SID52/gcgdata/geneseq/emb1/AA1991.DAT:*
13: /SID52/gcgdata/geneseq/emb1/AA1992.DAT:*
14: /SID52/gcgdata/geneseq/emb1/AA1993.DAT:*
15: /SID52/gcgdata/geneseq/emb1/AA1994.DAT:*
16: /SID52/gcgdata/geneseq/emb1/AA1995.DAT:*
17: /SID52/gcgdata/geneseq/emb1/AA1996.DAT:*
18: /SID52/gcgdata/geneseq/emb1/AA1997.DAT:*
19: /SID52/gcgdata/geneseq/emb1/AA1998.DAT:*
20: /SID52/gcgdata/geneseq/emb1/AA2000.DAT:*
21: /SID52/gcgdata/geneseq/emb1/AA2001.DAT:*
22: /SID52/gcgdata/geneseq/emb1/AA2002.DAT:*
23: /SID52/gcgdata/geneseq/emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1069	97.8	570	18	AAW17767
2	828	75.8	570	18	AAW17766
3	826	75.6	570	18	AAW17768
4	825	75.5	570	16	AAW78142
5	825	75.5	570	18	AAW17765
6	736	67.3	572	22	ABW57850
7	595	54.4	530	22	ABW57857
8	587.5	53.8	567	22	ABW57857
9	582	53.2	554	22	ABW57866
10	573	52.4	565	22	ABW57746

11	563.5	51.6	566	22	ABW61983	Drosophila melanog
12	563	51.5	572	22	ABW57867	Drosophila melanog
13	560	51.2	554	22	ABW59161	Drosophila melanog
14	555	50.8	542	22	ABW57790	Drosophila melanog
15	541.5	49.5	602	23	AAW47598	Drosophila cell cy
16	470	43.0	541	22	ABW57789	Drosophila melanog
17	469	42.9	568	22	ABW57831	Drosophila melanog
18	465	42.5	551	22	ABW57788	Drosophila melanog
19	463.5	42.4	513	19	AAW57863	C. felis esterace,
20	463.5	42.4	528	22	AAW57862	C. felis esterace,
21	463.5	42.4	528	22	AAW57862	C. felis esterace,
22	428	39.2	495	19	AAW57869	C. felis esterace,
23	428	39.2	530	19	AAW57855	C. felis esterace,
24	428	39.2	530	19	AAW57857	C. felis esterace,
25	428	39.2	530	22	AAW57851	C. felis esterace,
26	428	39.2	550	19	AAW57853	C. felis esterace,
27	428	39.2	550	19	AAW57854	C. felis esterace,
28	428	39.2	550	22	AAW57854	C. felis esterace,
29	425	38.9	505	19	AAW57851	C. felis esterace,
30	425	38.9	505	19	AAW57851	C. felis esterace,
31	425	38.9	505	22	AAW57852	C. felis esterace,
32	425	38.9	505	22	AAW57852	C. felis esterace,
33	425	38.9	550	19	AAW57864	C. felis esterace,
34	425	38.9	550	19	AAW57864	C. felis esterace,
35	420.5	38.5	527	22	ABW62353	C. felis esterace,
36	411	37.6	576	22	ABW64915	C. felis esterace,
37	400.5	36.6	562	22	ABW64708	C. felis esterace,
38	397	36.3	530	19	AAW57867	C. felis esterace,
39	397	36.3	530	19	AAW57867	C. felis esterace,
40	375	34.3	570	19	AAW57860	C. felis esterace,
41	375	34.3	570	19	AAW57860	C. felis esterace,
42	375	34.3	570	22	AAW57860	C. felis esterace,
43	375	34.3	595	19	AAW57859	C. felis esterace,
44	375	34.3	595	19	AAW57859	C. felis esterace,
45	375	34.3	595	22	AAW57861	C. felis esterace,
					AAW57861	C. felis esterace,

ALIGNMENTS

RESULT 1	
AAW17767	standard; Protein; 570 AA.
ID	AAW17767
AC	AAW17767
XX	
DT	08-AUG-1997 (first entry)
XX	
DE	Md-alpha-E7 malathion resistant mutant.
XX	
KW	Malathion carboxylesterase; organophosphate; insecticide; pesticide; remediation; bioremediation; decontamination.
XX	
OS	Musca domestica Rutgers strain.
XX	
FT	Key Location/Qualifiers
FT	Misc-difference 251
FT	/note="Ser-251 is tryptophan in the susceptible allele expression product"
XX	
PN	W09719176-A1.
XX	
PD	29-MAY-1997.
XX	
PE	22-NOV-1996; 96WO-A000746.
XX	
PR	23-NOV-1995; 95AU-0006751.
XX	
PA	(CSIR) COMMONWEALTH SCI & IND RES ORG.
XX	
PI	Boyce T, Brownlie JC, Campbell PM, Claudianos C,
XX	Newcomb RD, Oakeshott JG, Robin GC, Russell RJ, Smyth K;

CC from the esterase (AAW17765) of a malathion susceptible clone of
CC Lucilia cuprina by a subclon. of the tryptophan residue at amino
CC acid position 251 by a leucine residue. This mutation is situated
CC at the base of the active site gorge, 6.5 Angstroms from the active
CC site serine. The RM80on amino acid sequence is a consensus deduced
CC from the DNA sequences of 3 resistant clones (RM8 A-C) and their
CC comparison to reference susceptible clone Lc743 (AAT68596) of
CC Lc-alpha-E7. The enzyme is capable of hydrolysing carboxylester
CC and/or dimethylloxon organophosphates and can be formulated for use
CC in bioremediation strategies for treatment of soil or water.

XX Sequence 570 AA;

Query Match

Best Local Similarity 74.6%; Score 826; DB 18; Length 570;
Matches 153; Conservative 25; Mismatches 27; Indels 0; Gaps 0;

QY 1 QTFPIGKPTGSEDCLYLNTYTDLPDKRPVWVFHGGGFIFGAGANRMVGPDYFMK 60
DB 97 QVDFITGKVGSEDCLYLNTYTDLPDKRPVWVFHGGGFIFGAGANRMVGPDYFMK 156
QY 61 PVVLVTVQYRLGVLGFLSKSENLNPGNAGLKDQVVALRMFKNIAIFGGVDNITVFG 120
DB 157 DVLINIOYRLGALGFLSLNSEDLPNGNAGLKDQVVALRMFKNIAIFGGVDNITVFG 216
QY 121 ESAGASTHYMMITEQTRGLFHRGIMMSGNSMCSSASTECOSRALTMARVKGGEENEK 180
DB 217 ESAGASTHYMMITEQTRGLFHRGIMSGNAICPLANTCQCHRAFTLAKLAGYKGEDNDK 276
QY 181 DLEFLMKANPYDLIKEEPOVLTPE 205
DB 277 DVLEFLMKAKPDILKLEKVTLE 301

RESULT 4

AAW78142

AC AAR78142;

DT 22-DEC-1995 (first entry)

DE OP-sensitive esterase E3.

KW Esterase; E3; bioremediation; organophosphate; carbamate;

KW insecticide; pesticide; water decontamination; meat decontamination.

OS Lucilia cuprina.

PN WO9519440-A1.

PD 20-JUL-1995.

PF 13-JAN-1995; 95WO-AU00016.

PR 13-JAN-1994; 94AU-0003347.

PA (CSIR) COMMONWEALTH SCI & IND RES ORG.

PI Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;

PI Parker AG, Robin GC, Russell RJ, Smyth K;

DR WPI: 1995-263870/34.

DR N-PSDB: AAO91561.

PT Pure E3 esterase from Lucilia cuprina and related DNA - used to

PS eliminate residues of organo:phosphate and carbamate pesticides from

CC water, meat etc.
CC Example 3; Page 12-17; 38pp; English.
CC cDNA from organophosphate (OP)-sensitive L. cuprina pupa cDNA
CC library was amplified using cluster-specific esterase primers.

CC Isolated clone Lc743, a probable full-length cDNA, was expressed
CC using a baculovirus vector in insect cells and shown to encode
CC an OP-susceptible E3 esterase useful in bioremediation.

XX Sequence 570 AA;

Query Match

Best Local Similarity 74.6%; Score 825; DB 16; Length 570;
Matches 153; Conservative 25; Mismatches 27; Indels 0; Gaps 0;

QY 1 QTFPIGKPTGSEDCLYLNTYTDLPDKRPVWVFHGGGFIFGAGANRMVGPDYFMK 60
DB 97 QVDFITGKVGSEDCLYLNTYTDLPDKRPVWVFHGGGFIFGAGANRMVGPDYFMK 156
QY 61 PVVLVTVQYRLGVLGFLSKSENLNPGNAGLKDQVVALRMFKNIAIFGGVDNITVFG 120
DB 157 DVLINIOYRLGALGFLSLNSEDLPNGNAGLKDQVVALRMFKNIAIFGGVDNITVFG 216
QY 121 ESAGASTHYMMITEQTRGLFHRGIMMSGNSMCSSASTECOSRALTMARVKGGEENEK 180
DB 217 ESAGASTHYMMITEQTRGLFHRGIMSGNAICPLANTCQCHRAFTLAKLAGYKGEDNDK 276
QY 181 DLEFLMKANPYDLIKEEPOVLTPE 205
DB 277 DVLEFLMKAKPDILKLEKVTLE 301

RESULT 5

AAW17765

AC AAW17765;

DT 08-AUG-1997 (first entry)

DE Lc-alpha-E7 malathion susceptible clone Lc743 esterase E3.

KW Malathion carboxylesterase; organophosphate; insecticide;

KW pesticide; remediation; bioremediation; decontamination; esterase.

OS Lucilia cuprina.

PN WO9719176-A1.

PD 29-MAY-1997.

PF 22-NOV-1996; 96WO-AU00746.

PR 23-NOV-1995; 95AU-0006751.

PA (CSIR) COMMONWEALTH SCI & IND RES ORG.

PI Boyce T, Brownlie JC, Campbell PM, Claudianos C;

PI Newcomb RD, Oakeshott JG, Robin GC, Russell RJ, Smyth K;

DR WPI: 1997-298113/27.

DR N-PSDB: AAT68596.

PT DNA encoding enzyme that degrades organophosphate pesticides -

PT useful for decontamination of soil, water, food etc

PS Disclosure; Fig 1; 52pp; English.

CC Esterase E3 (AAW17765) from a malathion susceptible strain of

CC Lucilia cuprina differs from an esterase enzyme (see also

CC AAW17768) from malathion resistant RM8 strains by a Trp for Leu
CC subclon. at amino acid position 251, owing to a mutation in the
CC encoding DNA sequence (see also AAT68596). The resistant enzyme,

Best Local Similarity 50.2%: Pred. No. 9, 6e-55; Matches 112; Conservative 31; Mismatches 62; Indels 18; Gaps 1.

QY	1	QPDFTISGKRTSGEDCLYLVNVTYNDLNPDKRRPVWFIFHGSGFIFGEANNNWGPDYFMKK	60
		11:	
Db	81	QHFHFVFEMTDSGEDCLYLVNVTYKNTLPTRKPMVPMWVIYGGQFGEASRECSPLYLRE	140
QY	61	PVVLVTVOYRTGLV-----GFLSLKSENLVNNGNGLKQOVALRRF	102
		11:	
Db	141	DVVVVISINRLPLGTINDTETWKKHLEINSLPGFLCLDDPELDVPGMGAKQOVALKRV	200
QY	103	KSNIATFGGDVNIIVVFGSAGASTHYWMLTEQFRGIFPHRITMNSGNSMCSASTECOS	162
		11:	
Db	201	KANCRSFGSDSANLITFDSDASGSAVHTMTITEQHHGLKFKATCSGNLTSPFAVTPORN	260
QY	163	RALTAKRRVKGGENEDDLEFLMKANPYDLIKEEPOVLTPPE	205
		1:	
Db	261	WPRRLAVAGAGTAGENNTDYMVELFNAGSGEITKANGSELCLIDE	303

DT 26-MAR-2002 (first entry)
XX
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 4275.
XX
XX Drosophila: developmental biology; cell signalling; insecticide;
KM pharmaceutical.

The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from *Drosophila*. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (AAB57737-AB572072).

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Query Match	51.28;	Score 560;	DB 22;	Length 554;
Best Match				

Matches 109; Conservative 24; Mismatches 55; Indels 0; Gaps 0;

QY 1 QTDIFSGKPTGSEDCLYINVTNDLNPDKRRPVWFIFGGGFIFGEANRMNMGDPYFK 60
 Db 86 QRMMLGIVESEDCGLHNVYKALKSEKPLPVYITGGGFOKEASRDYSPYFKK 145
 QY 61 PVLVTYVYRGLVGLFSLKSENLVPGNAGLKDQVMAIRFKSNIAIFGGDVNITVFG 120
 Db 146 PVFVFAIRYRLAALGFLSLKDPKLDVPCNAGLKDQVMAIRFQSNIAHFNGDPNITLMG 205
 QY 121 ESAGASTHYMMITTEQTRGLFHRGIMSGNSMCSASTECOSRALTMAKRVGKGEENK 180
 Db 206 ESAGASVHYMMITTEQTRGLFHRKAIMOSGALSEWVSPDNMAFLAONLTKGDEKDA 265
 QY 181 DILEFLMK 188
 Db 266 DVLSEFLSK 273

RESULT 14

ABB57790
 ID ABB57790 standard; Protein; 542 AA.

AC ABB57790;
 DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 162.

KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmacological.

OS Drosophila melanogaster.

XX MO200171042-A2.

PD 27-SEP-2001.

PF 23-MAR-2001; 2001MO-US09231.

PR 23-MAR-2000; 2000US-191637P.

PR 11-JUL-2000; 2000US-0614150.

XX (PEKE) PE CORP NY.

PI Venter JC, Adams M, Li PMD, Myers EW;

DR WPI; 2001-656860/75.

DR N-PSDB; ABL01893.

PT New isolated nucleic acid detection reagent for detecting 1000 or more
 genes from Drosophila and for elucidating cell signalling and cell-cell

PT Interactions -

PS Disclosure; SEQ ID NO 162; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent.
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
 CC sequences (AB101840-AB116175) and the encoded proteins
 CC (AB57737-AB572072).

CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/Published_pct_sequences.

XX Sequence 542 AA;

Query Match 50.8%; Score 555; DB 22; Length 542;
 Best Local Similarity 54.3%; Pred. No. 7.2e-54;
 Matches 113; Conservative 24; Mismatches 59; Indels 12; Gaps 2;

QY 8 KPT-----GSEDCLYINVTNDLNPDKRRPVWFIFGGGFIFGEANRMNMGDPYF 57
 Db 71 KPTQGLYTRIEGGEDCLYINVTNSKOLKSEKPLPVYITGGATVTEARRELXGPYF 130
 QY 58 MKRPVLTVYRGLVGLFSLKSENLVPGNAGLKDQVMAIRFKSNIAIFGGDVNIT 117
 Db 131 MKRDVYLTIANRVDCITGLSLKPSLKVPGNAGLKDQVMAIRFKSNIAIFGGDVNIT 190
 QY 118 VEGESAGASTHYMMITTEQTRGLFHRGIMSGNSMCSASTECOSRALTMAKRVGKGE 177
 Db 191 VEGESAGGCTHFMCTEQTRGLFHRKAIMSGTGHVNYMANPAEDFAFLAQNFTGEN 250
 QY 178 NEKDILEFLMKANPYDLKEEPOVLTP 205
 Db 251 DDAKYLEYLGVPARDLVNH--NLTP 276

RESULT 15

AAM47598
 ID AAM47598 standard; Protein; 602 AA.

AC AAM47598;

DT 12-FEB-2002 (first entry)

DE Drosophila cell cycle progression protein #27.

KW Antiproliferative; cytostatic; cardiant; immunosuppressive; meiosis;
 KW antineoplastic; antiproliferative; dermatological; antifungal; mitosis;
 KW antiparasitic; antimalarial; antineoplastic; antitubercular; cell division;
 KW cell cycle progression protein; tumour; proliferative disorder;
 KW cardiovascular; autoimmune; dermatological disorder.

XX Drosophila sp.

XX MO200172774-A2.

PD 04-OCT-2001.

PF 23-MAR-2001; 2001MO-GH01297.

PR 24-MAR-2000; 2000GB-0007268.

XX (CYCL-) CYCLACEL LTD.

PI Deak P, Glover DM, Midgley C;

DR WPI; 2002-055132/07.

PT Polynucleotides encoding cell cycle progression proteins, useful for
 treating a tumor or a proliferative disorder -

PS Claim 8; Page 164; 213pp; English.

XX The present invention relates to Drosophila cell cycle progression
 CC proteins (AAM47572-AAM47608) and their coding sequences and proteins are useful for
 CC (AAM490366-ABA90520). The coding sequences and proteins are useful for
 CC identifying a substance capable of affecting the function of the
 CC corresponding gene, a substance capable of inhibiting the cell division
 CC cycle, or capable of inhibiting mitosis and/or meiosis. They can also be
 CC used in a method for treating a tumor or proliferative disorder,
 CC cardiovascular disorders (such as stenosis and cardiomyopathy),
 CC autoimmune disorders (such as glomerulonephritis and Rheumatoid
 CC arthritis), dermatological disorders (such as psoriasis),
 CC antineoplastic, antifungal and antiparasitic disorders (such as
 CC malaria).

XX Sequence 602 AA;

Query Match 49.5%; Score 541.5; DB 23; Length 602;
 Best Local Similarity 53.7%; Pred. No. 2.8e-52;
 Matches 109; Conservative 29; Mismatches 56; Indels 9; Gaps 2;

```

QY 1 QTFISGKPTGSEDCLYLNVTYNDLNPDKKRPVWFIHGGEFIFGEANRWYGPDYFMKK 60
Db 143 QTHMEFRKYAGSEDCLYLNVTYNDLNPDKKRPVWFIHGGEFIFGEANRWYGPDYFMKK 194
QY 61 PVVLYTVQYRLGVYGLSLSENINVPNGAGLKDQVNALNWEKSNIAIFGDDVNDITVFG 120
Db 195 -VVIVTAVYRLGALGPLSLDDPOLNVPNGAGLKDQVNALNWEKSNIAIFGDDVNDITVFG 253
QY 121 ESAGGASTHYWMITEOTRGLEFHGIMSGNSMSSASTECOSRALTMKRVGYKGEENEK 180
Db 254 ESAGGASTHYWMITEOTRGLEFHGIMSGNSMSSASTECOSRALTMKRVGYKGEENEK 313
QY 181 DLEFLMKANPYDLIKEEPVLT 203
Db 314 AIFEFRLMSMSGELVKATATVLS 336

```

Search completed: April 4, 2003, 09:13:04
 Job time : 18.9846 secs

GenCore version 5.1.4-p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2003, 09:10:33; Search time 6.92664 Seconds
(without alignments)
2872.940 Million cell updates/sec

Title: US-09-776-910-15

Perfect score: 1093
Sequence: 1 QTFDISGKPTGSEDLXLYNV.....KANPYDLIKEPQVLTPERM 207

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

1: PIR73:*
2: PIR73:*
3: PIR73:*
4: PIR73:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	458	41.9	540	2	carboxylesterase (EC 3.1.1.1) B2 - southern house mosquito
2	454	41.5	540	2	esterase B1 - sout
3	447	40.9	503	2	carboxylesterase (EC 3.1.1.1) B2 - southern house mosquito
4	446	40.8	540	2	carboxylesterase (EC 3.1.1.1) B2 - southern house mosquito
5	359	32.8	564	2	juvenile-hormone e
6	354	32.4	578	2	protein T28C12.4b
7	354	32.4	658	2	hypothetical prote
8	345	31.6	564	1	carboxylesterase (EC 3.1.1.1) B2 - southern house mosquito
9	344.5	31.5	603	2	hypothetical prote
10	344	31.5	548	2	hypothetical prote
11	343.5	31.4	596	2	acetylcholinestera
12	341	31.2	614	2	acetylcholinestera
13	340	31.1	489	2	para-nitrobenzyl e
14	340	31.1	614	2	acetylcholinestera
15	338	30.9	552	2	carboxylesterase (EC 3.1.1.1) B2 - southern house mosquito
16	337	30.8	583	2	hypothetical prote
17	337	30.8	583	2	hypothetical prote
18	336	30.7	602	1	cholinesterase (EC 3.1.1.1) B2 - southern house mosquito
19	335.5	30.7	581	2	cholinesterase (EC 3.1.1.1) B2 - southern house mosquito
20	335	30.6	614	2	acetylcholinestera
21	334.5	30.6	599	1	juvenile hormone e
22	334.5	30.6	599	1	acetylcholinestera
23	334.5	30.6	599	1	acetylcholinestera
24	334	30.6	565	2	carboxylesterase (EC 3.1.1.1) B2 - southern house mosquito
25	333	30.5	612	2	steroid esterase (EC 3.1.1.1) B2 - southern house mosquito
26	331	30.3	567	1	steroid esterase (EC 3.1.1.1) B2 - southern house mosquito
27	331	30.3	599	2	steroid esterase (EC 3.1.1.1) B2 - southern house mosquito
28	329.5	30.1	561	2	carboxylesterase (EC 3.1.1.1) B2 - southern house mosquito
29	329	30.1	597	2	steroid esterase (EC 3.1.1.1) B2 - southern house mosquito

30	328.5	30.1	584	2	acetylcholinesterase (EC 3.1.1.1) B2 - southern house mosquito
31	326	29.8	561	2	carboxylesterase (EC 3.1.1.1) B2 - southern house mosquito
32	325.5	29.8	561	2	carboxylesterase (EC 3.1.1.1) B2 - southern house mosquito
33	324.5	29.7	595	2	glutathione S-transferase (EC 2.3.2.1) B2 - southern house mosquito
34	324	29.6	593	1	triacylglycerol 11
35	324	29.6	561	2	carboxylesterase (EC 3.1.1.1) B2 - southern house mosquito
36	321	29.4	745	2	triacylglycerol 11
37	320	29.3	554	2	carboxylesterase (EC 3.1.1.1) B2 - southern house mosquito
38	318	29.1	549	2	carboxylesterase (EC 3.1.1.1) B2 - southern house mosquito
39	316	28.9	562	2	carboxylesterase (EC 3.1.1.1) B2 - southern house mosquito
40	315.5	28.9	545	2	carboxylesterase (EC 3.1.1.1) B2 - southern house mosquito
41	315.5	28.9	559	1	carboxylesterase (EC 3.1.1.1) B2 - southern house mosquito
42	315	28.8	554	2	carboxylesterase (EC 3.1.1.1) B2 - southern house mosquito
43	314.5	28.8	620	2	acetylcholinesterase (EC 3.1.1.1) B2 - southern house mosquito
44	314	28.7	502	2	probable esterase
45	314	28.7	566	2	carboxylesterase (EC 3.1.1.1) B2 - southern house mosquito

ALIGNMENTS

RESULT 1

S53370 carboxylesterase (EC 3.1.1.1) B2 - southern house mosquito

C:Species: Culex pipiens quinquefasciatus (southern house mosquito)

C>Date: 15-Jul-1995 #sequence_revision 08-Sep-1995 #text_change 21-Jul-2000

C:Accession: S53370; S44211

R:Vaughan, A.; Rodriguez, M.; Hemingway, J.

Biochem. J. 305, 651-658, 1995

A:File: The independent gene amplification of electrophoretically indistinguishable

A:Reference number: S53370; M01D:95134253; PMID:7530448

A:Accession: S53370

A:Molecule type: mRNA

A:Residues: 1-540 <VAD>

A:Cross-references: EMBL:232694; NID:q475067; PIDN:CA83643.1; PID:q475068

A:Experimental source: strain PeIR

A:Superfamily: cholinesterase; cholinesterase homology

C:Keywords: carboxylic ester hydrolase

Query Match	41.9%; Score 458; DB 2; Length 540;
Best Local Similarity	44.0%; Pred. No. 8.9e-36;
Matches	88; Conservative 40; Mismatches 72; Indels 0; Gaps 0;
QY	8 KPTGSEDCLYLVNTDNDPKRPVMTFHGGGFTFGANRWGPDVFMKKPVITV 67
DB	77 KIVGCEDSKINFAKEINPSKPLPMLYIGGGFTGELGPDVLGKDIYVSE 136
QY	68 QYRLVGLFSLKSENUNPGNAGLDQYVALRWFKNIAIFGQVDNITVFGESAGAS 127
DB	137 NYRIGALGFICQSEDDGVPGNAGLDQYVALRWFKNIAIFGQVDNITVFGESAGAS 196
QY	128 THVMATTEOTRGLEHFGIMSGNSMCSASTECOSRALTMAKRVGKGENEKDILEFTM 187
DB	197 VOYHILSDASKDLFORAIYWSGSTYNSWLTQRNMVETLAKRIGMDGGGSGALRFK 256
QY	188 KANPYDLIKEPQVLTPERM 207
DB	257 AAKPEDIVANOEKRLTDQDM 276

RESULT 2

A35986 esterase B1 - southern house mosquito

C:Species: Culex pipiens quinquefasciatus (southern house mosquito)

C>Date: 16-Nov-1990 #sequence_revision 13-Jan-1993 #text_change 21-Jul-2000

C:Accession: A35986

R:Mouches, C.; Pupulin, Y.; Agarwal, M.; Lemieux, L.; Hertzog, M.; Beyssat

Proc. Natl. Acad. Sci. U.S.A. 87, 2574-2578, 1990

A:Title: Characterization of amplification core and esterase B1 gene responsible for

A:Reference number: A35986; M01D:90207238; PMID:2320576

A:Accession: A35986

A:Status: preliminary

A:Molecule type: DNA

RESULT 6

Protein T28C12.4b [imported] - *Caenorhabditis elegans*

C/Species: *Caenorhabditis elegans*

C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001

C/Accession: F89068

R:anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A>Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biology

A/Reference number: A75000; M01D:99069613; PMID:9851916

A/Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C_eleg

A/Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A/Accession: F89068

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-578 <STO>

A/Cross-references: GB:chr_V; PIDN:AAB66160.1; PID:g2315734; GSPDB:GN00023; CESP:T28C12.

C/Genetics:

A:Gene: T28C12.4b

A:Map position: 5

C:Superfamily: cholinesterase; cholinesterase homology

Query Match 32.4%; Score 354; DB 2; Length 578;

Best Local Similarity 42.0%; Pred. No. 8.8e-26;

Matches 79; Conservative 29; Mismatches 62; Indels 18; Gaps 5;

12 SEDCLYLVNTNDLNPDKRPVWFVFIHGGGFIHGGEANRWYGPYFMK----KPVLYTV 67

DB 95 SEDCLYLVNFAPKIRIDKRPVLFYIHGGGYVDSAEF--YTAKNICKLVLSREIIVTF 152

OY 68 QYRLGVGLSLKSENLNVPNGALIKDQVMAIRMFKSNIAIFGSDVDNITVFGESAGAS 127

DB 153 HVRIGLFLGLSTGDD--VCPGNYGLFDMLEAMRWVHANISFGCPENITISGOSAGAA 210

OY 128 THYMMATEQTRGLFHRGIMSGNSMCSAST---ECOSRALTMARVYKGE-----E 177

DB 211 ADLISFSPITKGLFKRKTYMGNSYCHWMTSTNSHDIRCYCKMAKRLGKPOLNANKRE 270

OY 178 NEKDILEF 185

DB 271 ESDVDFNF 278

RESULT 7

T32053

hypothetical protein T28C12.4a - *Caenorhabditis elegans*

C/Species: *Caenorhabditis elegans*

C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 01-Dec-2000

C/Accession: T32053; T32054

R:Ledwith, J.; Wohldmann, P.; Graves, T.; Bradshaw, H.

submitted to the EMBL Data Library, July 1997

A>Description: The sequence of *C. elegans* cosmid T28C12.

A/Reference number: 221117

A/Accession: T32053

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-658 <LED>

A/Cross-references: EMBL:AF016679; PIDN:AAB66159.1; GSPDB:GN00023; CESP:T28C12.4a

A/Experimental source: strain Bristol N2; clone T28C12

A/Accession: T32054

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 81-658 <LE2>

A/Cross-references: EMBL:AF016679; PIDN:AAB66160.1; GSPDB:GN00023; CESP:T28C12.4b

A/Experimental source: strain Bristol N2; clone T28C12

C/Genetics:

A:Gene: CESP:T28C12.4a; CESP:T28C12.4b

A:Map position: 5

A/Intons: 70/1; 96/3; 137/3; 192/3; 366/2; 423/1; 480/3; 573/2

C:Superfamily: cholinesterase; cholinesterase homology

Query Match 32.4%; Score 354; DB 2; Length 658;

Best Local Similarity 42.0%; Pred. No. 1e-25;

Matches 79; Conservative 29; Mismatches 62; Indels 18; Gaps 5;

OY 12 SEDCLYLVNTNDLNPDKRPVWFVFIHGGGFIHGGEANRWYGPYFMK----KPVLYTV 67

DB 175 SEDCLYLVNFAPKIRIDKRPVLFYIHGGGYVDSAEF--YTAKNICKLVLSREIIVTF 232

OY 68 QYRLGVGLSLKSENLNVPNGALIKDQVMAIRMFKSNIAIFGSDVDNITVFGESAGAS 127

DB 233 HVRIGLFLGLSTGDD--VCPGNYGLFDMLEAMRWVHANISFGCPENITISGOSAGAA 290

OY 128 THYMMATEQTRGLFHRGIMSGNSMCSAST---ECOSRALTMARVYKGE-----E 177

DB 291 ADLISFSPITKGLFKRKTYMGNSYCHWMTSTNSHDIRCYCKMAKRLGKPOLNANKRE 350

OY 178 NEKDILEF 185

DB 351 ESDVDFNF 358

RESULT 8

336787

carboxylesterase (EC 3.1.1.1) F84 precursor - green peach aphid

C/Species: *Myzus persicae* (green peach aphid)

C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C/Accession: S36787

R:Field, L.M.; Williamson, M.S.; Moores, G.D.; Devonshire, A.L.

Biochem. J. 294, 563-574, 1993

A>Title: Cloning and analysis of the esterase genes conferring insecticide resistance

A/Reference number: S36786; M01D:93384534; PMID:8573571

A/Accession: S36787

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-564 <REF>

A/Cross-references: EMBL:X74555; NID:g397512; PIDN:CA52649.1; PID:g397513

C:Superfamily: cholinesterase; cholinesterase homology

C/Keywords: carboxylic ester hydrolase

F:52-552/Domain: cholinesterase homology <CHE>

Query Match 31.6%; Score 345; DB 1; Length 564;

Best Local Similarity 41.8%; Pred. No. 6.2e-25;

Matches 82; Conservative 30; Mismatches 62; Indels 22; Gaps 7;

OY 3 DFISG-KPTGSEDCLYLVNTNDLNPDKK----RPVWFVFIHGGGFIHGGEANRWYGPYFMK 57

DB 93 EFGSGSKITIGQEDCLFLNVYTPKLPQENSAGDILNNTIVHIIHGGGYEGE--ILYGPYL 150

OY 58 M-KRPVLYTVQYRLGVGLSLKSENLNVPNGALIKDQVMAIRMFKSNIAIFGSDVDNIT 116

DB 151 LDNNDVYVVSINVRIGVIGFASDGDYL--PGNNGLDQVAAALRWIOONTIVARQGDPSV 208

OY 117 TVFGSAGCASTHYMMATEQTRGLFHRGIMSGNSMCSASTECOSRALTMARVYKGE 176

DB 209 TITGMSAGASSVHNHILISPMKGLFNRAIIQSGSAFCWMTVAE-----NVAQTKTYAN 262

OY 177 -----ENEKDILEFL 186

DB 263 ILGCPTNNSVEIVECL 278

RESULT 9

S70849

cholinesterase (EC 3.1.1.8) - mouse

N:Alternate names: butyrylcholine esterase

C/Species: *Mus musculus* (house mouse)

C/Date: 28-Oct-1996 #sequence_revision 08-Nov-1996 #text_change 18-Jun-1999

C/Accession: S70849; S15680; A39768

R:Taylor, P.

submitted to the EMBL Data Library, August 1992

A/Reference number: S70849

A/Accession: S70849

A/Molecule type: nucleic acid

A:Residues: 1-603 <TAY>
 A:Cross-references: EMBL:M99492; NID:9191579; PIDN:AAA37328.1; PID:9191580
 R:Rachinsky, T.L.; Camp, S.; Li, Y.; Ekstrom, T.J.; Newton, M.; Taylor, P.
 Neuron 5, 317-327, 1990
 A:Title: Molecular cloning of mouse acetylcholinesterase: tissue distribution of alternate
 A:Reference number: J00314; MUID:90380429; PMID:2400605
 A:Accession: S15680
 A:Status: nucleic acid sequence not shown
 A:Molecule type: nucleic acid
 A:Residues: 30-128, 'P', 130-603 <RAC>
 A:Cross-references: EMBL:M99492
 R:Arpagaus, M.; Chalmers, A.; Masson, P.; Newton, M.; Vaughan, T.A.; Bartels, C.F.; Nog
 J. Biol. Chem. 266, 6966-6974, 1991
 A:Title: Use of the polymerase chain reaction for homology probing of butyrylcholinester
 A:Reference number: A39768; MUID:91201348; PMID:2016308
 A:Accession: A39768
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 97-128, 'P', 130-237 <ARP>
 C:Superfamily: cholinesterase; cholinesterase homology
 C:Keywords: carboxylic ester hydrolase; glycoprotein
 F:57-557/Domain: cholinesterase homology <CHE>

Query Match 31.5%; Score 344.5; DB 2; Length 603;
 Best Local Similarity 41.5%; Pred. No. 7.5e-25;
 Matches 81; Conservative 39; Mismatches 68; Indels 7; Gaps 5;

QY 12 SEDLLYLVTVYNDLPDKRPVVFHGGFIFGEANRMVGPDEYMK-KPVYLVTVQYR 70
 Db 118 SEDLLYLVTVYNDLPDKRPVVFHGGFIFGEANRMVGPDEYMK-KPVYLVTVQYR 70
 QY 71 LGVIFLSEKENVNGLKQVMAIRKSNIAIFGGVDNITVFESAGASTHY 130
 Db 177 VGAGFLAFRE-NDPAGNMGFLDQDIALQVORNIAPFGNPSITIFESAGASVSL 235
 QY 131 MITEQTRGLFHRCIMNSMCSA--STECOSRALYMAKRGVYGFENEDIEFLM 187
 Db 236 HLLCPQSPYPLFTRALLESQSNMAYAKHDEANRRLTLAKFTGC-SKENEEMIKCLR 294
 QY 188 KANYDYDIKEPOVL 202
 Db 295 SKDQELIRNERFVL 309

RESULT 10

hypothetical protein F56C11.6 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 31-Jan-2000
 C:Accession: T32907
 R:Lin-Wollam, A.; Wohldmann, P.; Morris, M.
 submitted to the EMBL Data Library, January 1998
 A:Description: The sequence of C. elegans cosmid F56C11.
 A:Reference number: Z21244
 A:Accession: T32907
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-548 <TIN>
 A:Cross-references: EMBL:AF043697; PIDN:AMB97558.1; GSPDB:GN00019; CESP:F56C11.6
 C:Experimental source: strain Bristol N2; clone F56C11
 C:Genetics:
 A:Gene: CESP:F56C11.6
 A:Map position: 1
 A:Introns: 29/3; 264/1; 340/1; 398/3; 447/1; 490/2
 C:Superfamily: cholinesterase; cholinesterase homology

Query Match 31.5%; Score 344; DB 2; Length 548;
 Best Local Similarity 40.2%; Pred. No. 7.4e-25;
 Matches 84; Conservative 34; Mismatches 65; Indels 26; Gaps 8;

QY 4 FTSGKPTGSEDLTVNYT---NDLNPDKRPVVFHGGFIFGEANRMVGPDEYMK 59
 Db 85 FNVYTKSEHRLSNVFTPKWSEWEPD-GPVMVFTHGGFAVHSSN--YGCASIR 141

QY 60 ----KPVYLVTVQYRGLVGLFLSKSNLVNPGNAGLKQVMAIRKSNIAIFGGVDN 115
 Db 142 NLCTKDDVVVTVINRLVLFETTGDEYVCR--NLTGIMQDTALEWQENTOSFRDPPN 199
 QY 116 IYVGEESAGASTHYMITEQTRGLFHRCIMNSMCSA--STECOSRALYMAKRGVYGF 172
 Db 200 VTFICQSGAGASVDLCLSPHSGRLNRAIPMAGNCECPAMTSSQQLSREFARYLG 259
 QY 173 YKGEENE-KDILEFL-----MKANP 191
 Db 260 WEGDDNSEDLLQFDQDPLXKTEMGINP 288

RESULT 11

ACRYE
 acetylcholinesterase (EC 3.1.1.7) precursor, 11S form [validated] - Pacific electric
 N:Alternate names: acetylcholinesterase, asymmetric form
 C:Species: Torpedo californica (Pacific electric ray)
 C:Date: 17-Mar-1987 #sequence_revision 08-Nov-1996 #text_change 15-Sep-2000
 A:Accession: A00773; A60820; A31962; B31962; A23902; B41117; S15677
 R:Schumacher, M.; Camp, S.; Maulet, Y.; Newton, M.; Macphée-Quigley, K.; Taylor, S.S.
 Nature 319, 407-409, 1986

A:Title: Primary structure of Torpedo californica acetylcholinesterase deduced from 1
 A:Reference number: A00773; MUID:86118676; PMID:3753747
 A:Accession: A00773
 A:Molecule type: mRNA
 A:Residues: 'NS', 11-596 <SCH>

A:Cross-references: GB:X03439; NID:964389
 A:Experimental source: electric organ
 A:Note: parts of this sequence, including the amino and carboxyl ends of the mature p
 R:Schumacher, M.; Camp, S.; Maulet, Y.; Newton, M.; Macphée-Quigley, K.; Taylor, S.S.
 Fed. Proc. 45, 2976-2981, 1986

A:Title: Primary structure of acetylcholinesterase: implications for regulation and f
 A:Reference number: A60820; MUID:87054662; PMID:3536598
 A:Accession: A60820
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 22-596 <SC2>

A:Cross-references: GB:X03439; NID:964389
 A:Experimental source: clones AChE-11 and AChE-18
 A:Note: revision to sequence A00773
 A:Accession: B31962
 A:Molecule type: DNA; mRNA
 A:Residues: 499-565 <SC4>

A:Cross-references: GB:X03439; NID:964389
 A:Experimental source: clone AChE-1
 R:Macphée-Quigley, K.; Taylor, P.; Taylor, S.
 J. Biol. Chem. 260, 12185-12189, 1985

A:Title: Primary structures of the catalytic subunits from two molecular forms of ace
 A:Reference number: A23902; MUID:86008285; PMID:3300071
 A:Accession: A23902
 A:Molecule type: protein
 A:Residues: 22, 'B', 24-45; 214-237 <MAC>

A:Note: active site Ser identification
 R:Kreienkamp, H.D.; Weise, C.; Rada, R.; Aaviksaar, A.; Hucho, F.
 Proc. Natl. Acad. Sci. U.S.A. 88, 6117-6121, 1991
 A:Title: Anticodon subunits of the catalytic center of acetylcholinesterase from Torped
 A:Reference number: A41117; MUID:91296772; PMID:2068091
 A:Accession: B41117
 A:Molecule type: protein
 A:Residues: 100-108 <KRE>

A:Note: substrate binding site
 R:Maulet, Y.; Camp, S.; Gbney, G.; Rachinsky, T.L.; Ekstrom, T.J.; Taylor, P.
 Neuron 4, 289-301, 1990
 A:Title: Single gene encodes glycopospholipid-anchored and asymmetric acetylcholines

C:Keywords: carboxylic ester hydrolase
F:24-478/Domain: cholinesterase homology <CHE>

Query Match 31.1%; Score 340; DB 2; Length 489;
Best Local Similarity 41.2%; Pred. No. 1.5e-24;
Matches 82; Conservative 26; Mismatches 83; Indels 8; Gaps 5;

QY 9 PTGSEDCLYLVNTDLPDKRPVWFTHGGGFIHGGEANRMWY-GPDYEMKKRPVLTVT 67
Db PROSEDCLYLVNVFAPD-TPSKNLPMVMWTHGCAFYLGAGSPLYDGSKLAQGEIVYTL 134
QY 68 QYRLGVGFLSKSENLVNPENAGLKQVVALRMFKSNIAIFGSDVNDITVFGESAGAS 127
Db NTRLGPFGFHLSSFNENAYSDNLLDQAAALKVRENISAFGGDPNVITVFGESAGAS 194
QY 128 THVMITEQTRGLFHRGIMSGNSMCSASTECOSRALTMARVGYKGEMENDILEFLM 167
Db IVALAMPAAKGLFQKALMESGASR-TWTKEQAASTSAFLQVIGT---NEGO-LDKLH 248
QY 188 KANPYDLKEEPOVLTPE 206
Db TVSAEDLKKADQLRIAEK 267

RESULT 14

JH0811
acetylcholinesterase (EC 3.1.1.7) catalytic chain precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 18-Jun-1999

C:Accession: JH0811

R:legay, C.; Bon, S.; Vernier, P.; Coussem, F.; Massoulié, J.
J. Neurochem. 60, 337-346, 1993

A:Title: Cloning and expression of a rat acetylcholinesterase subunit: generation of mu

A:Reference number: JH0811; MUID:93107932; PMID:8417155

A:Accession: JH0811

A:Molecule type: mRNA

A:Residues: 1-614 <LEG>

A:Cross-references: GB:S50879; NID:9262092; PIDN:AAB24566.1; PID:9262093

A:Experimental source: striatum

C:Comment: This protein is responsible for hydrolysis of acetylcholine at cholinergic sy

C:Superfamily: cholinesterase; cholinesterase homology

C:Keywords: carboxylic ester hydrolase; glycoprotein; membrane protein; muscle; nerve; r

F:1-31/Domain: signal sequence #status predicted <SIG>

F:32-614/Product: acetylcholinesterase catalytic chain #status predicted <CAT>

F:63-569/Domain: cholinesterase homology <CHE>

F:100-127-288-303,440-560/Disulfide bonds: #status predicted

F:234,365,478/Active site: Ser, Glu, His #status predicted

F:296,381,495/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 31.1%; Score 340; DB 2; Length 614;

Best Local Similarity 39.3%; Pred. No. 2.1e-24;

Matches 79; Conservative 37; Mismatches 77; Indels 8; Gaps 5;

QY 12 SEDCLYLVNTDLPDKRPVWFTHGGGFIHGGEANRMWYGPDPYFMK-KPVVLTVOYR 70
Db SEDCLYLVNTWTPPTSPPLVIMYGGFGYSGASILDVYDGRFLAQVEGTIVLSMNR 183
QY 71 LGVLGFLSKSENLVNPENAGLKQVVALRMFKSNIAIFGSDVNDITVFGESAGASTHY 130
Db VGTFGFLAPGSR-EAPGNVGLLDQRLAQWQENIAAFGSDPMSVTLFGESAGASVGM 242
QY 131 NMITEQTRGLFHRGIMSG--NSMCSAST-ECOSRALTMARVGYK--GEENKDLIE 184
Db HTLSLPSRSLFHRVAVLGSTGPNMATVSGARRRATILAVLVCPPGAGAGNDTELIS 302
QY 185 FLMKANPYDLKEEPOVLTPE 205
Db 303 CLTRPADLDVHEWVLPQE 323

RESULT 15

S36786

carboxylesterase (EC 3.1.1.1) E4 - green peach aphid

C:Species: Myzus persicae (green peach aphid)

C:Date: 09-Jun-1994 #sequence_revision 01-Dec-1995 #text_change 18-Jun-1999

C:Accession: S36786

R:Field, L.M.; Williamson, M.S.; Moores, G.D.; Devonshire, A.L.
Biochem. J. 294, 569-574, 1993

A:Title: Cloning and analysis of the esterase genes conferring insecticide resistance

A:Reference number: S36786; MUID:93384534; PMID:8373371

A:Accession: S36786

A>Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-552 <FIE>

A:Cross-references: EMBL:X74554; NID:9397510; PIDN:CAAS2648.1; PID:9397511

C:Superfamily: cholinesterase; cholinesterase homology

C:Keywords: carboxylic ester hydrolase

F:52-552/Domain: cholinesterase homology <CHE>

Query Match 30.9%; Score 338; DB 2; Length 552;

Best Local Similarity 41.3%; Pred. No. 2.8e-24;

Matches 81; Conservative 30; Mismatches 63; Indels 22; Gaps 7;

QY 3 DPLSG-KPTGSEDCLYLVNTDLPDKK---RPVWFTHGGGFIHGGEANRMWYGPDPY 57
Db EFGSGSKIIIGDCLFLNVYTPKLPQENSAGDLMNVIVIHGGGYFEGG--IITGPHYL 150
QY 58 M-KRPVLTVOYRLGVGFLSKSENLVNPENAGLKQVVALRMFKSNIAIFGSDVNDI 116
Db LNNDFEYVYSTRIGVLGFASTGQVLT--GNCKLQVVALRMFKSNIAIFGSDVNDI 208
QY 117 TVFGESAGASTHYMMITEQTRGLFHRGIMSGNSMCSASTECOSRALTMARVGYKGE 176
Db TITGMSAGASVHNHLISPMKGLFNRAIIQSGAFCHMSTAE-----NVAQTKTYIAN 262
QY 177 -----ENKDLIEFL 186
Db 263 IMGCPPTNNSVETLVECL 278

Search completed: April 4, 2003, 09:17:20
Job time : 8.92664 secs

GenCore version 5.1.4.P5-4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2003, 09:09:07 ; Search time 3.86293 Seconds
(without alignments)
2222.559 Million cell updates/sec

Title: us-09-776-910-15

Perfect score: 1093
Sequence: 1 QPDTISGKRTGSEDCLYLV.....KANPYDLKEPQVLTBERM 207

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	454	41.5	540	EST1_CULP1	P16854 culex pipie
2	359	32.8	564	EST1_HELV1	P12992 heliothis v
3	357.5	32.7	574	CHLE_HORSE	P81908 equus caball
4	348	31.6	613	ACES_BOVIN	P23795 bos taurus
5	344.5	31.5	564	ESTF_MYZPE	P35502 myzus persi
6	343.5	31.4	586	CHLE_MOUSE	P00311 mus musculu
7	343.5	31.4	586	ACES_TORCA	P04058 torpeda cal
8	342	31.3	611	ACES_FELCA	P06763 felis silve
9	341	31.2	581	ACES_BUNFA	P092035 bungarus fa
10	341	31.2	614	ACES_MOUSE	P21836 mus musculu
11	340	31.1	614	ACES_RABIT	P37136 rattus norv
12	338	30.9	552	ESTF_MYZPE	P029499 oryctolagus
13	336	30.7	602	CHLE_HUMAN	P35501 myzus persi
14	336	30.7	581	CHLE_RABIT	P06276 homo sapien
15	335.5	30.7	581	ES10_RAT	P21927 oryctolagus
16	335	30.6	565	ES10_RAT	P16303 rattus norv
17	335	30.6	614	ACES_HUMAN	P22303 homo sapien
18	334.5	30.6	590	ACES_TORMA	P07692 torpeda mar
19	334.5	30.6	767	ACES_CHICK	P36196 gallus galli
20	333	30.5	489	PNEB_BACSU	P37967 gallus galli
21	333	30.5	612	BAL_RAT	P07882 rattus norv
22	331.5	30.3	357	CHLI_BRALA	P095000 branchiost
23	331	30.3	567	EST1_HUMAN	P234121 homo sapien
24	331	30.3	567	EST1_HUMAN	P234121 homo sapien
25	330.5	30.2	561	EST5_RAT	P063010 rattus norv
26	329	30.1	597	BAL_BOVIN	P30122 bos taurus
27	329	30.1	634	ACES_BRARE	P063108 rattus norv
28	326	29.8	561	EST3_RAT	P063108 rattus norv
29	325.5	29.7	561	EST4_RAT	P063108 rattus norv
30	324.5	29.4	633	ACES_ELEEL	P042275 electrophor
31	321	29.4	561	EST1_MESAU	P064419 mesocricetu
32	321	29.4	742	BAL_HUMAN	P19835 homo sapien
33	320	29.3	554	ESTM_MOUSE	P063880 mus musculu

34	318	29.1	549	1	EST1_RAT	P10959 rattus norv
35	316	28.9	562	1	EST2_MOUSE	P064176 mus musculu
36	315	28.8	554	1	ESTN_MOUSE	P23953 mus musculu
37	314.5	28.8	620	1	ACEL_CABER	P27459 caenorhabdi
38	314.5	28.8	620	1	ACEL_CABER	P27459 caenorhabdi
39	314	28.7	566	1	EST1_PIG	P29550 sus scrofa
40	310.5	28.4	629	1	ACES_LEPDE	P27677 leptotars
41	310	28.4	532	1	EST2_RABIT	P14943 oryctolagus
42	310	28.4	545	1	ESTC_DROPS	P25725 drosophila
43	309.5	28.3	545	1	ESMB_DROPS	P25726 drosophila
44	308.5	28.2	542	1	EST6_DROMA	P47982 drosophila
45	308.5	28.2	547	1	ESTA_DROPS	P25727 drosophila

ALIGNMENTS

RESULT 1	EST1_CULP1	STANDARD	PRT	540 AA.
ID	EST1_CULP1			
AC	P16854;			
DT	01-AUG-1990 (Rel. 15, Created)			
DT	01-AUG-1990 (Rel. 15, Last sequence update)			
DT	01-FEB-1994 (Rel. 28, Last annotation update)			
DE	Esterase B1 precursor (EC 3.1.1.1).			
GN	B1.			
OS	Culex pipiens (House mosquito).			
OC	Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;			
OC	Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;			
OC	Culicoidae; Culex.			
OX	NCBI_TaxID=7175;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=TEM-R;			
RX	MEDLINE=90207238; PubMed=2320576;			
RA	Mouches C., Pauplin Y., Agarwal M., Lemieux L., Herzog M.,			
RA	Abadon M., Beysseat-Arnaout V., Hyrien O., de Saint Vincent B.R.,			
RA	Georgiou G.P., Pasteur N.;			
RT	*Characterization of amplification core and esterase B1 gene			
RT	responsible for insecticide resistance in Culex *;			
RL	Proc. Natl. Acad. Sci. U.S.A. 87:2574-2578(1990)			
CC	- FUNCTION: OVERPRODUCTION OF NONSPECIFIC ESTERASES IS A COMMON			
CC	MECHANISM OF RESISTANCE TO ORGANOPHOSPHATE INSECTICIDES.			
CC	- CARBOXYLIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a			
CC	carboxylic anion.			
CC	- MISCELLANEOUS: THERE ARE TWO SUCH ESTERASES: A AND B. ALLELES OF			
CC	BOTH A AND B ARE KNOWN.			
CC	- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@sib-sib.ch).			
CC	-----			
DR	EMBL, M3328; AAA28289.1; -			
DR	PIR, A35986; A35986.			
DR	HSSP, P21836; IMAA.			
DR	InterPro, IPR002018; CarboxylesteraseB.			
DR	InterPro, IPR000379; Ser_estrs_site.			
DR	Pfam: PF00135; Coesterase; 1.			
DR	PROSITE: PS00122; CARBOXYLESTERASE_B.2; FALSE_NEG.			
DR	PROSITE: PS00941; CARBOXYLESTERASE; MultiGene family; Signal.			
KW	Hydroxylase; Serine esterase; Glycoprotein; MultiGene family; Signal.			
FT	SIGNAL	1	?	
FT	CHAIN	?	540	
FT	ACT_SITE	191	191	ESTERASE B1.
FT	ACT_SITE	442	442	BY SIMILARITY.
FT	DISULFID	68	81	BY SIMILARITY.
FT	CARBOHYD	452	452	(POTENTIAL).
FT	SEQUENCE	540 AA:	60806 MW:	F73B25B3A7157C95 CRC64;

Query Match 41.5%; Score 454; DB 1; Length 540;
 Best Local Similarity 43.5%; Pred. No. 6, 2e-35;
 Matches 87; Conservative 41; Mismatches 72; Indels 0; Gaps 0;

OY 8 KPTGSDCLYNTVNDLNPKRPPVWFTHGGFTFGANRWYGPDPYMKRPVLT 67
 DB 77 KIVGDEDLKTNVAKETNPSTPLVMIYTGCGFTGTELTGYPDFLVQKDIYLSF 136
 OY 68 QYRLGVLGFLSKSENLNPNAGLKQVVALRFRKSNIAIEGDDVNTIVGESAGAS 127
 DB 137 NYRIGALGFLCCQSGDGVGNAGLKQVVALRFRKSNIAIEGDDVNTIVGESAGAS 196
 OY 128 THYMMITEQRTGLFRHIGMISGNSMSSASTECOSRALTWKRVGKGENEDILEFIM 187
 DB 197 VOYHLISDASKDLFQRIIVMSGSTYSMSLIRQNNVEXLAKAIGMDGGSGALRFLR 256
 OY 188 KANFYDLKEEPPVLPFERM 207
 DB 257 RAKPEDIVAHQEKLTDDM 276

RESULT 2

ESTD_HELVI STANDARD; PRT; 564 AA.
 AC P12992;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DE Juvenile hormone esterase precursor (EC 3.1.1.59) (JH esterase).
 OS Heliothis virescens (Noctuid moth) (Owllet moth).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;
 OC Diptera; Noctuidae; Noctuidae; Heliothinae; Heliothis.
 NCBI_Taxid=7102;
 [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 20-54.
 RA MEDLINE=89308671; PubMed=2745451;
 RT Hanzlik T.N., Yehia A.I.A.-A., Harshman L.G., Hammock B.D.;
 RT "Isolation and sequencing of cDNA clones coding for juvenile hormone
 RT esterase from *Heliothis virescens*. Evidence for a catalytic mechanism
 RT for the serine carboxylesterases different from that of the serine
 RT proteases.";
 RT J. Biol. Chem. 264:12419-12425(1989).
 RL [2]
 RN REVISIONS.
 RA Hanzlik T.N.;
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: JH ESTERASE PLAYS A CRUCIAL ROLE IN THE DECREASE OF
 CC JH ACTIVITY IN LEPIDOPTERAN INSECTS, BY HYDROLYZING THE METHYL
 CC ESTER OF JH. IT IS ALSO INVOLVED IN THE TRANSPORT OF JH.
 CC -1- CATALYTIC ACTIVITY: Methyl (2E,6E)-(10R,11S)-10,11-epoxy-3,7,11-
 CC trimethyltrideca-2,6-dienoate + H(2)O = (2E,6E)-(10R,11S)-10,11-
 CC epoxy-3,7,11-trimethyltrideca-2,6-dienoate + methanol.
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 CC THIS SWISS-PROT ENTRY IS COPYRIGHT. IT IS PRODUCED THROUGH A COLLABORATION
 CC BETWEEN THE SWISS INSTITUTE OF BIOINFORMATICS AND THE EMBL OUTSTATION -
 CC THE EUROPEAN BIOINFORMATICS INSTITUTE. THERE ARE NO RESTRICTIONS ON ITS
 CC USE BY NON-PROFIT INSTITUTIONS AS LONG AS ITS CONTENT IS IN NO WAY
 CC MODIFIED AND THIS STATEMENT IS NOT REMOVED. USAGE BY AND FOR COMMERCIAL
 CC ENTITIES REQUIRES A LICENSE AGREEMENT (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC EMBL: J04955; AAB88629.1. -
 DR PIR: A34325; A34325.
 DR HSSP: P37967; 10E3.
 DR InterPro: IPR002018; Carbesteraseb.
 DR InterPro: IPR000379; Ser_estr_site.
 DR Pfam: PF00135; Coesterase; 1.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; FALSE_NEG.
 DR Hydrolase; Serine esterase; Glycoprotein; Signal.
 KW

FT SIGNAL 1 19
 FT CHAIN 20 564 JUVENILE HORMONE ESTERASE.
 FT ACT_SITE 220 220 BY SIMILARITY.
 FT ACT_SITE 351 351 BY SIMILARITY.
 FT ACT_SITE 465 465 BY SIMILARITY.
 FT DISULFID 89 109 BY SIMILARITY.
 FT CARBOHYD 81 81 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 180 180 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 402 402 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 515 515 N-LINKED (GLCNAC...) (POTENTIAL).
 FT VARIANT 29 29 V -> L.
 FT VARIANT 52 52 F -> P.
 SO SEQUENCE 564 AA; 62614 MW; D140E5DD91914E8D CRC64;

Query Match 32.8%; Score 359; DB 1; Length 564;
 Best Local Similarity 42.5%; Pred. No. 5, 1e-26;
 Matches 71; Conservative 30; Mismatches 44; Indels 22; Gaps 4;

OY 1 QTFPISGKPTG-----SDCLYLVNY-----TNDLNDPKRPPVWFTHGGFTFG 45
 DB 91 QTVLVGRILMAASEMSEACIVANIHVPMQSLPRVGTPL-----RLIVTHGGFAFG 145
 OY 46 EANRNWYGPDPYMKRPVLTVOYRLGVGLSKSENLNPNAGLKQVVALRFRKSN 105
 DB 146 SCHEDLHCEPELVTKVYITFTNRYLVNFGELSMNT--TKIPNAGLRDQVTLRWQVN 203
 OY 106 IAFSGDVNTIVFEGSAGASTHYMMITEQRTGLFRHIGMISGNSM 152
 DB 204 AKNFGDPSDITLACOSAGASNAHLTLTKATEGLFRKAILMSGTGM 250

RESULT 3

CHIE_HORSE STANDARD; PRT; 574 AA.
 ID CHIE_HORSE
 AC P81908;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cholinesterase (EC 3.1.1.8) (Acetylcholine acylhydrolase) (Choline
 DE esterase II) (Butyrylcholine esterase) (Pseudocholinesterase) (Bq-
 DE BChE).
 GN Equus caballus (Horse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 NCBI_Taxid=9796;
 [1]
 RP SEQUENCE.
 RC TISSUE=Plasma;
 RA Moored D.R., Luo C., Garcia G.E., Doctor B.P.;
 RT "Amino acid sequence of horse serum butyrylcholinesterase.";
 RT (In) Doctor B.P., Taylor P., Quinn D.M., Rotundo R.L., Gentry M.K.
 RL (eds.);
 RL Structure and function of cholinesterases and related proteins,
 RL pp.145-146, Plenum Press, New York and London (1998).
 CC -1- CATALYTIC ACTIVITY: An acetylcholine + H(2)O = choline + a
 CC carboxylic acid anion.
 CC -1- SUBUNIT: HOMOTETRAMER. THE TETRAMER IS COMPOSED OF TWO DIMERS. THE
 CC TWO SUBUNITS IN A DIMER ARE LINKED BY A DISULFIDE BOND.
 CC -1- TISSUE SPECIFICITY: PRESENT IN MOST CELLS EXCEPT ERYTHROCYTES.
 CC -1- MISCELLANEOUS: CHOLINESTERASE IS HIGHLY REACTIVE WITH
 CC ORGANOPHOSPHATE ESTERS.
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 DR HSSP: P21836; 1MA.
 DR InterPro: IPR002018; Carbesteraseb.
 DR InterPro: IPR000997; Cholinesterase.
 DR InterPro: IPR000379; Ser_estr_site.
 DR Pfam: PF00135; Coesterase; 1.
 DR PROSITE: PS00878; CHOLINESTERASE.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
 DR Hydrolase; Serine esterase; Glycoprotein.
 KW ACT_SITE 198 198 BY SIMILARITY.

[illegible]

PRINTS; PR00878; CHOLNESTRAE.

PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.

DR PROSITE: PS00941; CARBOXYL ESTERASE B.2; 1.
 KW Hydrolyase; Serine esterase; Glycoprotein; Signal.
 FT SIGNAL 1 29
 FT CHAIN 30 603
 FT ACT_SITE 227 227
 FT ACT_SITE 354 354
 FT ACT_SITE 467 467
 FT ACT_SITE 94 121
 FT DISULFID 281 292
 FT DISULFID 429 548
 FT DISULFID 600 600
 FT CARBOHYD 86 86
 FT CARBOHYD 135 135
 FT CARBOHYD 270 270
 FT CARBOHYD 370 370
 FT CARBOHYD 484 484
 FT CARBOHYD 510 510
 FT CARBOHYD 515 515
 FT CONFLICT 129 129
 SQ SEQUENCE 603 AA; 68521 MW; 719B1B220D1E5367 CRC64;
 Query Match 31.5%; Score 344.5; DB 1; Length 603;
 Best Local Similarity 41.5%; Pred. No. 1.3e-24;
 Matches 81; Conservative 39; Mismatches 68; Indels 7; Gaps 5;
 QY 12 SEDCLYLVYNDLNPDKRPVWFHGGGFEGEANRMYGPDYEMK-KPVVLVTVQYR 70
 DB 118 SEDCLYLVWIRKPKR-KNATVWVWITGGGFQGTSSLPYDGKFLARVRVIVSMYR 176
 QY 71 LGVIGFLSKSENLVPCNAGIKDOVALRMFKSNIAIFGDDVNIIVPESAGGASTHY 130
 DB 177 VQALGFLEAPG-NPAPAPNMGIFDDQALALWVORHIAAFGSPKSTIFGESAGASVSL 235
 QY 131 MMITETRGLEFRGIMSGNSMCSA--STECOSRALTYMKRVYKGEENKIDILEFLM 187
 DB 236 HILCPQSYLFLTRAILLESGSSNAPVAVHPEARNRITLTKAFGC-SKENEMEMIKCLR 294
 QY 188 KANPYDLIKEPOVL 202
 DB 295 SKDPOELINERFVL 309
 RESULT 7
 ACES_TORCA STANDARD; PRT; 586 AA.
 ID ACES_TORCA
 AC P04058;
 DT 01-NOV-1986 (Rel. 03, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE acetylcholinesterase precursor (EC 3.1.1.7) (Ache).
 OS Torpedo californica (Pacific electric ray).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Squalia; Hynostomata; Pristigastera; Batoida;
 OC Torpediniformes; Torpedinidae; Torpedinidae; Torpedo.
 OX NCBI_Taxid=7787;
 RN [1]
 RP SEQUENCE OF 10-586 FROM N.A.
 RX MEDLINE=86118676; PubMed=3753747;
 RA Schumacher M., Camp S., Maulet Y., Newton M., McPhee-Quigley K.,
 RA Taylor S.S., Friedman T., Taylor P.;
 RA "Primary structure of Torpedo californica acetylcholinesterase
 RA deduced from its cDNA sequence.";
 RL Nature 319:407-409(1986).
 RN [2]
 RP SEQUENCE OF 1-9 FROM N.A.
 RX MEDLINE=89066695; PubMed=3198606;
 RA Schumacher M.;
 RA "Multiple messenger RNA species give rise to the structural diversity
 RA in acetylcholinesterase.";
 RL J. Biol. Chem. 263:18979-18987(1988).
 RN [3]
 RP SEQUENCE OF 552-558.
 RX MEDLINE=88087239; PubMed=3335534;
 RA Gibney G., MacPhee-Quigley K., Thompson B., Vedvick T., Low M.G.,
 RA Taylor S.S., Taylor P.;
 RA "Divergence in primary structure between the molecular forms of
 RA acetylcholinesterase.";
 RL J. Biol. Chem. 263:1140-1145(1988).
 RN [4]
 RP ALTERNATIVE SPLICING.
 RX MEDLINE=90166618; PubMed=2306366;
 RA Maulet Y., Camp S., Gibney G., Rachinsky T.L., Ekstrom T.J.,
 RA Taylor P.;
 RA "Single gene encodes glycopospholipid-anchored and asymmetric
 RA acetylcholinesterase forms: alternative coding exons contain inverted
 RA repeat sequences.";
 RL Neuron 4:289-301(1990).
 RN [5]
 RP DISULFIDE BONDS.
 RX MEDLINE=87008586; PubMed=3759980;
 RA McPhee-Quigley K., Vedvick T.S., Taylor P., Taylor S.S.;
 RA "Profile of the disulfide bonds in acetylcholinesterase.";
 RL J. Biol. Chem. 261:13565-13570(1986).
 RN [6]
 RP STRUCTURE OF THE GPI-ANCHOR.
 RX MEDLINE=94079692; PubMed=8257440;
 RA Mehler A., Varon L., Silman I., Homans S.W., Ferguson M.A.;
 RA "Structure of the glycosyl-phosphatidylinositol membrane anchor of
 RA acetylcholinesterase from the electric organ of the electric fish,
 RA Torpedo californica.";
 RL Biochem. J. 296:473-479(1993).
 RN [7]
 RP GPI-ANCHOR.
 RX MEDLINE=96176849; PubMed=8597567;
 RA Bucht G., Hjalmarsson K.;
 RA "Residues in Torpedo californica acetylcholinesterase necessary for
 RA processing to a glycosyl phosphatidylinositol-anchored form.";
 RL Biochim. Biophys. Acta 1252:223-232(1996).
 RN [8]
 RP MUTAGENESIS.
 RX MEDLINE=91017542; PubMed=2217185;
 RA Gibney G., Camp S., Dionne M., McPhee-Quigley K., Taylor P.;
 RA "Mutagenesis of essential functional residues in
 RA acetylcholinesterase.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:7546-7550(1990).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
 RX MEDLINE=91343928; PubMed=1678899;
 RA Sussman J.L., Harel M., Frolow F., Oefner C., Goldman A., Tokor L.,
 RA Silman I.;
 RA "Atomic structure of acetylcholinesterase from Torpedo californica: a
 RA prototypic acetylcholine-binding protein.";
 RL Science 253:872-879(1991).
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF COMPLEX WITH PASCICULIN.
 RX MEDLINE=96363673; PubMed=8747462;
 RA Harel M., Kleywegt G.J., Ravelli R.B., Silman I., Sussman J.L.;
 RA "Crystal structure of an acetylcholinesterase-fasciculin complex:
 RA interaction of a three-fingered toxin from snake venom with its
 RA target.";
 RL Structure 3:1355-1366(1995).
 RN [11]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE=97143314; PubMed=8989325;
 RA Raves M.L., Harel M., Pang Y.P., Silman I., Kozikowski A.P.,
 RA Sussman J.L.;
 RA "Structure of acetylcholinesterase complexed with the nootropic
 RA alkalioid, (-)-huperzine A.";
 RL Natl. Struct. Biol. 4:57-63(1997).
 RN [12]
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
 RX MEDLINE=99249780; PubMed=10231521;
 RA Bartolucci C., Perola E., Cellai L., Brufani M., Lamba D.;
 RA "Back door" opening implied by the crystal structure of a
 RA carbamoylated acetylcholinesterase.";
 RL Biochemistry 38:5714-5719(1999).

[illegible]

```

Query Match          31.4%; Score 343.5; DB 1; Length 586;
Best Local Similarity 41.0%; Pred. No.1:se-24;
Matches      80; Conservative    31; Mismatches   77; Indels       7; Gaps
QY      12 SEDCLYNVNTNDLNEDKKRPVFTHGGGFIFEANRMNNGYDPE-MKKPVLYTVVOYR 70
        |||||:::||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB       112 SEDCLYLNIWVSPSR-KSTVTWMVIYGGSFSSSLDYDNKRYLATIEEVLYKSLSYR 170
        |||||:::||||:||||:||||:||||:||||:||||:||||:||||:
QY      71 LGVLGFLSIKSENLNVPGAGLKDQVALMRFKNALITFGVDNYTIFGSGASAGATHY 130
        :||||:||||:||||:||||:||||:||||:||||:||||:
DB       171 VGAFGEFALHGSO-EAPGVGLGDQRNALOWHDNIQFCGGRPKYTTFIGESAGASYGM 229
        :||||:||||:||||:||||:||||:||||:||||:||||:
QY      131 MITTEOTRLFRHGIIMSGNSGCCSAS---TECSRATLMARKVGKGPNKIILEFIEM 187
        :::::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:
DB       230 HILSPGSRIPLFRRAIIQGSGPNCMAVSVAEGRRAVELGNLCNNLSDE-ELIHCLR 288
        :::::||:::||:::||:::||:::||:::||:::||:::||:::||:
QY      188 KANDPYDLKEPOYL 202
        :||::|||::|
DB       289 EKKPFELLIDVENVL 303
        :||::|||::|

RESULT # 8
ACCES_FELICA STANDARD; PRT; 611 AA.
AC AC 062763: 062762:
DT DT 16-OCT-2001 (Rel. 40, Created)
DT DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Acetylcholinesterase precursor (EC 3.1.1.7) (Ache).
GN ACHE.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_Trxid=9685;
[1]
SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE=20334351; PubMed=10874122;
RA Barfels C.F., Xie W., Miller-Lindholm A.K., Schopfer L.M.,
RA Lockridge O.;
RT "Determination of the DNA sequences of acetylcholinesterase and
RT butyrylcholinesterase from cat and demonstration of the existence of
RT both in cat plasma.";
RC Blochem. Pharmacol. 60:479-487(2000);
CC -I- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE (BY
CC SIMILARITY).
CC -I- CATALYTIC ACTIVITY: Acetylcholine + H2O = choline + acetate.
CC -I- SUBUNIT: ISOFORM H GENERATES GPI-ANCHORED DIMERS; DISULFIDE

```


SQ SEQUENCE 581 AA; 64722 MW; 436C3CBE457E399F CRC64;
 Query Match 31.2%; Score 341; DB 1; Length 581;
 Best Local Similarity 38.5%; Pred. No. 2,6e-24;
 Matches 85; Conservative 34; Mismatches 74; Indels 28; Gaps 6;
 QY 12 SEDCLVINYNDLNPDKRPVWFTHGGGFTFGGANRMVY-GPDYFMKKPVVLTVOYR 70
 D 122 SEDCLVINYNDLNPDKRPVWFTHGGGFTFGGANRMVY-GPDYFMKKPVVLTVOYR 180
 QY 71 LGVLGFLSKSENLVNPAGNAGLKDQVVALRMFKSNIAIFGSDVNTVFGESAGASTHY 130
 D 181 VGAGFGFLGPG-SPEARGNGGLDORALQWNTNHPGNGPRATVFGESAGASVGM 239
 QY 131 MMTETQRLFRHGMGSGMSGSSAS--TECQSRALTMARVYKGENEKDLEFLM 187
 D 240 HLSTQSRFLFRHGMGSGMSGSSAS--TECQSRALTMARVYKGENEKDLEFLM 187
 QY 188 KANPYDLKEEPQVLT-----TPERM 207
 D 299 SKNPDLIDEMSVLPYKSTFPEPPVVIDGFFPDTPERM 339
 RESULT 10
 ACES_MOUSE STANDARD; PRT; 614 AA.
 ID P21836;
 DT 01-MAY-1991 (rel. 18, Created)
 DT 01-MAY-1991 (rel. 18, Last sequence update)
 DT 16-OCT-2001 (rel. 40, Last annotation update)
 DE Acetylcholinesterase precursor (EC 3.1.1.7) (Ache).
 GN ACHE.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=90380429; PubMed=2400605;
 RA Rachtinsky T.L., Camp S., Li Y., Ekstrom T.J., Newton M., Taylor P.;
 RT "Molecular cloning of mouse acetylcholinesterase: tissue distribution
 of alternatively spliced mRNA species."; *Neuron* 5:317-327(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA STRAIN=129/Sv;
 RA MEDLINE=21138439; PubMed=11239002;
 RA Wilson M.D., Riemer C., Martindale D.W., Schnupf P., Boright A.P.,
 RA Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Tsui L.-C.,
 RA Miller W., Koop B.F.;
 RT "Comparative analysis of the gene-dense ACHE/TFP2 region on human
 chromosome 7q22 with the orthologous region on mouse chromosome 5."; *Nucleic Acids Res.* 29:1352-1365(2001).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS) OF COMPLEX WITH FASCICULIN.
 RA MEDLINE=96067648; PubMed=8521480;
 RA Bourne Y., Taylor P., Marchot P.;
 RT "Acetylcholinesterase inhibition by fasciculin: crystal structure of
 the complex."; *Cell* 83:503-512(1995).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RA MEDLINE=99115643; PubMed=9915834;
 RA Bourne Y., Taylor P., Bougis P.E., Marchot P.;
 RT "Crystal structure of mouse acetylcholinesterase. A peripheral site-
 occluding loop in a tetrameric assembly."; *J. Biol. Chem.* 274:2963-2970(1999).
 CC -1- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.
 CC -1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
 CC -1- SUBUNIT: ISOPFORM H GENERATES MULTIPLE ANCHORED DIMERS, DISULFIDE
 CC LINKED. ISOPFORM T GENERATES MULTIPLE STRUCTURES, RANGING FROM
 CC MONOMERS AND DIMERS TO COLLAGEN-TAILED AND HYDROPHOBIC-TAILED
 CC FORMS, IN WHICH CATALYTIC TETRAMERS ARE ASSOCIATED WITH ANCHORING

CC CC PROTEINS THAT ATTACH THEM TO THE BASAL LAMINA OR TO CELL
 CC CC MEMBRANES. IN THE COLLAGEN-TAILED FORMS, ISOPFORM T SUBUNTS ARE
 CC CC ASSOCIATED WITH A SPECIFIC COLLAGEN, COLO, WHICH TRIGGERS THE
 CC CC FORMATION OF ISOPFORM T TETRAMERS, FROM MONOMERS AND DIMERS (BY
 CC CC SIMILARITY).
 CC CC -1- ALTERNATIVE PRODUCTS: 2 ISOPFORMS; H AND T (SHOWN HERE); MAY BE
 CC CC PRODUCED BY ALTERNATIVE SPLICING.
 CC CC -1- TISSUE SPECIFICITY: PREDOMINATES IN MOST EXPRESSING TISSUES
 CC CC EXCEPT ERYTHROCYTES WHERE A GLYCOPHOSPHOLIPID-ATTACHED FORM OF
 CC CC ACHE PREDOMINATES.
 CC CC -1- MISCELLANEOUS: SYNAPSES USUALLY CONTRAIN ASYMMETRIC MOLECULES OF
 CC CC CHOLINESTERASE. WITH A COLLAGEN-LIKE PART DISULFIDE-BONDED TO THE
 CC CC CATALYTIC PART. A DIFFERENT, GLOBULAR TYPE OF CHOLINESTERASE
 CC CC OCCURS ON THE OUTER SURFACES OF CELL MEMBRANES, INCLUDING THOSE OF
 CC CC ERYTHROCYTES.
 CC CC -1- MISCELLANEOUS: THIS IS THE CATALYTIC SUBUNIT OF AN ASYMMETRIC OR
 CC CC SOLUBLE FORM OF ACHE.
 CC CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 CC CC
 CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC CC the European Bioinformatics Institute. There are no restrictions on its
 CC CC use by non-profit institutions as long as its content is in no way
 CC CC modified and this statement is not removed. Usage by and for commercial
 CC CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC CC or send an email to license@isb-sib.ch).
 CC CC
 CC CC EMBL: X56518; CAA39667.1; -
 CC CC DR EMBL: AF312033; AAK28816.1; -
 CC CC DR PIR: JH0314; JH0314.
 CC CC DR PDB: 1MAH; 03-APR-96.
 CC CC DR PDB: 1MAA; 20-APR-99.
 CC CC DR MGI: 87876; Ache.
 CC CC DR InterPro: IPR002018; CarbesteraseB.
 CC CC DR InterPro: IPR000997; Cholinesterase.
 CC CC DR InterPro: IPR000379; Ser_estrs_site.
 CC CC DR Pfam: PF00135; Coesterase; 1.
 CC CC DR PRINTS: PR00878; CARBOXYLESTERASE_B.1; 1.
 CC CC DR PROSITE: PS00122; CARBOXYLESTERASE_B.2; 1.
 CC CC DR PROSITE: PS00941; CARBOXYLESTERASE_B.2; 1.
 CC CC KM Hydrolyase; Serine esterase; Synapse; Membrane; Nerve; Muscle; Signal;
 CC CC KW Neurotransmitter degradation; Glycoprotein; Alternative splicing;
 CC CC 3D-structure. 1
 CC CC FT SIGNAL. 31
 CC CC FT CHAIN. 32 614 ACETYLCHOLINESTERASE.
 CC CC FT ACT_SITE. 234 234
 CC CC FT ACT_SITE. 365 365
 CC CC FT ACT_SITE. 478 478
 CC CC FT DISULFID. 100 127
 CC CC FT DISULFID. 288 303
 CC CC FT DISULFID. 440 560
 CC CC FT DISULFID. 611 611
 CC CC FT CARBOHYD. 296 296
 CC CC FT CARBOHYD. 381 381
 CC CC FT CARBOHYD. 495 495
 CC CC SQ SEQUENCE 614 AA; 68168 MW; 65E2512463C21172 CRC64;
 Query Match 31.2%; Score 341; DB 1; Length 614;
 Best Local Similarity 39.8%; Pred. No. 2,7e-24;
 Matches 80; Conservative 36; Mismatches 77; Indels 8; Gaps 5;
 QY 12 SEDCLVINYNDLNPDKRPVWFTHGGGFTFGGANRMVY-GPDYFMKKPVVLTVOYR 70
 D 124 SEDCLVINYNDLNPDKRPVWFTHGGGFTFGGANRMVY-GPDYFMKKPVVLTVOYR 183
 QY 71 LGVLGFLSKSENLVNPAGNAGLKDQVVALRMFKSNIAIFGSDVNTVFGESAGASTHY 130
 D 184 VGAGFGFLGPG-SPEARGNGGLDORALQWNTNHPGNGPRATVFGESAGASVGM 242
 QY 131 MMTETQRLFRHGMGSGMSGSSAS--TECQSRALTMARVYKGENEKDLEFLM 184
 D 243 HLSTQSRFLFRHGMGSGMSGSSAS--TECQSRALTMARVYKGENEKDLEFLM 184

QY 185 FLKMANPYDLKEEPOVLTPE 205
 Db 303 CLRTRPAQDLVDHNMVLPQE 323

RESULT 11
 ACES_RAT STANDARD; PRT; 614 AA.
 ID ACES_RAT STANDARD; PRT; 614 AA.
 AC P37136;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Acetylcholinesterase precursor (EC 3.1.1.7) (AChE);
 GN AChE.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus;
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM T).
 RX MEDLINE=93107932; PubMed=8417155;
 RA Legay C., Bon S., Vernier P., Cousen F., Massoulié J.;
 RT "Cloning and expression of a rat acetylcholinesterase subunit:
 RT generation of multiple molecular forms and complementarity with a
 RT Torpedo collagenic subunit";
 RL J. Neurochem. 60:337-346(1993).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS H AND R).
 RX MEDLINE=93114454; PubMed=8417973;
 RA Legay C., Bon S., Massoulié J.;
 RT "Expression of a cDNA encoding the glycolipid-anchored form of rat
 RT acetylcholinesterase";
 RL FEBS Lett. 315:163-166(1993).
 CC -1- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.
 CC -1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
 CC -1- SUBUNIT: OLIGOMER COMPOSED OF DISULFIDE-LINKED HOMODIMERS.
 CC CATALYTIC FORMS H (GPI-ANCHOR DIMER) AND T (ASYMMETRIC COLLAGEN-
 CC TAILED), WHICH DIFFER IN THEIR C-TERMINUS, ACCOUNT FOR ALL TYPES
 CC OF KNOWN AChE FORMS.
 CC -1- ALTERNATIVE PRODUCTS: 3 isoforms; T (shown here), H and R; are
 CC produced by alternative splicing. It is not known whether isoform
 CC R is functional.
 CC -1- TISSUE SPECIFICITY: HAS BEEN FOUND IN CENTRAL NERVOUS SYSTEM AND
 CC MUSCLE. FOUND IN EMBRYONIC LIVER AND SPLEEN BUT NOT IN ADULT
 CC LIVER.
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLSTERASE/LIPASE FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; S50879; AAB24586.1; -;
 CC EMBL; X70140; CAA49717.1; -;
 CC EMBL; X70141; CAA49718.1; -;
 CC PIR; JH0811; JH0811.
 CC HSSP; P21836; IMAA.
 CC InterPro; IPR002018; CarbesteraseB.
 CC InterPro; IPR000097; Cholinesterase.
 CC InterPro; IPR000379; Ser_estrs-site.
 CC Pfam; PF00135; Coesterase; 1.
 CC PRINTS; PR00878; CHOLNSTRASE.
 CC PROSITE; PS00122; CARBOXYLSTERASE_B_1; 1.
 CC PROSITE; PS00941; CARBOXYLSTERASE_B_2; 1.
 CC Hydrolase; Serine esterase; Synapse; Membrane; Nerve; Muscle; Signal;
 CC Neurotransmitter degradation; Glycoprotein; Alternative splicing.
 CC SIGNAL 1 31
 CC CHAIN 32 614
 CC ACT_SITE 234 365
 CC ACT_SITE 365 365
 CC BY SIMILARITY.

FT ACT_SITE 478 478 BY SIMILARITY.
 FT DISULFID 100 127 BY SIMILARITY.
 FT DISULFID 288 303 BY SIMILARITY.
 FT DISULFID 440 560 BY SIMILARITY.
 FT DISULFID 611 611 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 381 381 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 495 495 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPIC 575 614 DTLEAEHOMKAEFHFWSSYVWYKNOFHYSKORCSDL
 FT -> ATPEPTGCSRAFGAEPKRALSTSLFELHSG
 FT LKWL (IN ISOFORM H).
 FT DTLEAEHOMKAEFHFWSSYVWYKNOFHYSKORCSDL
 FT -> GRRGVKGQGHKAKARVGRIGERGKGRM (IN
 FT ISOFORM R).
 SO SEQUENCE 614 AA; 68196 MW; 2EDAE7D46282E7C0 CR664;
 Query Match 31.1%; Score 340; DB 1; Length 614;
 Best Local Similarity 39.3%; Pred. No. 3,4e-24;
 Matches 79; Conservative 37; Mismatches 77; Indels 8; Gaps 5;

QY 12 SEDCLYLVNTNDLNPDKRPVWVFTHGGFGEANRMWYGPDPYMK-KPVLYVVOYR 70
 Db 124 SEDCLYLVNTNPDPKRPVWVFTHGGFGEANRMWYGPDPYMK-KPVLYVVOYR 183
 QY 71 LGVGLFLSKSENLNPNAGLKDQYVALMFKSNIAIFGDVNDITVGEASGASTHY 130
 Db 184 VGTGFLALPGSR-EAPGNVGLDQRLAQVOENIAAFGSDPMSTVLTCESAGASVGM 242
 QY 131 MMTTEQRLGFLHFGIMMSG--NSMCSAST-EGOSRALTKARVGR---GEENEDILE 184
 Db 243 HILSPSRSLFHRVAVLQSGTPNGPMATVSGAEARRATLLARLVGPGAGGNDTLLS 302

QY 185 FLKMANPYDLKEEPOVLTPE 205
 Db 303 CLRTRPAQDLVDHNMVLPQE 323

RESULT 12
 ACES_RABIT STANDARD; PRT; 584 AA.
 ID ACES_RABIT STANDARD; PRT; 584 AA.
 AC 029499;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Acetylcholinesterase precursor (EC 3.1.1.7) (AChE) (Fragment).
 GN AChE.
 OS Oryctolagus cuniculus (Rabbit).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Muscle;
 RX MEDLINE=95010096; PubMed=7925428;
 RA Djillo O., Lhermitte Y., Tountant J., Chatonnet A.;
 RT "Acetylcholinesterase and butyrylcholinesterase expression in adult
 RT rabbit tissues and during development.";
 RL Eur. J. Biochem. 225:115-124(1994).
 CC -1- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.
 CC -1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
 CC -1- SUBUNIT: OLIGOMER COMPOSED OF DISULFIDE-LINKED HOMODIMERS.
 CC -1- MISCELLANEOUS: SYNAPSES USUALLY CONTAIN ASYMMETRIC MOLECULES OF
 CC CHOLINSTERASE, WITH A COLLAGEN-LIKE PART DISULFIDE-BONDED TO THE
 CC CATALYTIC PART. A DIFFERENT, GLOBULAR TYPE OF CHOLINSTERASE
 CC OCCURS ON THE OUTER SURFACES OF CELL MEMBRANES, INCLUDING THOSE OF
 CC ERYTHROCYTES.
 CC -1- MISCELLANEOUS: THIS IS THE CATALYTIC SUBUNIT OF AN ASYMMETRIC OR
 CC SOLUBLE FORM OF AChE.
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLSTERASE/LIPASE FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sdb.ch/announce/>
 CC or send an email to license@sdb.ch).

DR EMBL: U05036; AAA53235.1; -
 DR HSSP: P22303; 2CLJ.
 DR InterPro: IPR002018; Carboxylesterase.
 DR InterPro: IPR000379; Ser-esterase.
 DR Pfam: PF00135; Coesterase; 1.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
 DR Hydrolyase; Serine esterase; Synapse; Membrane; Nerve; Muscle; signal;
 KW Neurotransmitter degradation; Glycoprotein.
 FT NON_TER 1
 FT SIGNAL 1
 FT CHAIN 1
 FT ACT_SITE 2 584
 FT ACT_SITE 204 204
 FT ACT_SITE 335 335
 FT ACT_SITE 448 448
 FT DISULFID 70 97
 FT DISULFID 258 273
 FT DISULFID 410 530
 FT DISULFID 581 581
 FT CARBOHYD 266 266
 FT CARBOHYD 351 351
 FT CARBOHYD 465 465
 FT SEQUENCE 584 AA; 64630 MW; 2AE157F3063649FE CRC64;

Query Match 31.0%; Score 339; DB 1; Length 584;
 Best Local Similarity 39.4%; Pred. No. 4e-24;
 Matches 80; Conservative 35; Mismatches 76; Indels 12; Gaps 6;

QY 12 SEDCLYLVNTYNDLMDPKRPVWVFHGGGFTFGEANRN-WGPDVEMKKPVLVVVOYR 70
 DB 94 SEDCLYLVNTYNDLMDPKRPVWVFHGGGFTFGEANRN-WGPDVEMKKPVLVVVOYR 153
 QY 71 LGVLGFLSKSENVLNPGNAGLKDQVMAALRMFKSNIAIFGQVDNITVGEASGASTHY 130
 DB 154 VGAFGFTCLPGSR-EAPGNVGLDQRLALQVQENVAAGFPGDPAVTLGEGSAGASVGL 212
 QY 131 MWITEQTRGLFHRGIMSG--NSMSSAST-ECQSALTMARV-----GYGEEHEKDI 182
 DB 213 HLLSPSRRLFRRAVLQSGAPNGPVAIVGVEARRRATLLARLVCCPGAGG--NDTEL 270
 QY 183 LEFLMKANPYDLIKEPQVLTPE 205
 DB 271 VACLRTRPADLDVDEHWRVLPGE 293

RESULT 13
 ESTE_MYZPE STANDARD; PRT; 552 AA.
 AC P35501:
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE Esterase B4 precursor (EC 3.1.1.1) (Carboxyl-ester hydrolase).
 OS Myzus persicae (peach-potato aphid).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha;
 OC Aphidiformes; Aphidoidea; Aphididae; Macrosiphini; Myzus.
 NCBI_TaxID=13164;
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 24-63.
 RC STRAIN=R3 / isolate 794J;
 RA MEDLINE=93384534; PubMed=8373731;
 RA Field L.M., Williamson M.S., Moores G.D., Devonshire A.L.;
 RT "Cloning and analysis of the esterase genes conferring insecticide
 resistance in the peach-potato aphid, Myzus persicae (Sulzer).";
 RL Biochem. J. 294:569-574(1993).
 CC -1- FUNCTION: OVERPRODUCTION OF NONSPECIFIC ESTERASES IS A COMMON
 CC MECHANISM OF RESISTANCE TO ORGANOPHOSPHATE INSECTICIDES.

CC -1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
 CC carboxylic anion.
 CC -1- MISCELLANEOUS: THIS ESTERASE CONFERS INSECTICIDE RESISTANCE.
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sdb.ch/announce/>
 CC or send an email to license@sdb.ch).

DR EMBL: X74554; CAA52648.1; -
 DR PIR: S36786; S36786.
 DR HSSP: P21836; 1MAA.
 DR InterPro: IPR002018; Carboxylesterase.
 DR InterPro: IPR000379; Ser-esterase.
 DR Pfam: PF00135; Coesterase; 1.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; FALSE_NEG.
 KW Hydrolyase; Serine esterase; Glycoprotein; signal.
 FT SIGNAL 1
 FT CHAIN 24 23
 FT ACT_SITE 214 214
 FT ACT_SITE 339 339
 FT ACT_SITE 463 463
 FT DISULFID 89 106
 FT DISULFID 266 277
 FT CARBOHYD 81 81
 FT CARBOHYD 269 269
 FT CARBOHYD 371 371
 FT CARBOHYD 404 404
 FT CARBOHYD 443 443
 FT SEQUENCE 552 AA; 61348 MW; B97B67272DEF7209 CRC64;

Query Match 30.9%; Score 338; DB 1; Length 552;
 Best Local Similarity 41.3%; Pred. No. 4.6e-24;
 Matches 81; Conservative 30; Mismatches 63; Indels 22; Gaps 7;

QY 3 DFISG-KPTGSEDCYLVNTYNDLMDPKR-----RPVWVFHGGGFTFGEANRNWYGPDYF 57
 DB 93 EFGSGSKITIGEDCLFLNNTYTRKLPQENSAGDLNVIHIGGGYFGSG--ILVGFHL 150
 QY 58 M-KRPVLTVOYRIGVLGFLSKSENVLNPGNAGLKDQVMAALRMFKSNIAIFGQVDNI 116
 DB 151 LDNDPYYVYVYIRGLVGLFASGTGDLT--GNNGIKDQVMAALRWIQOINIVAFGGDPNSV 208
 QY 117 TVFGESAGASTHYMMITQETGLFHRGIMSGNSMSSASTECQSALTMARVYKGE 176
 DB 209 TTGMSAGASVYHNLISPMKGLFRKAITQSGAFCWSTAL-----NVAKRTYIAN 262
 QY 177 -----ENEKDLLEFL 186
 DB 263 IMGCPITNSVEIVECL 278

RESULT 14
 CHEL_HUMAN STANDARD; PRT; 602 AA.
 AC P06276:
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cholinesterase precursor (EC 3.1.1.8) (Acetylcholine acylhydrolase)
 DE (Pseudocholinesterase II) (Butyrylcholine esterase)
 DE BCHE OR CHEI.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_TaxID=9606;
 RN [1]

QY 12 SEDCLYLVNTNDLPDKRRVWFIHGCGFIFGEANRMWGPDPYFK-KPVVLVTVQYR 70
 |||||
 Db 117 SEDCLYLVNTNDLPDKRRVWFIHGCGFIFGEANRMWGPDPYFK-KPVVLVTVQYR 70
 |||||
 QY 71 LGVIGFELSKSENLVPGNAGLKDQVALRMFKSNIAIFGDDVNTIVGESAGASTHY 130
 :|||||
 Db 176 VGALGFLLPG-NPEAPGNMGLFPODLALQWVKNIAPFGNPKSVTLFGESAGASVSL 234
 :|||||
 QY 131 MATEOTRGLFRHGMGNSMCSAST---ECOSRALTMARKVGYGGENEKDILEFLM 187
 :|||
 Db 235 HILSPGSHLPTRALILQSGSNAPWATSLYEARNRTLLAKLTC-SRENETEIIKCLR 293
 :|||
 QY 188 KANPYDLIKEPOVL---TP 204
 :|||
 Db 294 NKDQETILLNEAFVVPYGT 313
 :|||

RESULT 15

CHLE RABIT STANDARD: PRT: 581 AA.
 AC P21927;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Cholinesterase precursor (EC 3.1.1.8) (acetylcholine acetylhydrolase)
 DE (Choline esterase II) (butyrylcholine esterase)
 DE (pseudocholinesterase)
 GN BCHE.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID:9986;
 RN 11)
 RP SEQUENCE FROM N.A.
 RC STRAIN-New Zealand;
 RC MEDLINE-90326526; PubMed-2374720;
 RA Jbllo O.; Roudani S.; Chatonnet A.;
 RT "Complete sequence of rabbit butyrylcholinesterase.";
 RL Nucleic Acids Res. 18:3990-3990(1990).
 RN 12)
 RP SEQUENCE OF 75-215 FROM N.A.
 RC TISSUE-Liver;
 RC MEDLINE-91201348; PubMed-2016308;
 RA Arpagus M.; Chatonnet A.; Masson P.; Newton M.; Vaughan T.A.;
 RA Bartels C.F.; Nogueira C.P.; La Du B.N.; Lockridge O.;
 RT "Use of the polymerase chain reaction for homology probing of
 butyrylcholinesterase from several vertebrates.";
 RL J. Biol. Chem. 266:6966-6974(1991).
 CC -1- CATALYTIC ACTIVITY: An acetylcholine + H(2)O = choline + a
 carboxylic acid anion.
 CC -1- SUBUNIT: HOMOTETRAMER. THE TETRAMER IS COMPOSED OF TWO DIMERS. THE
 TWO SUBUNITS IN A DIMER ARE LINKED BY A DISULFIDE BOND.
 CC -1- TISSUE SPECIFICITY: PRESENT IN MOST CELLS EXCEPT ERYTHROCYTES.
 CC -1- MISCELLANEOUS: CHOLINESTERASE IS HIGHLY REACTIVE WITH
 ORGANOPHOSPHATE ESTERS.
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL ESTERASE/LIPASE FAMILY.

This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 or send an email to license@sib-sib.ch).

DR EMBL: X52090; CAA36308.1;
 DR EMBL: X52091; CAA36308.1; JOINED.
 DR EMBL: X52092; CAA36308.1; JOINED.
 DR EMBL: M62779; AAA31169.1;
 DR PIR: S10255; S10255.
 DR PIR: C39768; C39768.
 DR HSSP: P21836; IMAA.

DR InterPro: IPR002018; CarbesteraseB.
 DR InterPro: IPR000997; Cholinesterase.
 DR InterPro: IPR000379; Ser_estrs_site.
 DR Pfam: PF00135; Coesterase_1.
 DR PRINTS: PR00878; CHOLINESTERASE.
 DR PROSITE: PS00122; CARBOXYL ESTERASE B.1; 1.
 DR PROSITE: PS00941; CARBOXYL ESTERASE B.2; 1.
 KW Hydrolyase; Serine esterase; Glycoprotein; Signal.
 FT SIGNAL 1
 FT CHAIN 8
 FT ACT_SITE 205 581
 FT ACT_SITE 332 205
 FT ACT_SITE 332 332
 FT ACT_SITE 445 445
 FT DISULFID 72 99
 FT DISULFID 259 270
 FT DISULFID 407 526
 FT DISULFID 578 578
 FT CARBOHYD 64 64
 FT CARBOHYD 113 113
 FT CARBOHYD 248 248
 FT CARBOHYD 263 263
 FT CARBOHYD 348 348
 FT CARBOHYD 462 462
 FT CARBOHYD 488 488
 FT CARBOHYD 492 492
 FT CARBOHYD 493 493
 SQ SEQUENCE 581 AA; 66156 MW; FE8B199E7B32EB0A CRC64;
 Query Match 30.7%; Score 335.5; DB 1; Length 581;
 Best Local Similarity 40.3%; Pred. No. 8,4e-24;
 Matches 77; Conservative 40; Mismatches 67; Indels 7; Gaps 5;

QY 12 SEDCLYLVNTNDLPDKRRVWFIHGCGFIFGEANRMWGPDPYFK-KPVVLVTVQYR 70
 |||||
 Db 96 SEDCLYLVNTNDLPDKRRVWFIHGCGFIFGEANRMWGPDPYFK-KPVVLVTVQYR 70
 |||||
 QY 71 LGVIGFELSKSENLVPGNAGLKDQVALRMFKSNIAIFGDDVNTIVGESAGASTHY 130
 :|||||
 Db 155 VGALGFLLPG-NPEAPGNMGLFPODLALQWVKNIAPFGNPKSVTLFGESAGASVSL 234
 :|||||
 QY 131 MATEOTRGLFRHGMGNSMCSAST---SASTECOSRALTMARKVGYGGENEKDILEFLM 187
 :|||
 Db 214 HILSPGSHLPTRALILQSGSNAPWATSLYEARNRTLLAKLTC-SRENETEIIKCLR 293
 :|||
 QY 188 KANPYDLIKEP 198
 :|||
 Db 273 NKDQETILLNE 283

Search completed: April 4, 2003, 09:13:40
 Job time: 6.86293 secs

GenCore version 5.1.4-p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2003, 09:09:58 ; Search time 20.6467 Seconds
(without alignments)
2065.788 Million cell updates/sec

Title: US-09-776-910-15

Perfect score: 1093
Sequence: 1 QTFDISGKPTGSEDCLYLVN.....KANPYDLIKEPQVLTPEKM 207

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL.21.*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_prodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1053	96.3	570	5	09XZ70 musca domes
2	840	76.9	570	5	09Y409 haematobia
3	825	75.5	570	5	025252
4	736	67.3	556	5	024201 dirosophila
5	736	67.3	572	5	09V1B5 dirosophila
6	735.5	67.3	345	5	09N153 dirosophila
7	595	54.4	530	5	09I7L5 dirosophila
8	595	54.4	549	5	024204 dirosophila
9	593	54.3	565	5	09N159 dirosophila
10	587.5	53.8	567	5	09V1B3 dirosophila
11	586.5	53.7	558	5	024202 dirosophila
12	585	53.5	297	5	09N151 dirosophila
13	582	53.2	554	5	09V1B0 dirosophila
14	579	53.0	286	5	09N152 dirosophila
15	573	52.4	553	5	024194 dirosophila
16	573	52.4	563	5	09V1C3 dirosophila

17	568	52.0	572	5	024203	024203 dirosophila
18	567	51.9	401	5	09N160	09N160 dirosophila
19	563.5	51.6	566	5	09W243	09W243 dirosophila
20	563	51.5	572	5	09V1B1	09V1B1 dirosophila
21	560	51.2	554	5	09V1C2	09V1C2 dirosophila
22	560	51.2	566	5	09V1N0	09V1N0 dirosophila
23	559	51.1	564	5	09N161	09N161 dirosophila
24	556	50.9	554	5	024195	024195 dirosophila
25	555	50.8	554	5	09S030	09S030 dirosophila
26	555	50.8	542	5	024198	024198 dirosophila
27	555	50.8	542	5	09V1B9	09V1B9 dirosophila
28	542	49.6	446	5	09N155	09N155 dirosophila
29	504.5	46.2	532	5	061726	061726 anisopterom
30	503.5	46.1	532	5	061727	061727 anisopterom
31	481	44.0	532	5	061597	061597 culix pipie
32	480	43.9	540	5	08W089	08W089 culix pipie
33	478	43.7	540	5	09G095	09G095 culix pipie
34	478	43.7	540	5	08W088	08W088 culix pipie
35	475	43.5	360	5	09G091	09G091 dirosophila
36	475	43.5	467	5	09V156	09V156 culix pipie
37	475	43.5	467	5	09V159	09V159 culix pipie
38	475	43.5	540	5	023733	023733 culix quing
39	475	43.5	540	5	09V156	09V156 culix quing
40	470	43.0	541	5	024197	024197 dirosophila
41	470	43.0	541	5	09V1C0	09V1C0 dirosophila
42	469	42.9	568	5	09V1B6	09V1B6 dirosophila
43	468.5	42.9	435	5	09N154	09N154 dirosophila
44	466.5	42.7	526	5	076177	076177 aphs gossy
45	466	42.6	540	5	09V1920	09V1920 culix tarsa

ALIGNMENTS

RESULT 1

09XZ70 PRELIMINARY; PRT; 570 AA.

AC 09XZ70;

DT 01-NOV-1999 (TREMUREL. 12, Created)

DT 01-NOV-1999 (TREMUREL. 12, Last sequence update)

DT 01-MAR-2002 (TREMUREL. 20, Last annotation update)

DE Carboxylesterase MdaE7 (EC 3.1.1.1).

GN MDAE7.

OS Musca domestica (House fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Muscidae; Muscidae; Musca.

NCBI_TaxID=7370;

CC [1]

RP SEQUENCE FROM N.A.

RC STRAIN=RUTGERS DIAZINON-R.

RX MEDLINE=9381228; PubMed=10451921;

RA Claudianos C., Russell R.J., Oakeshott J.G.;

RT "The same amino acid substitution in orthologous esterases confers

RT organophosphate resistance on the house fly and a blowfly.";

RL Insect Biochem. Mol. Biol. 29:675-686(1999).

CC -1 SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.

DR EMBL; AF133341; AAD29685.1;

DR HSSP; P37967; 10E3.

DR InterPro: IPR002018; CarboxylesteraseB.

DR InterPro: IPR000379; Ser esters_site.

DR Pfam; PF00135; Coesterase_1.

DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.

DR HydroLase.

SO SEQUENCE 570 AA; 65421 MW; 08AFEBEF284003BB CRC64;

Query Match 96.3%; Score 1053; DB 5; Length 570;

Best Local Similarity 96.6%; Pred. No. 2,5e-91;

Matches 200; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 QTFDISGKPTGSEDCLYLVNVTNDINPDKRRPVWFIHGCFITGEANRMWYGDYEPKK 60
|||||
DB 97 QTFDISGKPTGSEDCLYLVNVTNDINPDKRRPVWFIHGCFITGEANRMWYGDYEPKK 156

```

QY 61 PVLVTVOYRLGVLGFLSLKSENLANVPGNAGLKDQVMAIRWFKSNIAIFGGDVNITVFG 120
DB 157 PVLVTVOYRLGVLGFLSLKSENLANVPGNAGLKDQVMAIRWFKSNIANANGGDVNITVFG 216
QY 121 ESAGGASTHYMTTEQTRGLFRHGMISGNSMCSASTCQSBALTMARVYKGEENK 180
DB 217 ESAGGASTHYMTTEQTRGLFRHGMISGNSMCSASTCQSBALTMARVYKGEENK 276
QY 181 DLEFLMKANPYDLIKEEPOVLTPERM 207
DB 277 DLEFLMKANPYDLIKEEPOVLTPERM 303

RESULT 2
ID 090409 PRELIMINARY; PRT; 570 AA.
AC 090409;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
OS Alpha E7 esterase.
GN AE7.
OC Haemolobia irritans irritans.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Muscidae; Muscidae; Haemolobia.
OC NCBI_Taxid=75445;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CAMP COOLEY 4/97;
RX MEDLINE=20445807; PubMed=10989298;
RA Guerrero F.D.;
RT "Cloning of a horn fly cDNA, HialphaE7, encoding an esterase whose
transcript concentration is elevated in diazinon-resistant flies."
RL Insect Biochem. Mol. Biol. 30:1107-1115(2000).
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL: AF139082; AAF14517.1;
DR HSSP: P37967; 1OE3.
DR InterPro: IPR002018; CarbesteraseB.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF00135; Coesterase; 1.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
DR KJ Hydrolyase.
KW HYDROLASE.
SQ SEQUENCE 570 AA; 65613 MW; 18DA0A9A94AB970D CRC64;

Query Match 76.9%; Score 840; DB 5; Length 570;
Best Local Similarity 75.4%; Pred. No. 4e-71;
Matches 156; Conservative 20; Mismatches 31; Indels 0; Gaps 0;

```

```

DE 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DB Alpha esterase (LCAE7) (Carboxylesterase).
GN LCAE7.
OS Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Oestroidae; Calliphoridae; Lucilia.
OC NCBI_Taxid=7375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LS2;
RA Newcomb R.D.; East P.D.; Russell R.J.; Oakeshott J.G.;
RL Insect Mol. Biol. 5:0-0(0).
RN [2]
RP SEQUENCE OF 70-181 FROM N.A.
RC STRAIN=LS2;
RA Newcomb R.D.; East P.D.; Russell R.J.; Oakeshott J.G.;
RL Insect Mol. Biol. 0:0-0(0).
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL: U56636; AAB67728.1;
DR EMBL: U49421; AAA92012.1;
DR HSSP: P37967; 1OE3.
DR InterPro: IPR002018; CarbesteraseB.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF00135; Coesterase; 1.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
DR KJ Hydrolyase.
KW HYDROLASE.
SQ SEQUENCE 570 AA; 65416 MW; 399D723A0F338FD CRC64;

Query Match 75.5%; Score 825; DB 5; Length 570;
Best Local Similarity 74.6%; Pred. No. 1.1e-69;
Matches 153; Conservative 25; Mismatches 27; Indels 0; Gaps 0;

```


DR InterPro: IPR000379; Ser_estrs_site.
 DR Pfam: PF00135; Coesterase; 1.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
 KW Hydrolase.
 FT NON_TER 1 1
 FT NON_TER 556 556
 SQ SEQUENCE 556 AA; 63397 MW; AF0680A1D3C34425 CRC64;
 Query Match 67.3%; Score 736; DB 5; Length 556;
 Best Local Similarity 67.5%; Pred. No. 2.8e-61;
 Matches 141; Conservative 25; Mismatches 41; Indels 2; Gaps 2;

OY 1 QDTDISKPTGSEDCILYLVNTDNLNPKRRPVMEFHGGGFIIEANRMYGPDYEMKK 60
 DB 81 QVQFVFDKVEGSEDCILYLVNTNPKRRPVMEFHGGGFIIEANRMYGPDYEMKE 140
 OY 61 PVLVTVQVRYLGLVGLFLSKSENINVPNGNGLKQDVMLRWFKSNIAIFGSDVDNITYFG 120
 DB 141 DVLVTVIQRGLGALGFMISKSPELNVPNGNGLKQDVMLRWFKSNIAIFGSDVDNITYFG 200
 OY 121 ESAGASTHYMMITDQGTGFLHFGILGMSGNSMCSA-STECOSRALTMAKRVGYKEENE 179
 DB 201 ESAGASTHYMMITDQGTGFLHFGILGMSGNSMCSA-STECOSRALTMAKRVGYKEENE 260
 OY 180 KDLEFLMKANPYDLKEEPOVLT-PERM 207
 DB 261 KDLEFLMKANPYDLKEEPOVLT-PERM 289

RESULT 5
 OYVIB5 PRELIMINARY; PRT; 572 AA.
 ID 09VIB5;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE ALPHA-EST7 OR CG112.
 GN ALPHA-EST7 OR CG112.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 RX SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 MEDLINE-20196006; PubMed-10731132;
 RA Adams M.D., Gelniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sulton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H.C., Blazer R.G., Champagne M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Plamkosh C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
 RA Burkova D., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cavley S., Danke C., Davenport L.B., Davies P.,
 RA de Pallos B., Delcher A., Deng Z., Mays A.D., Dew I., Diez S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegami C., Ketchum K.A.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kemison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mettel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Spier B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Sphar E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Sylvestre R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 RN 121
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY.
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nuno J., Paclab J., Paragas V., Park S., Phuanavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Gelniker S.,
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 DR EMBL: AE003671; AF54010.1; -.
 DR EMBL: AY051473; AA92897.1; -.
 DR HSSP: P21836; IMAA.
 DR Flybase: FBgn0015575; alpha-Est7.
 DR InterPro: IPR002018; Carbesterase.
 DR InterPro: IPR000379; Ser_estrs_site.
 DR Pfam: PF00135; Coesterase; 1.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
 DR Hydrolase.
 SQ SEQUENCE 572 AA; 65435 MW; 693D9360DA18AE27 CRC64;
 Query Match 67.3%; Score 736; DB 5; Length 572;
 Best Local Similarity 67.5%; Pred. No. 2.9e-61;
 Matches 141; Conservative 25; Mismatches 41; Indels 2; Gaps 2;

OY 1 QDTDISKPTGSEDCILYLVNTDNLNPKRRPVMEFHGGGFIIEANRMYGPDYEMKK 60
 DB 97 QVQFVFDKVEGSEDCILYLVNTNPKRRPVMEFHGGGFIIEANRMYGPDYEMKE 156
 OY 61 PVLVTVQVRYLGLVGLFLSKSENINVPNGNGLKQDVMLRWFKSNIAIFGSDVDNITYFG 120
 DB 157 DVLVTVIQRGLGALGFMISKSPELNVPNGNGLKQDVMLRWFKSNIAIFGSDVDNITYFG 216
 OY 121 ESAGASTHYMMITDQGTGFLHFGILGMSGNSMCSA-STECOSRALTMAKRVGYKEENE 179
 DB 217 ESAGASTHYMMITDQGTGFLHFGILGMSGNSMCSA-STECOSRALTMAKRVGYKEENE 276
 OY 180 KDLEFLMKANPYDLKEEPOVLT-PERM 207
 DB 277 KDLEFLMKANPYDLKEEPOVLT-PERM 305

RESULT 6
 OYVIB5 PRELIMINARY; PRT; 345 AA.
 ID 09VIB5;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Alpha-esterase 7 (Fragment).
 GN AEA7 OR AEA7.
 OS Drosophila buzzatii (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7264;
 RX SEQUENCE FROM N.A.
 RC Robin C., Claudianos C., Russell R.J., Oakeshott J.G.,
 RT "The alpha-esterase cluster of Drosophila buzzatii";
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 DR EMBL: AF216215; AAF26729.1; .
 DR HSPB: P21836; IMAA.
 DR FlyBase: FBgn0029447; DbnvAae7a.
 DR InterPro: IPR002018; CarbesteraeB.
 DR InterPro: IPR000379; Ser-estrs-site.
 DR Pfam: PF00135; Coesterase_1.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
 DR Hydrolyase.
 KW NON_TER 1
 FT 345 345
 SQ SEQUENCE 345 AA; 38472 MW; C08564A34E4EC97A CRC64;

Query Match 67.3%; Score 735.5; DB 5; Length 345;
 Best Local Similarity 68.0%; Pred. No. 1.6e-61;
 Matches 140; Conservative 27; Mismatches 38; Indels 1; Gaps 1;

QY 1 QDTFSGKPTGSEDCILYNTYNDLNDKRRPVWFHGGGFTFGANRMWGPDPYMK 60
 Db 28 QVHFVPEBRESSECLLYNTYNNLSAPKRPVWVHGGGFTFGANRDWGPDPYFKE 87
 QY 61 PVLVTVQYRLGVLGFLSLKSENLPVGNAGLKDQVVALWPKSNIAIFGVDNTVFG 120
 Db 88 DVVTVTVQYRLGALGFLSLKTPGLNVPVGNAGLKDQVVALWPKSNIAIFGVDNTVFG 147
 QY 121 ESAGASTHYMIMTEQTRGFHFGIMSGNSMCSA-STECOSRALFMKRVGYGEENE 179
 Db 148 ESAGASTHYMIMTDQGTGFLHFGILQSGSAIGPMAFNGDITSAFRIRAKLAGYGEEND 207
 QY 180 KDILEFLMKANPYDLIKEPQVLTPE 205
 Db 208 KDVLQFLQTVRARDLIRVEQVLTPE 233

RESULT 7

Q91715 PRELIMINARY; PRT; 530 AA.

AC 091715; 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Alpha-Est10 protein.
 GN ALPHA-EST10 OR CG1131.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RX MEDLINE-20196006; PubMed-10731132;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Tandel M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milos G.L.G.,
 RA Abill J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshanov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
 RA Burlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahler A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA de Pallos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwa C.,
 RA Jalali M., Kalish F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mohrly C., Morris J., Mostrel A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Spaden-Klamas I., Simpson M., Skupski M.P., Smith T.,
 RA Spler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.-E., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gbbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RL "The genome sequence of Drosophila melanogaster";
 CC Science 287:2185-2195(2000)
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 DR EMBL: AEO03671; AAC22202.1; .
 DR HSPB: P37967; I0E3.
 DR FlyBase: FBgn0015569; alpha-Est10.
 DR InterPro: IPR002018; CarbesteraeB.
 DR InterPro: IPR000997; Cholinesterase.
 DR InterPro: IPR000379; Ser-estrs-site.
 DR Pfam: PF00135; Coesterase_1.
 DR PRINTS: PR00878; CHOLINESTRASE.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
 DR Hydrolyase.
 KW SEQUENCE 530 AA; 59739 MW; FP9011F52DEA07F1 CRC64;

Query Match 54.4%; Score 595; DB 5; Length 530;
 Best Local Similarity 55.7%; Pred. No. 6.2e-46;
 Matches 113; Conservative 31; Mismatches 59; Indels 0; Gaps 0;

QY 1 QDTFISGKPTGSEDCILYNTYNDLNDKRRPVWFHGGGFTFGANRMWGPDPYMK 60
 Db 62 QTHMFEKRYAGSEDCILYNTYNNLSAPKRPVWVHGGGFTFGANRDWGPDPYFKE 121
 QY 61 PVLVTVQYRLGVLGFLSLKSENLPVGNAGLKDQVVALWPKSNIAIFGVDNTVFG 120
 Db 122 DVVTVTVQYRLGALGFLSLKTPGLNVPVGNAGLKDQVVALWPKSNIAIFGVDNTVFG 181
 QY 121 ESAGASTHYMIMTEQTRGFHFGIMSGNSMCSA-STECOSRALFMKRVGYGEENE 180
 Db 182 ESAGASTHYMIMTDQGTGFLHFGILQSGSAIGPMAFNGDITSAFRIRAKLAGYGEEND 241
 QY 181 DILEFLMKANPYDLIKEPQVLT 203
 Db 242 AIFELRSMGSEIVKATVLS 264

RESULT 8

Q24204 PRELIMINARY; PRT; 549 AA.

AC 024204; 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Alpha-esterase (Fragment).
 GN ALPHA-EST10 OR AE10 OR CG1131.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN 11
 RP SEQUENCE FROM N.A.
 RC Robin C., Medveczky K.M., Russell R.J., Oakeshott J.G.;
 RL J. Mol. Evol. 0:0-0(0).
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 DR EMBL: U51054; AAB01153.1; .
 DR HSPB: P21836; IMAA.
 DR FlyBase: FBgn0015569; alpha-Est10.

[illegible]

KW Hydrolase.
SQ SEQUENCE 567 AA; 64831 MW; 07DACC72786F14A CRC64;

Query Match 53.8%; Score 587.5; DB 5; Length 567;
Best Local Similarity 54.9%; Pred. No. 3.5e-47;
Matches 112; Conservative 32; Mismatches 60; Indels 1; Gaps 1;

QY 1 QDIFSGKPTGSEDCILYLVNTNDLPDKRPVWFHGGGFGEAGRNMYGDPYFMKK 60
DB 90 QVNIIVLKOVGSEDCILYLVNTRELPHRPLVLTWITGGGFQMGESRDLYSPDYITME 149
QY 61 PVLVTVQYRLGVLFGLSLKSENLVNPVGNAGLKQVMAALRWFKSNIAIFGGDVNITVFG 120
DB 150 HVLVVISIRLGLFGLSLADELDVPCNAGLKQVMAALRWVKNRCQFFGGDPDNITVFG 209
QY 121 ESAGASTHYMMITETQTLGFLFRGIMSGNSCSASTECO-SRALLMARKVYKGEENE 179
DB 210 ESAGASTHYMMITDQAGLFLFKTITIMSGSALAPMAOTPTHTNPYRLAQTGYTGAND 269
QY 180 KDIEFLMKANPYDLKEEPOVLTPE 205
DB 270 RDIFFALKKCKASSMLKVAEDITIME 295

RESULT 11

Q24202 PRELIMINARY; PRT; 558 AA.

AC Q24202.
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Alpha esterase (Fragment).
GN ALPHA-EST8 OR CG1121.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
FT NON_TER

SEQUENCE FROM N.A.
RA Robin C., Medveczky K.M., Russell R.J., Oakeshott J.G.;
RL J. Mol. Evol. 0:0-0(0).
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL: U51052; AAB01151.1; -.
DR HSSP: P37967; IOE3.
DR Flybase: FBgn0015576; alpha-Est8.
DR InterPro: IPR002018; Carboxylesterase.
DR Pfam: PF00135; Coesterase_1.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
KW Hydrolase.
FT NON_TER

SQ SEQUENCE 558 AA; 63916 MW; BFF6F62C8FF212720 CRC64;

Query Match 53.7%; Score 586.5; DB 5; Length 558;
Best Local Similarity 54.4%; Pred. No. 4.2e-47;
Matches 112; Conservative 33; Mismatches 60; Indels 1; Gaps 1;

QY 1 QDIFSGKPTGSEDCILYLVNTNDLPDKRPVWFHGGGFGEAGRNMYGDPYFMKK 60
DB 81 QVNIIVLKOVGSEDCILYLVNTRELPHRPLVLTWITGGGFQMGESRDLYSPDYITME 140
QY 61 PVLVTVQYRLGVLFGLSLKSENLVNPVGNAGLKQVMAALRWFKSNIAIFGGDVNITVFG 120
DB 141 HVLVVISIRLGLFGLSLADELDVPCNAGLKQVMAALRWVKNRCQFFGGDPDNITVFG 200
QY 121 ESAGASTHYMMITETQTLGFLFRGIMSGNSCSASTECO-SRALLMARKVYKGEENE 179
DB 201 ESAGASTHYMMITDQAGLFLFKTITIMSGSALAPMAOTPTHTNPYRLAQTGYTGAND 260
QY 180 KDIEFLMKANPYDLKEEPOVLTPE 205

DB 261 RDIFFALKKCKASSMLKVAEDITIME 286

RESULT 12

Q9N151 PRELIMINARY; PRT; 297 AA.

AC Q9N151.
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Alpha-esterase 9 (Fragment).
GN AEG9 OR AEG9.
OS Drosophila buzzatii (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7264;
RN [1]
FT NON_TER

SEQUENCE FROM N.A.
RA Robin C., Claudianos C., Russell R.J., Oakeshott J.G.;
RT "The alpha-esterase cluster of Drosophila buzzatii."
RL Submitted (DEC-1999) to the EMBL/GenBank/DBD databases.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL: AF216217; AAF26731.1; -.
DR HSSP: P37967; IOE3.
DR Flybase: FBgn0029445; DbuzAEG9.
DR InterPro: IPR002018; Carboxylesterase.
DR Pfam: PF00135; Coesterase_1.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
KW Hydrolase.
FT NON_TER

SQ SEQUENCE 297 AA; 33635 MW; 89CF7761871B362D CRC64;
Query Match 53.5%; Score 585; DB 5; Length 297;
Best Local Similarity 54.6%; Pred. No. 2.5e-47;
Matches 112; Conservative 33; Mismatches 60; Indels 0; Gaps 0;

QY 1 QDIFSGKPTGSEDCILYLVNTNDLPDKRPVWFHGGGFGEAGRNMYGDPYFMKK 60
DB 81 QKHFVEMTGSSEDCILYLVNTKNLYPVKPMVWMTITGGGFQFEASRECYSPDYITRE 140
QY 61 PVLVTVQYRLGVLFGLSLKSENLVNPVGNAGLKQVMAALRWFKSNIAIFGGDVNITVFG 120
DB 141 DVVVISIRLGLFGLSLADELDVPCNAGLKQVMAALRWVKNRCQFFGGDPDNITVFG 200
QY 121 ESAGASTHYMMITETQTLGFLFRGIMSGNSCSASTECO-SRALLMARKVYKGEENE 180
DB 201 DSAGSASTHYMMITETQTLGFLFKTITIMSGSALAPMAOTPTHTNPYRLAQTGYTGAND 260
QY 181 DILEFLMKANPYDLKEEPOVLTPE 205
DB 261 EWVEFLKNAKGSIDITKANGELCTIXE 285

RESULT 13

Q9VIB0 PRELIMINARY; PRT; 554 AA.

AC Q9VIB0.
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Alpha-EST9 protein.
GN ALPHA-EST9 OR CG1128.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
FT NON_TER

SEQUENCE FROM N.A.
RC STRAIN-BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananidis P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S.J., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos L.G.,
 RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brockstein P., Brotler P.,
 RA Burlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,
 RA Fostel C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,
 RA Jatelli M., Kalush F., Karpen G.H., Ke Z., Kenison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclik J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Sytkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of Drosophila melanogaster".
 RL Science 287:2185-2195(2000).
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 DR EMBL: AE003671; AAF54014.1; -.
 DR HSSP: P37967; 10E3.
 DR FLYBASE: FBgn0015577; alpha-Est9.
 DR InterPro: IPR002018; Carboxylesterase.
 DR InterPro: IPR000997; Carboxylesterase.
 DR InterPro: IPR000379; Ser-estrs-site.
 DR Pfam: PF00135; Coesterase; 1.
 DR PRINTS: PR00878; CHOLNESTRASE.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
 DR HydroLase.
 SQ SEQUENCE 554 AA; 63670 MW; 0A72368389DFPC2B CRC64;

Query Match 53.2%; Score 582; DB 5; Length 554;
 Best Local Similarity 54.6%; Pred. No. 1, le-46;
 Matches 112; Conservative 31; Mismatches 62; Indels 0; Gaps 0;

QY 1 QTPDISGKPTGSEDCILYNTYNDLNPDKRPVVFTHGGGTFEGANRWGPDYFMKK 60
 DB 81 OHFVEMTDSGSEDCILYNTYNTYNDLNPDKRPVVFTHGGGTFEGANRWGPDYFMKK 140
 QY 61 PVLVTVYVRLVGLVGLSLKSENLPVGNAGLKDQVMAIRFMSNTAIFGVDVNTVFG 120
 DB 141 DVVAVSINRRLGFLGLDLPDELVPNGAGLKDQVMAIRFMSNTAIFGVDVNTVFG 200
 QY 121 ESAGGASTHYMTTEQTRGLFHGIMSGMSKSSASTEGQSALTMARVYKGEENK 180
 DB 201 DSAGASVHYMTTEQTRGLFHGIMSGMSKSSASTEGQSALTMARVYKGEENK 260
 QY 181 DLEFLMKANPYDLKEEPOVLTPE 205
 DB 261 DVEFLKNAKGSEIKANGELCID 285

RESULT 14

09NI52
 ID 09NI52 PRELIMINARY; PRT: 286 AA.
 AC 09NI52
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Alpha-esterase 8 (Fragment).
 GN AEA OR AEB.
 OS Drosophila buzzatii (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCB1_TaxID=7264;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Robin C., Claudianos C., Russell R.J., Oakeshott J.G.,
 RT "The alpha-esterase cluster of Drosophila buzzatii".
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 DR EMBL: AF216216; AAF26730.1; -.
 DR HSSP: P21836; 1MAA.
 DR FLYBASE: FBgn0029446; DhuzaaE8a.
 DR InterPro: IPR002018; Carboxylesterase.
 DR InterPro: IPR000379; Ser-estrs-site.
 DR Pfam: PF00135; Coesterase; 1.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; UNKNOWN_1.
 DR HydroLase.
 KW NON_TER
 FT NON_TER
 SQ SEQUENCE 286 AA; 32409 MW; ADCCAFED124D2A953 CRC64;

Query Match 53.0%; Score 579; DB 5; Length 286;
 Best Local Similarity 53.2%; Pred. No. 8, 7e-47;
 Matches 109; Conservative 36; Mismatches 60; Indels 0; Gaps 0;
 QY 1 QTPDISGKPTGSEDCILYNTYNDLNPDKRPVVFTHGGGTFEGANRWGPDYFMKK 60
 DB 28 QVNLVYLKQVSGSEDCILYNTYNTYNDLNPDKRPVVFTHGGGTFEGANRWGPDYFMKK 87
 QY 61 PVLVTVYVRLVGLVGLSLKSENLPVGNAGLKDQVMAIRFMSNTAIFGVDVNTVFG 120
 DB 88 HVLVTVYVRLVGLVGLSLKSENLPVGNAGLKDQVMAIRFMSNTAIFGVDVNTVFG 147
 QY 121 ESAGGASTHYMTTEQTRGLFHGIMSGMSKSSASTEGQSALTMARVYKGEENK 180
 DB 148 ESAGGASTHYMTTEQTRGLFHGIMSGMSKSSASTEGQSALTMARVYKGEENK 207
 QY 181 DLEFLMKANPYDLKEEPOVLTPE 205
 DB 208 EIFKHLQCKASSMLRMAEGIVIME 232

RESULT 15
 ID 024194 PRELIMINARY; PRT: 553 AA.
 AC 024194;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Alpha-esterase E1.
 GN ALPHA-EST1 OR AEL OR CG1031.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCB1_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=CANTON S;
 RX MEDLINE=97056255; PubMed=8900595;
 RA Russell R.J., Robin G.C., Kostakos P., Newcomb R.D., Boyce T.M.,
 RA Medveczky K.M., Oakeshott J.G.;

RT	"Molecular cloning of an alpha-esterase gene cluster on chromosome 3 of <i>Drosophila melanogaster</i> ."			
RL	Insect Biochem. Mol. Biol. 26:235-247(1996).			
CC	-1. SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLTERASE/LIPASE FAMILY.			
DR	EMBL; U51043; BAB01142.1; -.			
DR	HSSP; P21836; 1MAH.			
DR	FLYBASE: FBgn0015568; alpha-Est1.			
DR	InterPro: IPR002018; CarboxylesteraseB.			
DR	InterPro: IPR000379; Ser_estrs.site.			
DR	Pfam: PF00135; Coesterase; 1.			
KM	Hydrolase.			
FT	147	150	POLY-VAL.	
SQ	SEQUENCE	553 AA;	63620 MW;	D30E8803BEADAD5 CRC64;

FILE REFERENCE: Attorney Docket No. 6235515 50179-051
 CURRENT APPLICATION NUMBER: US/09/068,960A
 CURRENT FILING DATE: 1998-05-20
 EARLIER APPLICATION NUMBER: PCT/AU96/00746
 EARLIER FILING DATE: 1996-11-22
 EARLIER APPLICATION NUMBER: AU 6751
 EARLIER FILING DATE: 1995-11-23
 NUMBER OF SEQ ID NOS: 43
 SOFTWARE: Patentln Ver. 2.0
 SEQ ID NO 13
 LENGTH: 570
 TYPE: PRT
 ORGANISM: Musca domestica
 US-09-068-960-13

Query Match 97.2%; Score 1062; DB 4; Length 570;
 Best Local Similarity 97.1%; Pred. No. 3.9e-121;
 Matches 201; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 QDFTSGKPTGSEDCLYNYNTDNLNDPKRPVWFTHGGGFTFGEANRMWYGPDYFMKK 60
 Db 97 QDFTSGKPTGSEDCLYNYNTDNLNDPKRPVWFTHGGGFTFGEANRMWYGPDYFMKK 156
 QY 61 PVLVTVOYRLGVGLFLSKSENINVPNGNGLKDOVVALRMFNSNIAIFGGDVNITVFG 120
 Db 157 PVLVTVOYRLGVGLFLSKSENINVPNGNGLKDOVVALRMFNSNIAIFGGDVNITVFG 216
 QY 121 ESAGASTHYMMITEQTRGLFHRGIMSGNSKCSASTECOSRALTMAKRVGKGEENK 180
 Db 217 ESAGASTHYMMITEQTRGLFHRGIMSGNSKCSASTECOSRALTMAKRVGKGEENK 276
 QY 181 DLEFLMKANPYDLIKEEPOVLTPERM 207
 Db 277 DLEFLMKANPYDLIKEEPOVLTPERM 303

RESULT 3
 US-09-068-960-43
 Sequence 43, Application US/09068960A
 Patent No. 6235515
 GENERAL INFORMATION:
 APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.
 TITLE OF INVENTION: MALATHION CARBOXYLESTERASE
 FILE REFERENCE: Attorney Docket No. 6235515 50179-051
 CURRENT APPLICATION NUMBER: US/09/068,960A
 EARLIER APPLICATION NUMBER: PCT/AU96/00746
 EARLIER FILING DATE: 1998-05-20
 EARLIER FILING DATE: 1996-11-22
 EARLIER APPLICATION NUMBER: AU 6751
 EARLIER FILING DATE: 1995-11-23
 NUMBER OF SEQ ID NOS: 43
 SOFTWARE: Patentln Ver. 2.0
 SEQ ID NO 43
 LENGTH: 207
 TYPE: PRT
 ORGANISM: Lucilia cuprina
 US-09-068-960-43

Query Match 75.6%; Score 826; DB 4; Length 207;
 Best Local Similarity 74.6%; Pred. No. 5.9e-93;
 Matches 153; Conservative 25; Mismatches 27; Indels 0; Gaps 0;

QY 1 QDFTSGKPTGSEDCLYNYNTDNLNDPKRPVWFTHGGGFTFGEANRMWYGPDYFMKK 60
 Db 1 QDFTSGKPTGSEDCLYNYNTDNLNDPKRPVWFTHGGGFTFGEANRMWYGPDYFMKK 60
 QY 61 PVLVTVOYRLGVGLFLSKSENINVPNGNGLKDOVVALRMFNSNIAIFGGDVNITVFG 120
 Db 61 PVLVTVOYRLGVGLFLSKSENINVPNGNGLKDOVVALRMFNSNIAIFGGDVNITVFG 120
 QY 121 ESAGASTHYMMITEQTRGLFHRGIMSGNSKCSASTECOSRALTMAKRVGKGEENK 180
 Db 121 ESAGASTHYMMITEQTRGLFHRGIMSGNSKCSASTECOSRALTMAKRVGKGEENK 180
 QY 121 ESAGASTHYMMITEQTRGLFHRGIMSGNSKCSASTECOSRALTMAKRVGKGEENK 180
 Db 121 ESAGASTHYMMITEQTRGLFHRGIMSGNSKCSASTECOSRALTMAKRVGKGEENK 180

QY 181 DLEFLMKANPYDLIKEEPOVLTPERM 205
 Db 181 DLEFLMKANPYDLIKEEPOVLTPERM 205

RESULT 4
 US-09-068-960-2
 Sequence 2, Application US/09068960A
 Patent No. 6235515
 GENERAL INFORMATION:
 APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.
 TITLE OF INVENTION: MALATHION CARBOXYLESTERASE
 FILE REFERENCE: Attorney Docket No. 6235515 50179-051
 CURRENT APPLICATION NUMBER: US/09/068,960A
 EARLIER APPLICATION NUMBER: PCT/AU96/00746
 EARLIER FILING DATE: 1998-05-20
 EARLIER FILING DATE: 1996-11-22
 EARLIER APPLICATION NUMBER: AU 6751
 EARLIER FILING DATE: 1995-11-23
 NUMBER OF SEQ ID NOS: 43
 SOFTWARE: Patentln Ver. 2.0
 SEQ ID NO 2
 LENGTH: 570
 TYPE: PRT
 ORGANISM: Lucilia cuprina
 US-09-068-960-2

Query Match 75.6%; Score 826; DB 4; Length 570;
 Best Local Similarity 74.6%; Pred. No. 2.8e-92;
 Matches 153; Conservative 25; Mismatches 27; Indels 0; Gaps 0;

QY 1 QDFTSGKPTGSEDCLYNYNTDNLNDPKRPVWFTHGGGFTFGEANRMWYGPDYFMKK 60
 Db 97 QDFTSGKPTGSEDCLYNYNTDNLNDPKRPVWFTHGGGFTFGEANRMWYGPDYFMKK 156
 QY 61 PVLVTVOYRLGVGLFLSKSENINVPNGNGLKDOVVALRMFNSNIAIFGGDVNITVFG 120
 Db 157 PVLVTVOYRLGVGLFLSKSENINVPNGNGLKDOVVALRMFNSNIAIFGGDVNITVFG 216
 QY 121 ESAGASTHYMMITEQTRGLFHRGIMSGNSKCSASTECOSRALTMAKRVGKGEENK 180
 Db 217 ESAGASTHYMMITEQTRGLFHRGIMSGNSKCSASTECOSRALTMAKRVGKGEENK 276
 QY 181 DLEFLMKANPYDLIKEEPOVLTPERM 205
 Db 277 DLEFLMKANPYDLIKEEPOVLTPERM 301

RESULT 5
 US-09-068-960-4
 Sequence 4, Application US/09068960A
 Patent No. 6235515
 GENERAL INFORMATION:
 APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.
 TITLE OF INVENTION: MALATHION CARBOXYLESTERASE
 FILE REFERENCE: Attorney Docket No. 6235515 50179-051
 CURRENT APPLICATION NUMBER: US/09/068,960A
 EARLIER APPLICATION NUMBER: PCT/AU96/00746
 EARLIER FILING DATE: 1998-05-20
 EARLIER FILING DATE: 1996-11-22
 EARLIER APPLICATION NUMBER: AU 6751
 EARLIER FILING DATE: 1995-11-23
 NUMBER OF SEQ ID NOS: 43
 SOFTWARE: Patentln Ver. 2.0
 SEQ ID NO 4
 LENGTH: 570
 TYPE: PRT
 ORGANISM: Lucilia cuprina
 US-09-068-960-4

Query Match 75.6%; Score 826; DB 4; Length 570;
 Best Local Similarity 74.6%; Pred. No. 2.8e-92;

VERSION	KEYWORDS	EST.	GI:3478225
SOURCE	fruit fly.		
ORGANISM	Drosophila melanogaster		
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.		
REFERENCE	1 (bases 1 to 646)		
AUTHORS	Harvey, D., Broksstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S., and Rubin, G.M.		
TITLE	Bdgp/Hm1 Drosophila EST project		
JOURNAL	unpublished (2001)		
COMMENT	Contact: stapleton, M. Bdgp		
FEATURES	Lawrence Berkeley National Lab One Cyclotron Rd. Berkeley, CA 94720, USA Fax: 510 486 6796 Email: http://www.fruitfly.org/EST/estfruitfly.berkeley.edu Plate: 92 row: H column: 8 High quality sequence stop: 513. location/Qualifiers		
SOURCE	1. 646 /organism="Drosophila melanogaster" /db_xref="taxon:7227" /clone="GH09292" /clone_11b="GH Drosophila melanogaster head pot2" /sex="male and female" /dev_stage="adult" /lab_host="DHS - alpha" /note="Organ: head; Vector: pot2; Site_1: EcoRI; Site_2: XhoI; Sized fractionated cDNAs were directly ligated into pot2. Plasmid cDNA library." BASE COUNT 152 a 163 c 182 g 149 t ORIGIN		
Query Match:	14.2%; Score 243.4; DB 9; Length 646;		
Best Local Similarity	64.8%; Pred. No. 1.6e-55;		
Matches 361; Conservative	0; Mismatches 196; Indels 0; Gaps 0		
1	ATGCAATTCACAGTTAGTTGATGAGAAATTAAATGGAAGATTAAATGATGAAAT 60		
89	ATGAAATAGAACCTCGGCTTTGGAGAGCCTTGGCGGTGCGCCTCAAAACATCGAGCAT 148		
61	AAGTTTAACTATCGTTAACTAACTGAAACGGTGTGACTGAATATGGC 120		
149	AAAGTCACACATATCGCCAGTCGACCAATGAAACGTTGTGGCGACAGGAGTACGGC 208		
121	AAAGTAAAGCGGTTAAAGTTAACTGTGATGATGATTCCTACTACAGTTTGAAGGT 180		
209	CAGATGAGGGGATACAGCGTCTATCTCTACAGATGTCCCTACTACGTTTCAAGGAT 268		
181	ATACCGTACGCCCAACGCGCAGTGGGTGAGTGAAGTTAAAGACCCAGCGACCAACA 240		
269	ATCCCGTACGCCACGCTCGGTTGGGGAGTTGACGGTTTAAAGCCCTCAAGGGCCCAT 328		
241	CCCTGGATGGTGTGGTGATTTGGTCAATCAATAAAGATAAGCAGTGAAGTTGATTT 300		
329	CCCTGGAGCGAGTTGCGACATGCAACGCCAGCGAAGATTAAGCCGTCCAGGTGCAATT 388		
301	ATACGCGGCAAGTGTGTGGCTCAGAGATTGCTATTAAGTGTCTATACGAATAAT 360		
389	GTCTTCGATTAAGGTAGAAGGCTCCGAGGACTGCCCTCTATCTCATGTATACACACAA 448		
361	CTAATATCCGAATTAACAGTCCCGTTTAAATATACATCAATGATGATGATTTATATAC 420		
449	GTTGAAGCCCGACAAAGCTCGCCGGTTAAGTTGATTACAGGAGAGAGGCTTCAATTAT 508		
421	GTTGAATATCAATGATTAAGTGTCTGATTAATTAATTAATTAATTAATTAATTAATTA 480		
509	GGCGAGCCCAATGCGAATGATGAGCCCGGATTTACTTTATGAAGAAGATGTTGTTCTC 568		
481	ATTAACTATCAATATGTTTGGAGCTTCAAGTTTCTAAGTTTAAATTCAGAAGCCTT 540		

Db	569	GTACAGATACAGTACCGACTTGGGCTTTGGATTATATAGACTTAAGTCCCGGAGCTA	628
Qy	541	AATGTGCCCCGATATGC	557
Db	629	AATGTACCAAGAAATGC	645
RESULT 15			
LOCUS	AI293416	646 bp	mrna
DEFINITION	LP06524:5prime LP Drosophila melanogaster larval-early pupal POT2		
	U51050: Drosophila melanogaster alpha esterase (AE7) gene, partial		
	cds, mRNA sequence.		
ACCESSION	AI293416		
VERSION	AI293416.1	GI:3942823	
KEYWORDS	EST.		
SOURCE	fruit fly.		
ORGANISM	Drosophila melanogaster		
	Euarvota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		
	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
	Ephydroidea; Drosophilidae; Drosophila.		
REFERENCE	1 (bases 1 to 646)		
AUTHORS	Harvey,D., Brokslein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,		
	Lewis,S. and Rubin,G.M.		
TITLE	BDGP/HHMI Drosophila EST Project		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Stapleton, M.		
	BDGP		
	Lawrence Berkeley National Lab		
	One Cyclotron Rd, Berkeley, CA 94720, USA		
	Fax: 510 486 6798		
	Email: http://www.fruitfly.org/EST , est@fruitfly.berkeley.edu		
	Plate: 65 row: B column: 12		
	High quality sequence stop: 493.		
FEATURES	Location/Qualifiers		
Source	1..646		
	/organism="Drosophila melanogaster"		
	/db_xref="taxon:7227"		
	/clone="LP06524"		
	/clone_lib="LP Drosophila melanogaster larval-early pupal		
	POT2"		
	/sex="male and female"		
	/dev_stage="larvae-pupae"		
	/lab_host="DHS-alpha"		
	/note="Organ: whole body; Vector: POT2; Site:1: EcoRI;		
	Site:2: XhoI; Sized fractionated cDNAs were directly		
	ligated into POT2. Plasmid cDNA library.		
BASE COUNT	151 a 163 c 184 g 148 t		
ORIGIN			
Query Match	14.2%; Score 243.4; DB 9; Length 646;		
Best Local Similarity	64.8%; Pred. No. 1.6e-55;		
Matches 361; Conservative 0; Mismatches 196; Indels 0; Gaps 0;			
Qy	1	ATGATTTTCAACGTAGTTGATGAGAAATAAATGSAAGATTAAATGATTGAAAT	60
Db	89	ATGATTAAGAACCTCGGCTTTGGAGCCCTTGGCGGTGCGGCTCAAAACATCGACAT	148
Qy	61	AAGTTTAAATATCGTTTAACCTACCAATGAAACGGTGTAGCTGAACCTGAATATGTC	120
Db	149	AAAGTCACGACATATGCGCAATGCAATGAACAGTTGTGCGCGACACGAGTAACGC	208
Qy	121	AAAGTGAAGCGCGTTAAACGTTAACTGTGTCGATGATCTCTACTACGTTTGAAGGT	180
Db	209	CAAGTGAGGGGTATCAAGGCTATCTCTCATGATGTGCCCTACTTCAGCTTGAGGGT	268
Qy	181	ATACGTCAGCCCAACCGCCAGTGGGTGAGCTGAGATTTAAAGCAACCCAGGACACAA	240
Db	269	ATCCCGTACGCCCAAGCTCCGCTGGGGAGAGTTGCGGTTTAAAGCCCTCAGAGCGCCAT	328
Qy	241	CCCTGGATGGTGTGCGTATGTTGCCATATCAATAAGATTAAGTCAAGTCAAGTTGTTT	300

GenCore version 5.1.4_p5-4578
Copyright (c) 1993 - 2003 Comphen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 11, 2003, 00:41:37 ; Search time 40.5118 Seconds
(without alignments)
12967.505 Million cell updates/sec

Title: US-09-776-910-9

Perfect score: 1713

Sequence: 1 atgaattcaacgttagttt.....aacatagagatttatttag 1713

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/5A.COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PTOS.COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query % Match	Length	ID	Description
1	1713	100.0	1713	US-09-068-960-9	Sequence 9, Appl
2	1711.4	99.9	1713	US-09-068-960-1	Sequence 1, Appl
3	1711.4	99.9	1713	US-09-068-960-3	Sequence 3, Appl
4	1708.2	99.7	1713	US-09-068-960-5	Sequence 5, Appl
5	1703.4	99.4	1713	US-08-669-524-1	Sequence 1, Appl
6	1703.4	99.4	1713	US-09-068-960-7	Sequence 7, Appl
7	1678.2	98.0	1713	US-08-668-524-2	Sequence 2, Appl
8	956.6	55.8	1710	US-09-068-960-14	Sequence 14, Appl
9	179.6	10.5	1584	US-08-747-221B-51	Sequence 51, Appl
10	179.6	10.5	1584	US-08-747-221B-52	Sequence 52, Appl
11	179.6	10.5	1584	US-09-005-051-51	Sequence 51, Appl
12	179.6	10.5	1584	US-09-005-051-52	Sequence 52, Appl
13	179.6	10.5	2007	US-08-747-221B-36	Sequence 36, Appl
14	179.6	10.5	2007	US-08-747-221B-38	Sequence 38, Appl
15	179.6	10.5	2007	US-09-005-051-36	Sequence 36, Appl
16	179.6	10.5	2007	US-09-005-051-38	Sequence 38, Appl
17	142.2	8.3	1590	US-08-747-221B-23	Sequence 23, Appl
18	142.2	8.3	1590	US-09-005-051-23	Sequence 23, Appl
19	142.2	8.3	1650	US-08-747-221B-21	Sequence 21, Appl
20	142.2	8.3	1650	US-08-747-221B-22	Sequence 22, Appl
21	142.2	8.3	1650	US-09-005-051-21	Sequence 21, Appl
22	142.2	8.3	1650	US-09-005-051-22	Sequence 22, Appl
23	142.2	8.3	1792	US-08-747-221B-18	Sequence 18, Appl
24	142.2	8.3	1792	US-08-747-221B-20	Sequence 20, Appl
25	142.2	8.3	1792	US-09-005-051-18	Sequence 18, Appl
26	142.2	8.3	1792	US-09-005-051-20	Sequence 20, Appl
27	138.6	8.1	1650	US-08-747-221B-60	Sequence 60, Appl

c 28	138.6	8.1	1650	3	US-08-747-221B-61	Sequence 61, Appl
c 29	138.6	8.1	1650	4	US-09-005-051-60	Sequence 60, Appl
c 30	138.6	8.1	1650	4	US-09-005-051-61	Sequence 61, Appl
c 31	138.6	8.1	2144	3	US-08-747-221B-57	Sequence 57, Appl
c 32	138.6	8.1	2144	3	US-08-747-221B-59	Sequence 59, Appl
c 33	138.6	8.1	2144	4	US-09-005-051-57	Sequence 57, Appl
c 34	138.6	8.1	2144	4	US-09-005-051-59	Sequence 59, Appl
c 35	138	8.1	1515	3	US-08-747-221B-16	Sequence 16, Appl
c 36	138	8.1	1515	3	US-08-747-221B-17	Sequence 17, Appl
c 37	138	8.1	1515	4	US-09-005-051-16	Sequence 16, Appl
c 38	138	8.1	1515	4	US-09-005-051-17	Sequence 17, Appl
c 39	138	8.1	1982	3	US-08-747-221B-13	Sequence 13, Appl
c 40	138	8.1	1982	3	US-08-747-221B-15	Sequence 15, Appl
c 41	138	8.1	1982	4	US-09-005-051-13	Sequence 13, Appl
c 42	138	8.1	1982	4	US-09-005-051-15	Sequence 15, Appl
c 43	88.8	5.2	1694	3	US-09-136-421-11	Sequence 11, Appl
c 44	88.8	5.2	2989	1	US-07-927-851-1	Sequence 1, Appl
c 45	88.8	5.2	2989	1	US-08-453-323-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-068-960-9
; Sequence 9, Application US/09068960A
; Patent No. 6235515
; GENERAL INFORMATION:
; APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.
; TITLE OF INVENTION: MALATHION CARBOXYESTERASE
; FILE REFERENCE: Attorney Docket No. 6235515 50179-051
; CURRENT APPLICATION NUMBER: US/09/068,960A
; EARLIER FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: PCT/AU96/00746
; EARLIER FILING DATE: 1996-11-22
; EARLIER APPLICATION NUMBER: AU 6751
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patentlin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 1713
; TYPE: DNA
; ORGANISM: Lucilia cuprina
; US-09-068-960-9

Query Match 100.0%; Score 1713; DB 4; Length 1713;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 1713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGATTTTCAACGTTAGTTGATGAGAAATTTAAATGAAATTAATGATTAATGATTAATGAAAT	60
DB	1	ATGATTTTCAACGTTAGTTGATGAGAAATTTAAATGAAATTTAAATGATTAATGATTAATGAAAT	60
QY	61	AAAGTTTAAACCTATTCGTTAACTACCAATGAAAGCGTGTAGCTGAATGAAATGCG	120
DB	61	AAAGTTTAAACCTATTCGTTAACTACCAATGAAAGCGTGTAGCTGAATGAAATGCG	120
QY	121	AAAGTTTAAACCTATTCGTTAACTACCAATGAAAGCGTGTAGCTGAATGAAATGCG	180
DB	121	AAAGTTTAAACCTATTCGTTAACTACCAATGAAAGCGTGTAGCTGAATGAAATGCG	180
QY	181	ATACCGTAGCGCCCAACCGCCAGTGGTGAGTGAATTTAAAGACCCCGACCCACACA	240
DB	181	ATACCGTAGCGCCCAACCGCCAGTGGTGAGTGAATTTAAAGACCCCGACCCACACA	240
QY	241	CCCTGGATGCTGCTGCTGATTTGTCATCAATCAATCAATCAATCAATCAATCAATCAAT	300
DB	241	CCCTGGATGCTGCTGCTGATTTGTCATCAATCAATCAATCAATCAATCAATCAATCAAT	300
QY	301	ATACCGTAGCGCCCAACCGCCAGTGGTGAGTGAATTTAAAGACCCCGACCCACACA	360
DB	301	ATACCGTAGCGCCCAACCGCCAGTGGTGAGTGAATTTAAAGACCCCGACCCACACA	360

QY 361 CTAATCCCGAAGCTAAGCTCCGTTTGTATACATCATGATGCTGTTTATATC 420
 Db 361 CTAATCCCGAAGCTAAGCTCCGTTTGTATATACATCATGATGCTGTTTATATC 420
 QY 421 GGTGAATATCATGATATGATGATGCTGCTATTTTTCATTAAAGAGATGCTGTTG 480
 Db 421 GGTGAATATCATGATATGATGATGCTGCTATTTTTCATTAAAGAGATGCTGTTG 480
 QY 481 ATTAACATACATATGTTTGGAGCTCTAGGTTTCTAAGTTTAAATTCAGAGACCTT 540
 Db 481 ATTAACATACATATGTTTGGAGCTCTAGGTTTCTAAGTTTAAATTCAGAGACCTT 540
 QY 541 AATGCGCCGGTAATGCGGCTTAAGATCAATGATGCGCTGCTGTTGATTAATAAT 600
 Db 541 AATGCGCCGGTAATGCGGCTTAAGATCAATGATGCGCTGCTGTTGATTAATAAT 600
 QY 601 AATGCGCAACTTGTGGGCAATCCGATATATTCAGCTTGTGGTAAGCGCGGT 660
 Db 601 AATGCGCAACTTGTGGGCAATCCGATATATTCAGCTTGTGGTAAGCGCGGT 660
 QY 661 GCTGCTCTACCACTACATGATGTTAACGCAAACTCGGCTCTTTTCATGCTGT 720
 Db 661 GCTGCTCTACCACTACATGATGTTAACGCAAACTCGGCTCTTTTCATGCTGT 720
 QY 721 ATACTAATGCTGGGTAATGCTATTTTTCATGCTAATCCCAATGCTCAATGCTGCC 780
 Db 721 ATACTAATGCTGGGTAATGCTATTTTTCATGCTAATCCCAATGCTCAATGCTGCC 780
 QY 781 TTCACTTAGCCAAATGCGCGCTATAGGCTAGAGTAAATGATAGGATGTTTGGAA 840
 Db 781 TTCACTTAGCCAAATGCGCGCTATAGGCTAGAGTAAATGATAGGATGTTTGGAA 840
 QY 841 TTTCTTTGAAAGCCAGCAAGATTTAATAAACTGAGGAAAGTTTAACTCTA 900
 Db 841 TTTCTTTGAAAGCCAGCAAGATTTAATAAACTGAGGAAAGTTTAACTCTA 900
 QY 901 GAAGAGGCTCAAAATAGGATGCTGCTTTGGTCCCACTGCTGCAATGCAATGCAAGC 960
 Db 901 GAAGAGGCTCAAAATAGGATGCTGCTTTGGTCCCACTGCTGCAATGCAATGCAAGC 960
 QY 961 GCTGATGCTGCTTACCCAAACATCTCTGGGAAATGTTTAAACTGCTGGGTAATTCG 1020
 Db 961 GCTGATGCTGCTTACCCAAACATCTCTGGGAAATGTTTAAACTGCTGGGTAATTCG 1020
 QY 1021 ATACCCATGATGAGGTACACTCTATAGAGGCTCTATTTTTCATGCTAATTTCTAG 1080
 Db 1021 ATACCCATGATGAGGTACACTCTATAGAGGCTCTATTTTTCATGCTAATTTCTAG 1080
 QY 1081 CAAATGCTATGCTTGTTAAGAAATGGAACCTGTCTCAATTTTGGCAAGTGAATTG 1140
 Db 1081 CAAATGCTATGCTTGTTAAGAAATGGAACCTGTCTCAATTTTGGCAAGTGAATTG 1140
 QY 1141 GCTGATGCTAAGCAAGCCGCGCAAGACCTTGGAAATGGGCTCTAAATTAAGAGCT 1200
 Db 1141 GCTGATGCTAAGCAAGCCGCGCAAGACCTTGGAAATGGGCTCTAAATTAAGAGCT 1200
 QY 1201 CATGTTACAGAGAAACACCAAGCTGATATTTTATGATGCTGCTCTACATCTAT 1260
 Db 1201 CATGTTACAGAGAAACACCAAGCTGATATTTTATGATGCTGCTCTACATCTAT 1260
 QY 1261 TTTGCTGCTCCCATGATGCTTGTGCAATTAAGTTTCAATTCACACCTCCGCTACACCC 1320
 Db 1261 TTTGCTGCTCCCATGATGCTTGTGCAATTAAGTTTCAATTCACACCTCCGCTACACCC 1320
 QY 1321 GTCCTACTGATGCTGCTGCACTGCTGATGGAAGATCTTATCAATCCCTATGCTATATG 1380
 Db 1321 GTCCTACTGATGCTGCTGCACTGCTGATGGAAGATCTTATCAATCCCTATGCTATATG 1380
 QY 1381 CGTAGTGAAGCTGCTGTAAGGCTGTAGTCAATGCTGATGAATTAACCTATTTCTGCG 1440
 Db 1381 CGTAGTGAAGCTGCTGTAAGGCTGTAGTCAATGCTGATGAATTAACCTATTTCTGCG 1440
 QY 1441 AATCAATGGCCAAACGTAATGCTTAAAGAAATCGGCTGAATACAAAACAATGAAGTATG 1500

Db 1441 AATCAATGGCCAAACGTAATGCTTAAAGAAATCGGTAATCAAAAACAATGAAGCTATG 1500
 QY 1501 ACTGCTATATGATATACATTTTGGCACCACTGTAATCTTATAGCAATGAATTAAGCT 1560
 Db 1501 ACTGCTATATGATATACATTTTGGCACCACTGTAATCTTATAGCAATGAATTAAGCT 1560
 QY 1561 ATGGAATATGCTTCCGCTGATTCGAATTAAGAAATCCGATGAAGTATACAAAGTGTGAAT 1620
 Db 1561 ATGGAATATGCTTCCGCTGATTCGAATTAAGAAATCCGATGAAGTATACAAAGTGTGAAT 1620
 QY 1621 ATTAGTATGATATGAATATGATGCTGCTGAATGATGAATTAACATGAGGAG 1680
 Db 1621 ATTAGTATGATATGAATATGATGCTGCTGAATGATGAATTAACATGAGGAG 1680
 QY 1681 TCGATGTTGAAACATGATGATTTATTTAG 1713
 Db 1681 TCGATGTTGAAACATGATGATTTATTTAG 1713

RESULT 2
 US-09-068-960-1
 ; Sequence 1, Application US/09068960A
 ; Patent No. 6235515
 ; GENERAL INFORMATION:
 ; APPLICANT: Commonwealth Scientific and Industrial Resrch. Org.
 ; TITLE OF INVENTION: MALATHION CARBOXYL ESTERASE
 ; FILE REFERENCE: Attorney Docket No. 6235515 501/9-051
 ; CURRENT FILING DATE: 1998-05-20
 ; EARLIER APPLICATION NUMBER: PCT/AU96/00746
 ; EARLIER FILING DATE: 1996-11-22
 ; EARLIER APPLICATION NUMBER: AU 6751
 ; NUMBER OF SEQ ID NOS: 43
 ; SOFTWARE: Patentlin Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 1713
 ; TYPE: DNA
 ; ORGANISM: Lucilia cuprina
 US-09-068-960-1

Query Match 99.9%; Score 1711.4; DB 4; Length 1713;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1712; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAATTTCAAGCTTAGTTGATGAGAAATTTAAATGAGATTAATGATGAAT 60
 Db 1 ATGAATTTCAAGCTTAGTTGATGAGAAATTTAAATGAGATTAATGATGAAT 60
 QY 61 AAGTTTAACTATCGTTTAACTACCAATGAAGAGGTGAGCTGAACACTGATATGC 120
 Db 61 AAGTTTAACTATCGTTTAACTACCAATGAAGAGGTGAGCTGAACACTGATATGC 120
 QY 121 AAGGGAAGGCGTTAAACGTTTAACTGCTGATGATTTTCTCTACAGTTTGAAGGT 180
 Db 121 AAGGGAAGGCGTTAAACGTTTAACTGCTGATGATTTTCTCTACAGTTTGAAGGT 180
 QY 181 ATACGTCAGCCCAACGCCAGTGGTGAAGTGAATTAAGACCCGACGCCACA 240
 Db 181 ATACGTCAGCCCAACGCCAGTGGTGAAGTGAATTAAGACCCGACGCCACA 240
 QY 241 CCCTGGGATGCTGCTGATGTTGCAATCATTAAGATAGTCAAGTGAATTTT 300
 Db 241 CCCTGGGATGCTGCTGATGTTGCAATCATTAAGATAGTCAAGTGAATTTT 300
 QY 301 ATACGGGCAAGGCTGCTGCTGATGATGATTTTATACCTAGTGTCTATAGCAATAT 360
 Db 301 ATACGGGCAAGGCTGCTGCTGATGATGATTTTATACCTAGTGTCTATAGCAATAT 360
 QY 361 CTAATCCCGAAGCTAAGCTCCGTTTGTATATACATGATGATGCTGTTTATATC 420
 Db 361 CTAATCCCGAAGCTAAGCTCCGTTTGTATATACATGATGATGCTGTTTATATC 420

421 GGTGAAATCATGCTGATATGATGCTCGGATTAATTCATTAAGAAAGATGCTG 480
421 GGTGAAATCATGCTGATATGATGCTCGGATTAATTCATTAAGAAAGATGCTG 480
421 GGTGAAATCATGCTGATATGATGCTCGGATTAATTCATTAAGAAAGATGCTG 480
481 ATTAACATACAAATGCTGTTGGAGCTGCTGATTTCTAAGTTAAATGAGAGACTT 540
481 ATTAACATACAAATGCTGTTGGAGCTGCTGATTTCTAAGTTAAATGAGAGACTT 540
541 AATGCGCCGCTAAATGCGGCTTAAGATCAATGAGCTGCTGCTGATTAAT 600
541 AATGCGCCGCTAAATGCGGCTTAAGATCAATGAGCTGCTGCTGATTAAT 600
601 AATGCGCCGCTAAATGCGGCTTAAGATCAATGAGCTGCTGCTGATTAAT 660
601 AATGCGCCGCTAAATGCGGCTTAAGATCAATGAGCTGCTGCTGATTAAT 660
661 GCTGCTCTACCCACTATGATGTTAAACGAAACAACTCGGCTTTCTCATGCTG 720
661 GCTGCTCTACCCACTATGATGTTAAACGAAACAACTCGGCTTTCTCATGCTG 720
721 ATACTAATGCTGGGTAATGCTATTTGCTCAATGCTTAATACCAATGCTGCTG 780
721 ATACTAATGCTGGGTAATGCTATTTGCTCAATGCTTAATACCAATGCTGCTG 780
781 TTACACTTAGCAATTTGGCGGCTAATAGGCTAGGATTAAGATGCTTTGGAA 840
781 TTACACTTAGCAATTTGGCGGCTAATAGGCTAGGATTAAGATGCTTTGGAA 840
841 TTCTTTATGAAGCCAGACAGAGATTTAAATTAATGAGAAAGTTTAACTCTA 900
841 TTCTTTATGAAGCCAGACAGAGATTTAAATTAATGAGAAAGTTTAACTCTA 900
901 GAAGAGCGTACAAATTAAGCTATGCTTTGCTTTGCTTCCACTGTTGACCATATGAC 960
901 GAAGAGCGTACAAATTAAGCTATGCTTTGCTTTGCTTCCACTGTTGACCATATGAC 960
961 GCTGATGCTGCTTACCCAAATCCTCGGAAATGTTAAACTGCTGGGTAATG 1020
961 GCTGATGCTGCTTACCCAAATCCTCGGAAATGTTAAACTGCTGGGTAATG 1020
1021 ATACCACATGATGAGTAACTTCAATATGAGGCTATTTTCACTCAATTTCTTAA 1080
1021 ATACCACATGATGAGTAACTTCAATATGAGGCTATTTTCACTCAATTTCTTAA 1080
1081 CAAATGCCATGCTGTTAAGAAATTTGAACTTGTCAATTTGTGCAAGTAAATG 1140
1081 CAAATGCCATGCTGTTAAGAAATTTGAACTTGTCAATTTGTGCAAGTAAATG 1140
1141 GGTGATGCTGAGACGACCCGACAGACCTTGAATGGTGTAAATTAAGAAAGCT 1200
1141 GGTGATGCTGAGACGACCCGACAGACCTTGAATGGTGTAAATTAAGAAAGCT 1200
1201 CATGTTACAGAGAAACACCAACAGCTGATTTTATGATGCTTCTCATCAT 1260
1201 CATGTTACAGAGAAACACCAACAGCTGATTTTATGATGCTTCTCATCAT 1260
1261 TTCTGCTTCCCATGATGCTTGTGCAATTAAGCTTCAATCAACCTCGGCTACCC 1320
1261 TTCTGCTTCCCATGATGCTTGTGCAATTAAGCTTCAATCAACCTCGGCTACCC 1320
1321 GGTGATGCTGATGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 1380
1321 GGTGATGCTGATGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 1380
1381 CTAAGTGAAGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 1440
1381 CTAAGTGAAGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 1440
1441 AATCAATTTGGCCAAAGCTATGCTTAAAGATGCTGATGCTGATGCTGATGCT 1500
1441 AATCAATTTGGCCAAAGCTATGCTTAAAGATGCTGATGCTGATGCTGATGCT 1500

1501 ACTGATATGATGATACATTTTGGACCACTGGATCTTATAGCAATGAATGAAGT 1560
1501 ACTGATATGATGATACATTTTGGACCACTGGATCTTATAGCAATGAATGAAGT 1560
1561 ATGGAATATGCTGCTGAGTCAATTAAGAAATCCGATGAGTATACAGTGTGAAT 1620
1561 ATGGAATATGCTGCTGAGTCAATTAAGAAATCCGATGAGTATACAGTGTGAAT 1620
1621 ATTAGGATGATGATGAATATGATGATGCTGCAATGATGATGATGATGATGAT 1680
1621 ATTAGGATGATGATGAATATGATGATGCTGCAATGATGATGATGATGATGAT 1680
1681 TCGATGTTGAAAAACATAGATGATTTATTTAG 1713
1681 TCGATGTTGAAAAACATAGATGATTTATTTAG 1713

RESULT 3
US-09-068-960-3
; Sequence 3, Application US/09068960A
; Patent No. 6235515
; GENERAL INFORMATION:
; APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.
; TITLE OF INVENTION: MALATHION CARBOXYL ESTERASE
; FILE REFERENCE: Attorney Docket No. 6235515 50179-051
; CURRENT APPLICATION NUMBER: US/09/068,960A
; EARLIER FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: PCT/AN96/00746
; EARLIER FILING DATE: 1996-11-22
; EARLIER APPLICATION NUMBER: AU 6751
; EARLIER FILING DATE: 1995-11-23
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1713
; TYPE: DNA
; ORGANISM: Lucilia cuprina
US-09-068-960-3

Query Match 99.9%; Score 1711.4; DB 4; Length 1713;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1712; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 ATGAATTTCAACGTTAGTTGATGATGATGATGATGATGATGATGATGATGAT 60
1 ATGAATTTCAACGTTAGTTGATGATGATGATGATGATGATGATGATGATGAT 60
61 AAGTTTAACTATGCTTAACTAAGCAATGAAGGAGTGAAGTGAATGATGCTG 120
61 AAGTTTAACTATGCTTAACTAAGCAATGAAGGAGTGAAGTGAATGATGCTG 120
121 AAAGTGAAGCGTTAAACGTTTAACTGATGATGATGATGATGATGATGATGAT 180
121 AAAGTGAAGCGTTAAACGTTTAACTGATGATGATGATGATGATGATGATGAT 180
181 AATGGAAGAGCGTTAAACGTTTAACTGATGATGATGATGATGATGATGATGAT 240
181 AATGGAAGAGCGTTAAACGTTTAACTGATGATGATGATGATGATGATGATGAT 240
241 AATGGAAGAGCGTTAAACGTTTAACTGATGATGATGATGATGATGATGATGAT 300
241 AATGGAAGAGCGTTAAACGTTTAACTGATGATGATGATGATGATGATGATGAT 300
301 AATGGAAGAGCGTTAAACGTTTAACTGATGATGATGATGATGATGATGATGAT 360
301 AATGGAAGAGCGTTAAACGTTTAACTGATGATGATGATGATGATGATGATGAT 360
361 CTAATCCGAAAGCTAAGCTGCTGATGATGATGATGATGATGATGATGATGAT 420
361 CTAATCCGAAAGCTAAGCTGCTGATGATGATGATGATGATGATGATGATGAT 420
421 GGTGAAATCATGCTGATATGATGCTGCTGATTTTCAATTAAGAAAGATGCTG 480
421 GGTGAAATCATGCTGATATGATGCTGCTGATTTTCAATTAAGAAAGATGCTG 480

```

Db 421 GGTGAAATATCATGATATGATGCTGCTGATATTTTCATTAAAAAGAGTGTGTTG 480
QY 481 ATTAACATCAATATGCTTTGGAGCTAGAGTTTCTAAGTTTAATTCAACAACCTT 540
Db 481 ATTAACATCAATATGCTTTGGAGCTAGAGTTTCTAAGTTTAAATTCACAAACCTT 540
QY 541 AATGTGCCCCGATATGCGGCTTAAAGATCAAGTATGCGCTGCTGATTTAAAT 600
Db 541 AATGTGCCCCGATATGCGGCTTAAAGATCAAGTATGCGCTGCTGATTTAAAT 600
QY 601 AATGTGCCCCGATATGCGGCTTAAAGATCAAGTATGCGCTGCTGATTTAAAT 660
Db 601 AATGTGCCCCGATATGCGGCTTAAAGATCAAGTATGCGCTGCTGATTTAAAT 660
QY 661 GCTGCTTACCTACCTACATGATGTTAAACCAACCAACCTGCTTTTCATGCTGT 720
Db 661 GCTGCTTACCTACCTACATGATGTTAAACCAACCAACCTGCTTTTCATGCTGT 720
QY 721 ATACTAATGTGGGTAATGCTATTTGCTCATTTGGCTAATPACCAATGTCAACATGCTCC 780
Db 721 ATACTAATGTGGGTAATGCTATTTGCTCATTTGGCTAATPACCAATGTCAACATGCTCC 780
QY 781 TTACACTTAGCCAAATTTGGCGGCTATPAGGTTAGAGTAAATGATAGAGTGTGGAA 840
Db 781 TTACACTTAGCCAAATTTGGCGGCTATPAGGTTAGAGTAAATGATAGAGTGTGGAA 840
QY 841 TTTCTTAATGAAGCCACACAGAGATTAAATAAACTTGAAGAAAAGTTTAACTCTA 900
Db 841 TTTCTTAATGAAGCCACACAGAGATTAAATAAACTTGAAGAAAAGTTTAACTCTA 900
QY 901 GAAGAGCTTACCAATTAAGTATGCTATTTGCTTGTCCACTGTTGACCCATACAGCC 960
Db 901 GAAGAGCTTACCAATTAAGTATGCTATTTGCTTGTCCACTGTTGACCCATACAGCC 960
QY 961 GCTGATTTGCTTACCCAAACATCTCTGGGAAATGTTAAAGCTGTTGGGTAATTCG 1020
Db 961 GCTGATTTGCTTACCCAAACATCTCTGGGAAATGTTAAAGCTGTTGGGTAATTCG 1020
QY 1021 ATACCACTATGATGGGTAACACTTCAATATAGAGTCTATTTTCACTTCAATTTCTTAAG 1080
Db 1021 ATACCACTATGATGGGTAACACTTCAATATAGAGTCTATTTTCACTTCAATTTCTTAAG 1080
QY 1081 CAATATGCTATGCTTGTAAAGAAATGGAACCTGTGCAATTTTGTGCCAAGTGAATG 1140
Db 1081 CAATATGCTATGCTTGTAAAGAAATGGAACCTGTGCAATTTTGTGCCAAGTGAATG 1140
QY 1141 GCTGATGCTGACGACCGCCCGCAGACCTTGAATGAGTGTAAATTTAAAAAGCT 1200
Db 1141 GCTGATGCTGACGACCGCCCGCAGACCTTGAATGAGTGTAAATTTAAAAAGCT 1200
QY 1201 CATGTTACAGAGAAACCAACCAAGCTGATTAATTTTATGATCTTCTCTCATATCTAT 1260
Db 1201 CATGTTACAGAGAAACCAACCAAGCTGATTAATTTTATGATCTTCTCTCATATCTAT 1260
QY 1261 TTTGTTGTTCCCATGATGCTTGTGTCATTAAGTTCACATGACACTGCGGACGCC 1320
Db 1261 TTTGTTGTTCCCATGATGCTTGTGTCATTAAGTTCACATGACACTGCGGACGCC 1320
QY 1321 GTCATCTTATGCTGCTGACTTGTGATTCGGAAGATCTTATCAATCCCTATGCTATTAAG 1380
Db 1321 GTCATCTTATGCTGCTGACTTGTGATTCGGAAGATCTTATCAATCCCTATGCTATTAAG 1380
QY 1381 CGTAGTGAGTGCTGTTAAGGCTGTAGTCAATGCTGATTAATTAATTAATTTCTTCTG 1440
Db 1381 CGTAGTGAGTGCTGTTAAGGCTGTAGTCAATGCTGATTAATTAATTAATTTCTTCTG 1440
QY 1441 AATCAATTTGCGCAACGATATGCTTAAAGAAATCGCTGAATATCAAAACATTTGAACGTATG 1500
Db 1441 AATCAATTTGCGCAACGATATGCTTAAAGAAATCGCTGAATATCAAAACATTTGAACGTATG 1500
QY 1501 ACTGATATATGATATCAATTTGCGCAACGCTGATTAATTTCTTGAAGTGAAGGT 1560
Db 1501 ACTGATATATGATATCAATTTGCGCAACGCTGATTAATTTCTTGAAGTGAAGGT 1560

```

```

QY 1561 ATGGAATATGTTTCTGCGATCCATTAAGAAATCCGATGATATCAAGTGTGAAT 1620
Db 1561 ATGGAATATGTTTCTGCGATCCATTAAGAAATCCGATGATATCAAGTGTGAAT 1620
QY 1621 ATTAGTATGATTAATGAAGATGATGCTCCGAAATGATTAAGATTAACAATGGAG 1680
Db 1621 ATTAGTATGATTAATGAAGATGATGCTCCGAAATGATTAAGATTAACAATGGAG 1680
QY 1681 TCGATGTTGAAAACATTAAGATTTATTTAG 1713
Db 1681 TCGATGTTGAAAACATTAAGATTTATTTAG 1713

```

RESULT 4
US-09-068-960-5
; Sequence 5, Application US/09068960A
; Patent No. 623515
; GENERAL INFORMATION:
; APPLICANT: Commonwealth Scientific and Industrial Resrch. Org.
; TITLE OF INVENTION: MALATHION CARBOXYL ESTERASE
; FILE REFERENCE: Attorney Docket No. 623515 50179-051
; CURRENT APPLICATION NUMBER: US/09/068,960A
; EARLIER FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: PCT/AU96/00746
; EARLIER FILING DATE: 1996-11-22
; EARLIER APPLICATION NUMBER: AU 6751
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1713
; TYPE: DNA
; ORGANISM: Lucilia cuprina
US-09-068-960-5

Query Match 99.7%; Score 1708.2; DB 4; Length 1713;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1710; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

QY 1 ATGAATTTCAAGTGTGTTGATGAGAAATTAATGAAGATTAATGATGAAAT 60
Db 1 ATGAATTTCAAGTGTGTTGATGAGAAATTAATGAAGATTAATGATGAAAT 60
QY 61 AAGTTTTAACTATGTTTAACTACCAATGAACGCTGTAGCTGAACCTGAATATG 120
Db 61 AAGTTTTAACTATGTTTAACTACCAATGAACGCTGTAGCTGAACCTGAATATG 120
QY 121 AAGTGAAGGCTTTAAAGCTTAACCTGATGATGATGATGATGATGATGATG 180
Db 121 AAGTGAAGGCTTTAAAGCTGATGATGATGATGATGATGATGATGATGATG 180
QY 181 ATACCTAGGCCCAACCGCAGTGGTGAAGTGAATTTAAAGCAACCCAGGACCA 240
Db 181 ATACCTAGGCCCAACCGCAGTGGTGAAGTGAATTTAAAGCAACCCAGGACCA 240
QY 241 CCTGAGGATGCTGCTGATGTTGCAATCAATGAATTAAGTCAAGTGAATTT 300
Db 241 CCTGAGGATGCTGCTGATGTTGCAATCAATGAATTAAGTCAAGTGAATTT 300
QY 301 ATACGGGCAAGTGTGGCTCAGAGATGCTATACCTAAGTGTATACGAATAT 360
Db 301 ATACGGGCAAGTGTGGCTCAGAGATGCTATACCTAAGTGTATACGAATAT 360
QY 361 CTAAATCCCGAAATCAACGCTCCGTTTATGATATCAATACATGATGATGAT 420
Db 361 CTAAATCCCGAAATCAACGCTCCGTTTATGATATCAATACATGATGATGAT 420
QY 421 GGTGAATATCATGCTGATATGATGCTCTGATTAATTTCAATTAAGAGATG 480
Db 421 GGTGAATATCATGCTGATATGATGCTCTGATTAATTTCAATTAAGAGATG 480
QY 481 ATTAACATATATGCTTTGGAGCTAGTGTTCATTAATTTAAATTCAGAACT 540

```

|||||
Db 481 ATTAACATTAACAAATGCTTTGGAGGCTAGGTTTCTTAAGTTTAAATTCAGAGACCTT 540
Qy 541 AATGCGCCGCGTAATGCGGCTTTAAAGATCAATGCGCTTGGGTTGATTAATAAT 600
Db 541 AATGCGCCGCGTAATGCGGCTTTAAAGATCAATGCGCTTGGGTTGATTAATAAT 600
Qy 601 AATGCGCCGCGTAATGCGGCTTTAAAGATCAATGCGCTTGGGTTGATTAATAAT 600
Db 601 AATGCGCCGCGTAATGCGGCTTTAAAGATCAATGCGCTTGGGTTGATTAATAAT 600
Qy 661 GCTGCGCTTACCCATCAATGATGATTAACCGAACAACCTGCGGCTTTTCCATCGTGGT 720
Db 661 GCTGCGCTTACCCATCAATGATGATTAACCGAACAACCTGCGGCTTTTCCATCGTGGT 720
Qy 721 ATACTAATGTCGGGTAATGCTATTTGTCATGTCCTAATACCAATGTCACATCGGCC 780
Db 721 ATACTAATGTCGGGTAATGCTATTTGTCATGTCCTAATACCAATGTCACATCGGCC 780
Qy 781 TTCACCTTACCAAAATTTGGCGGCTAATAGGTAAGGATTAATGATTAAGATTTTGGAA 840
Db 781 TTCACCTTACCAAAATTTGGCGGCTAATAGGTAAGGATTAATGATTAAGATTTTGGAA 840
Qy 841 TTTCTTATGAAGCCAAAGCCACAGGATTTATATAAACTTGAGAAAAGTTTAACTCTA 900
Db 841 TTTCTTATGAAGCCAAAGCCACAGGATTTATATAAACTTGAGAAAAGTTTAACTCTA 900
Qy 901 GAAGAGGCTCAATTAAGTCAATGCTTCTTGTCCCATGTCAGCATATCGAGCC 960
Db 901 GAAGAGGCTCAATTAAGTCAATGCTTCTTGTCCCATGTCAGCATATCGAGCC 960
Qy 961 GCTGATTTGCTTCTTACCAAAATCTCGGGAATGTTAAACTGTTGGGTAATTCG 1020
Db 961 GCTGATTTGCTTCTTACCAAAATCTCGGGAATGTTAAACTGTTGGGTAATTCG 1020
Qy 1021 ATACCACATTAATGCTTAACTTCAATGAGGCTATTTTTCATCTCAATTTCTTAA 1080
Db 1021 ATACCACATTAATGCTTAACTTCAATGAGGCTATTTTTCATCTCAATTTCTTAA 1080
Qy 1081 CAATGCTTAACTTCAATGAGGCTATTTTTCATCTCAATTTCTTAA 1140
Db 1081 CAATGCTTAACTTCAATGAGGCTATTTTTCATCTCAATTTCTTAA 1140
Qy 1141 GCTGATGCTGAAGCAACCGCCAGAGACCTTGGAAATGGTCTTAAATTAAGAGCT 1200
Db 1141 GCTGATGCTGAAGCAACCGCCAGAGACCTTGGAAATGGTCTTAAATTAAGAGCT 1200
Qy 1201 CATGTTACAGAGAAACACCAAGCTGATTAATTTATGATCTTGTCTCAATCTAT 1260
Db 1201 CATGTTACAGAGAAACACCAAGCTGATTAATTTATGATCTTGTCTCAATCTAT 1260
Qy 1261 TTTGCTGTCCTCCATGATGCTTGTGCAATTAAGTTTAACTTCTTCAATCTAT 1320
Db 1261 TTTGCTGTCCTCCATGATGCTTGTGCAATTAAGTTTAACTTCTTCAATCTAT 1320
Qy 1321 GTCCTACTTGTATGCTTCACTTCAATGAGGATCTTATCAATCCATGATTTATG 1380
Db 1321 GTCCTACTTGTATGCTTCACTTCAATGAGGATCTTATCAATCCATGATTTATG 1380
Qy 1381 CGTAGTGGAGCTGTGTTAAGGCTTGAAGTCAATGATTAACCTTCTTCTG 1440
Db 1381 CGTAGTGGAGCTGTGTTAAGGCTTGAAGTCAATGATTAACCTTCTTCTG 1440
Qy 1441 AATCAATTTGGCCAAACGTAATGCTTAAGAAATGCGGTAATCAAAAACATTAAGATG 1500
Db 1441 AATCAATTTGGCCAAACGTAATGCTTAAGAAATGCGGTAATCAAAAACATTAAGATG 1500
Qy 1501 ACTGTAATGATTAATTTGGCCAACTGTAATCTTATAGCAATGAATTTGAAGT 1560
Db 1501 ACTGTAATGATTAATTTGGCCAACTGTAATCTTATAGCAATGAATTTGAAGT 1560
Qy 1561 ATGGAATAATGTTCTTGGATGCAATTAAGAAATCGATGAAGTATACAGTGTGTAAT 1620
Db 1561 ATGGAATAATGTTCTTGGATGCAATTAAGAAATCGATGAAGTATACAGTGTGTAAT 1620

Db 1561 ATGGAATAATGTTCTTGGATGCAATTAAGAAATCGATGAAGTATACAGTGTGTAAT 1620
Qy 1621 ATTAGGATGAATTAAGAAATGATGTCCTGAAGATGAAGATTAACATGAGGAG 1680
Db 1621 ATTAGGATGAATTAAGAAATGATGTCCTGAAGATGAAGATTAACATGAGGAG 1680
Qy 1681 TCGATGTTGAAAAACATAGAGATTTAATTTAG 1713
Db 1681 TCGATGTTGAAAAACATAGAGATTTAATTTAG 1713

RESULT 5
US-08-669-524-1
; Sequence 1, Application US/08669524
; Patent No. 5843758
; GENERAL INFORMATION:
; APPLICANT: RUSSELL, Robyn J.
; APPLICANT: NEWCOMB, Richard D.
; APPLICANT: ROBIN, Geoffrey C.
; APPLICANT: BOYCE, Thomas M.
; APPLICANT: CAMPBELL, Peter M.
; APPLICANT: PARKER, Anthony G.
; APPLICANT: OAKESHOTT, John G.
; TITLE OF INVENTION: ENZYME BASED BIOREMEDIATION
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lowe Price Leblanc & Becker
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/669,524
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Price, Robert L.
; REGISTRATION NUMBER: 22,685
; REFERENCE/DOCKET NUMBER: 1451-021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-684-1111
; TELEFAX: 703-684-1124
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1713 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-669-524-1

Query Match 99.4%; Score 1703.4; DB 2; Length 1713;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1707; Conservative 0; Mismatches 6; Indels 0; Caps 0;

Qy 1 ATGAATTTCAACGTTAGTTGATGAGAGAAATTAAGAAATGAAGTAAATGATTAATGATTAAT 60
Db 1 ATGAATTTCAACGTTAGTTGATGAGAGAAATTAAGAAATGAAGTAAATGATTAATGATTAAT 60
Qy 61 AAGTTTAACTATCGTTTAACTACCAATGAAGACGGTGTAGCTGAACATGAATATGCG 120
Db 61 AAGTTTAACTATCGTTTAACTACCAATGAAGACGGTGTAGCTGAACATGAATATGCG 120
Qy 121 AAGTGAAGAGCGTTTAAAGCTTTTAACTGTGTAGCATGATTCCTATCAAGTTTGAGGCT 180
Db 121 AAGTGAAGAGCGTTTAAAGCTTTTAACTGTGTAGCATGATTCCTATCAAGTTTGAGGCT 180

```

QY 181 ATACCGTAGCCCAACCGCCAGTGGGTGAGCTGAGATTTAAGACCCCAAGCCACA 240
DB 181 ATACCGTAGCCCAACCGCCAGTGGGTGAGCTGAGATTTAAGACCCCAAGCCACA 240
QY 241 CCCTGGGATGTGTGGGTGATTTGGCAATCAATAAGATGACAGTGAATTTT 300
DB 241 CCCTGGGATGTGTGGGTGATTTGGCAATCAATAAGATGACAGTGAATTTT 300
QY 301 ATACGCGGCAAAAGTGTGTGGGTGATTTGGCAATCAATAAGATGACAGTGA 360
DB 301 ATACGCGGCAAAAGTGTGTGGGTGATTTGGCAATCAATAAGATGACAGTGA 360
QY 361 CTAAATCCCAAACTAAACGCTCCGTTTGTATACATACATGAGTGTGTTTATC 420
DB 361 CTAAATCCCAAACTAAACGCTCCGTTTGTATACATACATGAGTGTGTTTATC 420
QY 421 GGTGAAATCATGTGTATGTATGTCTGATTTATTTCAATTAAGATGAGTGTG 480
DB 421 GGTGAAATCATGTGTATGTATGTCTGATTTATTTCAATTAAGATGAGTGTG 480
QY 481 ATTAACATCAATATCTGTTGGAGCTCTAGCTTCTAAGTTAAATTCAGAGACTT 540
DB 481 ATTAACATCAATATCTGTTGGAGCTCTAGCTTCTAAGTTAAATTCAGAGACTT 540
QY 541 AATGTGCGCGTAAATGCGGCTTAAAGATCAAGTCATGCGCTTGGATTAAAT 600
DB 541 AATGTGCGCGTAAATGCGGCTTAAAGATCAAGTCATGCGCTTGGATTAAAT 600
QY 601 AATTTGGCCCACTTTGGTGGCAATCCGATATATTTACAGCTTTGGTGAAGTCCG 660
DB 601 AATTTGGCCCACTTTGGTGGCAATCCGATATATTTACAGCTTTGGTGAAGTCCG 660
QY 661 GGTGCGCTCTACCCATCATGATGTATTAACGAAACAACTGCGGCTTTTCATCGT 720
DB 661 GGTGCGCTCTACCCATCATGATGTATTAACGAAACAACTGCGGCTTTTCATCGT 720
QY 721 ATACTAATGTGCGGTAAATGCTATTTGTCCATTTGCTAATACCAATGTCATGTC 780
DB 721 ATACTAATGTGCGGTAAATGCTATTTGTCCATTTGCTAATACCAATGTCATGTC 780
QY 781 TTACACCTTACCCAAATGCGGCTATTAAGGTGAGATTAAGTGAAGTGTGAA 840
DB 781 TTACACCTTACCCAAATGCGGCTATTAAGGTGAGATTAAGTGAAGTGTGAA 840
QY 841 TTCTTTATGAAGCCCAAGCAGAGATTTAATAAATCTTGAGAAAAAGTTTAACTA 900
DB 841 TTCTTTATGAAGCCCAAGCAGAGATTTAATAAATCTTGAGAAAAAGTTTAACTA 900
QY 901 GAAGAGCGTACAAATTAAGTCAATGTTTCTTTGCTCCACTGTGAGCCATATCAGC 960
DB 901 GAAGAGCGTACAAATTAAGTCAATGTTTCTTTGCTCCACTGTGAGCCATATCAGC 960
QY 961 GCTGATTTGCTTTACCCAAACATCTCGGGAATGTTAAACGCTTGGGTAATTCG 1020
DB 961 GCTGATTTGCTTTACCCAAACATCTCGGGAATGTTAAACGCTTGGGTAATTCG 1020
QY 1021 ATACCCACTATGATGGGTAACTTCAATGAGGCTAATTTTCACTTCAATTTTAA 1080
DB 1021 ATACCCACTATGATGGGTAACTTCAATGAGGCTAATTTTCACTTCAATTTTAA 1080
QY 1081 CAATGCGCTATGCTTTAAGGAATGGAATCTGTCAATTTTGTGCCAATGGAATG 1140
DB 1081 CAATGCGCTATGCTTTAAGGAATGGAATCTGTCAATTTTGTGCCAATGGAATG 1140
QY 1141 GCTGATGCTGAAGCAGCGCCAGAGACCTTGGAATGGTGTAAATTTAAAGGCT 1200
DB 1141 GCTGATGCTGAAGCAGCGCCAGAGACCTTGGAATGGTGTAAATTTAAAGGCT 1200
QY 1201 CATGTTACAGAGAAACACCAAGAGCTGATTAATTTATGATCTTGTCTCACATCAT 1260
DB 1201 CATGTTACAGAGAAACACCAAGAGCTGATTAATTTATGATCTTGTCTCACATCAT 1260

```

```

QY 1261 TTCTGTTCCCATGATCGTTTGTGCAATTACGTTTCAATCAACACCTCCGATACCC 1320
DB 1261 TTCTGTTCCCATGATCGTTTGTGCAATTACGTTTCAATCAACACCTCCGATACCC 1320
QY 1321 GTTACTTTGATGCTTCGACTTCGATTTGGAGATCTTTCAATCCCTATCGTATATG 1380
DB 1321 GTTACTTTGATGCTTCGACTTCGATTTGGAGATCTTTCAATCCCTATCGTATATG 1380
QY 1381 CGTAGTGAGCTGTGTTAAGGCTGTAGTCAATGCTGATGAATTAACCTATTTCTTCG 1440
DB 1381 CGTAGTGAGCTGTGTTAAGGCTGTAGTCAATGCTGATGAATTAACCTATTTCTTCG 1440
QY 1441 AATCAATTTGGCCAAAGCTATGCTTAAAGATCGCGTGAATTCAAACAAATTTGAAC 1500
DB 1441 AATCAATTTGGCCAAAGCTATGCTTAAAGATCGCGTGAATTCAAACAAATTTGAAC 1500
QY 1501 ACTGCTATGATGATACAAATTTGCCACAGCTGTAATCCTTATACCAATGAATGAAGT 1560
DB 1501 ACTGCTATGATGATACAAATTTGCCACAGCTGTAATCCTTATACCAATGAATGAAGT 1560
QY 1561 ATGGAATGTTTCTGAGATCCAAATTAAGAAATCCGATGAGTATCAAGTGTGTAAT 1620
DB 1561 ATGGAATGTTTCTGAGATCCAAATTAAGAAATCCGATGAGTATCAAGTGTGTAAT 1620
QY 1621 ATTAGTACGAAATGAAGAAATGATGTGCTGAAATGATTAAGATTAACCAATGGGA 1680
DB 1621 ATTAGTACGAAATGAAGAAATGATGTGCTGAAATGATTAAGATTAACCAATGGGA 1680
QY 1681 TCGATGTTTGAAGAAACATAGAGATTTATTTAG 1713
DB 1681 TCGATGTTTGAAGAAACATAGAGATTTATTTAG 1713

RESULT 6
US-09-960-7
: Sequence 7, Application US/09068960A
: Patent No. 6235515
: GENERAL INFORMATION:
: APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.
: TITLE OR INVENTION: MALATHION CARBOXYL ESTERASE
: FILE REFERENCE: Attorney Docket No. 6235515 50179-051
: CURRENT APPLICATION NUMBER: US/09/068,960A
: EARLIER FILING DATE: 1998-05-20
: EARLIER APPLICATION NUMBER: PCT/AU96/00746
: EARLIER FILING DATE: 1996-11-22
: EARLIER APPLICATION NUMBER: AU 6751
: NUMBER OF SEQ ID NOS: 43
: SOFTWARE: Patentln Ver. 2.0
: SEQ ID NO 7
: LENGTH: 1713
: TYPE: DNA
: ORGANISM: Lucilia cuprina
US-09-068-960-7

Query Match 99.48; Score 1703.4; DB 4; Length 1713;
Best Local Similarity 99.68; Pred. No. 0;
Matches 1707; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 ATGAAATTTCAACGTTAGTGTGATGAGAGAAATTAATAATGGAATTAATGATGAAT 60
DB 1 ATGAAATTTCAACGTTAGTGTGATGAGAGAAATTAATAATGGAATTAATGATGAAT 60
QY 61 AAGTTTAAACATATCGTTTAACTACCAATGAAGAAAGGTGATGCTGAAGTGAATG 120
DB 61 AAGTTTAAACATATCGTTTAACTACCAATGAAGAAAGGTGATGCTGAAGTGAATG 120
QY 121 AAAGTGAAGCGCTTAAAGCTTTAACTGTGACATGATTTCTTACTACAGTTTGAAG 180
DB 121 AAAGTGAAGCGCTTAAAGCTTTAACTGTGACATGATTTCTTACTACAGTTTGAAG 180
QY 181 ATACCGTAGCCCAACCGCCAGTGGGTGAGCTGAGATTTAAGACCCCAAGCCACA 240
DB 181 ATACCGTAGCCCAACCGCCAGTGGGTGAGCTGAGATTTAAGACCCCAAGCCACA 240

```

Db 181 ATACCTAGACCCCAACCCGAGTGGGTGAGCTGAGATTTAAAGCAACCCGAGGACCAACA 240
Qy 241 CCTGGGATGCTGTGGGATGTTGGCAATCAATAAGATAAGCTGCAAGTTGATTT 300
Db 241 CCTGGGATGCTGTGGGATGTTGGCAATCAATAAGATAAGCTGCAAGTTGATTT 300
Qy 301 ATACGAGGAAAGTGTGGCTCAGAGATTTGCTATACCTAAGTGTATACGATAT 360
Db 301 ATACGAGGAAAGTGTGGCTCAGAGATTTGCTATACCTAAGTGTATACGATAT 360
Qy 361 CTAAATCCGAAATCAACGTCCTTTTATATACATACATAGTGTGTTTATATC 420
Db 361 CTAAATCCGAAATCAACGTCCTTTTATATACATACATAGTGTGTTTATATC 420
Qy 421 GGTGAATATCATGCTATATGCTGCTGATATTTTATTAAGATGCTGCTG 480
Db 421 GGTGAATATCATGCTATATGCTGCTGATATTTTATTAAGATGCTGCTG 480
Qy 481 ATTAACATACATATGCTTGGAGCTAGTCTTCTAAGTTTAAATCAGACACTT 540
Db 481 ATTAACATACATATGCTTGGAGCTAGTCTTCTAAGTTTAAATCAGACACTT 540
Qy 541 AATGTGCCCCGATATGCTGCTTAAAGATCAATGCTGCTGCTGATTAAT 600
Db 541 AATGTGCCCCGATATGCTGCTTAAAGATCAATGCTGCTGCTGATTAAT 600
Qy 601 AATTTGGCCCACTTTGGTGGCATCCCGATATATACAGTCTTGGTAAAGTGGCT 660
Db 601 AATTTGGCCCACTTTGGTGGCATCCCGATATATACAGTCTTGGTAAAGTGGCT 660
Qy 661 GCTGCTCTACCTACATATGATGTTAACGAAACACTGCGCTTTTCCATCGTGT 720
Db 661 GCTGCTCTACCTACATATGATGTTAACGAAACACTGCGCTTTTCCATCGTGT 720
Qy 721 ATACTAATGTGGGATATGCTATTTGCTAATGCTAATACCAATGCTAATGCTGCC 780
Db 721 ATACTAATGTGGGATATGCTATTTGCTAATGCTAATACCAATGCTAATGCTGCC 780
Qy 781 TTACACCTTACCAATTTGGCGGCTATTAAGGTAGATATATAGATGTTTGGAA 840
Db 781 TTACACCTTACCAATTTGGCGGCTATTAAGGTAGATATATAGATGTTTGGAA 840
Qy 841 TTTCTTATGAAGCCCAAGCCAGATTTATATAAACTTGAGAAAAAGTTTAACTCTA 900
Db 841 TTTCTTATGAAGCCCAAGCCAGATTTATATAAACTTGAGAAAAAGTTTAACTCTA 900
Qy 901 GAAGAGGTCAAAATAGGTCATGTTCTTTGGTCCCACTGTGAGCCATATCAGACC 960
Db 901 GAAGAGGTCAAAATAGGTCATGTTCTTTGGTCCCACTGTGAGCCATATCAGACC 960
Qy 961 GCTGATGCTGCTTACCAACATCTCGGGAATGTTTAAACTGCTTGGGTAATTCG 1020
Db 961 GCTGATGCTGCTTACCAACATCTCGGGAATGTTTAAACTGCTTGGGTAATTCG 1020
Qy 1021 ATACCCATATGATGGTAACTCTATATAGAGGCTATTTTCACTTCAATTTCTAAG 1080
Db 1021 ATACCCATATGATGGTAACTCTATATAGAGGCTATTTTCACTTCAATTTCTAAG 1080
Qy 1081 CAATGCTATGCTGTTGAAGATTTGAACCTGTCTCAATTTTGGCCAACTGATTCG 1140
Db 1081 CAATGCTATGCTGTTGAAGATTTGAACCTGTCTCAATTTTGGCCAACTGATTCG 1140
Qy 1141 GCTGATGCTGATACGACCGCCAGAGACCTTGGAAATGGGTCGTAATTAAGAGCT 1200
Db 1141 GCTGATGCTGATACGACCGCCAGAGACCTTGGAAATGGGTCGTAATTAAGAGCT 1200
Qy 1201 CATGTACAGAGAAACCAACAGCTGATTAATTTATGATCTTTCTCTCATATAT 1260
Db 1201 CATGTACAGAGAAACCAACAGCTGATTAATTTATGATCTTTCTCTCATATAT 1260
Qy 1261 TTTGGTTCCTCCATGATGCTTTGCTGATTTTCAATTCACCTCCGGTACACC 1320
Db 1261 TTTGGTTCCTCCATGATGCTTTGCTGATTTTCAATTCACCTCCGGTACACC 1320

Qy 1321 GTCTACTGTATCGCTTGCAGCTTGCATGAGATCTTATCAATCCCTATTCGATATG 1380
Db 1321 GTCTACTGTATCGCTTGCAGCTTGCATGAGATCTTATCAATCCCTATTCGATATG 1380
Qy 1381 CCGTATGAGCGTGTGTTAAGGCTGTATGATCATGCTGATTAATTAACCTATTTCTCG 1440
Db 1381 CCGTATGAGCGTGTGTTAAGGCTGTATGATCATGCTGATTAATTAACCTATTTCTCG 1440
Qy 1441 AATCAATTTGCCCAACCTATGCTTAAAGATCGGCTGATCAAAACATTAAGAGCTATG 1500
Db 1441 AATCAATTTGCCCAACCTATGCTTAAAGATCGGCTGATCAAAACATTAAGAGCTATG 1500
Qy 1501 ACTGCTATATGATGATCAATTTGCCACCACTGCTATTCCTTATACCAATGAATGAAGT 1560
Db 1501 ACTGCTATATGATGATCAATTTGCCACCACTGCTATTCCTTATACCAATGAATGAAGT 1560
Qy 1561 ATGAAAAATGTTTCTGCGATCAATTAAGAAATCCGATGATATACAGTGTTCGAT 1620
Db 1561 ATGAAAAATGTTTCTGCGATCAATTAAGAAATCCGATGATATACAGTGTTCGAT 1620
Qy 1621 ATTAGTATGATGATTAAGATGATGCTGATTAAGATTAAGATTAAGATTAAGATTAAG 1680
Db 1621 ATTAGTATGATGATTAAGATGATGCTGATTAAGATTAAGATTAAGATTAAGATTAAG 1680
Qy 1681 TCGATGTTGAAAAACATAGATTTATTTAG 1713
Db 1681 TCGATGTTGAAAAACATAGATTTATTTAG 1713

RESULT 7
US-08-669-524-2
Sequence 2, Application US/08669524
Patent No. 5843758

GENERAL INFORMATION:
APPLICANT: RUSSELL, Robyn J.
APPLICANT: NEWCOMB, Richard D.
APPLICANT: ROBIN, Geoffrey C.
APPLICANT: BOYCE, Thomas M.
APPLICANT: CAMPBELL, Peter M.
APPLICANT: PARKER, Anthony G.
APPLICANT: OAKESHOTT, John G.
APPLICANT: SMITH, Kerlie A.
TITLE OF INVENTION: ENZYME BASED BIOREMEDIATION
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lowe Price Leblanc & Becker
STREET: 99 Canal Center Plaza, Suite 300
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,524
FILING DATE:

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Price, Robert L.
REGISTRATION NUMBER: 22,685
REFERENCE/DOCKET NUMBER: 1451-021
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1111
TELEFAX: 703-684-1124
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1713 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-669-524-2

Query Match 98.0%; Score 1678.2; DB 2; Length 1713;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 1680; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 1 ATGATTTCAACGTTAGTTGATGAGAAATTAATGAAGATTAATGATGAAT 60
DB 1 ATGATTTCAACGTTAGTTGATGAGAAATTAATGAAGATTAATGATGAAT 60
QY 61 AAGTTTTAACTATCGTTTAACTACCAATGAACGGGTGAGCTGAATGATG 120
DB 61 AAGTTTTAACTATCGTTTAACTACCAATGAACGGGTGAGCTGAATGATG 120
QY 121 AAGTGAAGGCGTTAAACGTTTAACTAGTGTGATGCTCTCTCTCTCTCT 180
DB 121 AAGTGAAGGCGTTAAACGTTTAACTAGTGTGATGCTCTCTCTCTCTCT 180
QY 181 ATACCGTACGCCAACCGCCAGTGGTGAAGCTGAGATTTAAAGCACCACCA 240
DB 181 ATACCGTACGCCAACCGCCAGTGGTGAAGCTGAGATTTAAAGCACCACCA 240
QY 241 CCCCTGGATGGTGGCGGATGTTGCAATCATTAAGTCAAGTGTGATTT 300
DB 241 CCCCTGGATGGTGGCGGATGTTGCAATCATTAAGTCAAGTGTGATTT 300
QY 301 ATACGGGCAAGTGTGGCTCAGAGATGCTATACCTAAGTGTCTATACAA 360
DB 301 ATACGGGCAAGTGTGGCTCAGAGATGCTATACCTAAGTGTCTATACAA 360
QY 361 CTAATCCGGAACCTAAACGTCCTTTTAACTATACATACATGCTGCTT 420
DB 361 CTAATCCGGAACCTAAACGTCCTTTTAACTATACATACATGCTGCTT 420
QY 421 GGTGAATATCTCGTGTATGTATGTCCTGATTTTCAATTAAGAGATG 480
DB 421 GGTGAATATCTCGTGTATGTATGTCCTGATTTTCAATTAAGAGATG 480
QY 481 ATTAACATACATATGCTTTGGAGCTCTAGGTTTCTAAGTTAAATGAAG 540
DB 481 ATTAACATACATATGCTTTGGAGCTCTAGGTTTCTAAGTTAAATGAAG 540
QY 541 AATGTCGGGTAATGCGGCTTAAAGATCAATGATGCGCTTGGATTTAA 600
DB 541 AATGTCGGGTAATGCGGCTTAAAGATCAATGATGCGCTTGGATTTAA 600
QY 601 AATGTCGGGTAATGCGGCTTAAAGATCAATGATGCGCTTGGATTTAA 660
DB 601 AATGTCGGGTAATGCGGCTTAAAGATCAATGATGCGCTTGGATTTAA 660
QY 661 GCTGCTCTACCACTACATGATGTTAAACGAACAACTGCGGCTTTTCA 720
DB 661 GCTGCTCTACCACTACATGATGTTAAACGAACAACTGCGGCTTTTCA 720
QY 721 ATACTAATGTCGGTAAATGCTATTTGTCATTTGCTAATACCAATGCG 780
DB 721 ATACTAATGTCGGTAAATGCTATTTGTCATTTGCTAATACCAATGCG 780
QY 781 TTGACCTTAGCAATGCGGCTTAAAGGTAAGGTAAGTAAAGTAAAGT 840
DB 781 TTGACCTTAGCAATGCGGCTTAAAGGTAAGGTAAGTAAAGTAAAGT 840
QY 841 TTCTTTTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 900
DB 841 TTCTTTTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 900
QY 901 GAAGAGCGTAAATGAAGTATGCTTTTGGTCCACTGTTGAGCATATCAG 960
DB 901 GAAGAGCGTAAATGAAGTATGCTTTTGGTCCACTGTTGAGCATATCAG 960
QY 961 GCTGATGTTGCTTACCAAAACATCCTCGGAAATGTTAAACTGCTGG 1020

DB 961 GCTGATGTTGCTTACCAAAACATCCTCGGAAATGTTAAANNCTGGGTAATTCG 1020
QY 1021 ATACCACTATGATGGGTAAACCTTCATATGAGGGCTATTTTCACTCAATTTAG 1080
DB 1021 ATACCACTATGATGGGTAAACCTTCATATGAGGGCTATTTTCACTCAATTTAG 1080
QY 1081 CAATGCTATGCTTTTAAAGAAATGGAACCTTGCTCAATTTTGTGCAAGTAATG 1140
DB 1081 CAATGCTATGCTTTTAAAGAAATGGAACCTTGCTCAATTTTGTGCAAGTAATG 1140
QY 1141 GCTGATGCTGAACGACCGCCAGAGACCTTGAATGGGTCTTAAATTTAAAGCT 1200
DB 1141 GCTGATGCTGAACGACCGCCAGAGACCTTGAATGGGTCTTAAATTTAAAGCT 1200
QY 1201 CATGTTACAGAGAAACACCAACAGCTGATTAATTTTATGATCTTGTCTCACA 1260
DB 1201 CATGTTACAGAGAAACACCAACAGCTGATTAATTTTATGATCTTGTCTCACA 1260
QY 1261 TTCTGCTCCCAATGATGCTTTTGAATTAAGCTTTCAATCACAACCTCGGTAC 1320
DB 1261 TTCTGCTCCCAATGATGCTTTTGAATTAAGCTTTCAATCACAACCTCGGTAC 1320
QY 1321 GCTGATGCTGAACGACCGCCAGAGACCTTGAATGGGTCTTAAATTTAAAGCT 1380
DB 1321 GCTGATGCTGAACGACCGCCAGAGACCTTGAATGGGTCTTAAATTTAAAGCT 1380
QY 1381 CTTAGTGAAGGCTGTTAAGGCTGTTAGTCAATGCTGATTAATTTTCACTTCTG 1440
DB 1381 CTTAGTGAAGGCTGTTAAGGCTGTTAGTCAATGCTGATTAATTTTCACTTCTG 1440
QY 1441 AATCAATGCGCAACAGTATGCTTAAAGAAATGCTTAAAGAAATGCTTAA 1500
DB 1441 AATCAATGCGCAACAGTATGCTTAAAGAAATGCTTAAAGAAATGCTTAA 1500
QY 1501 ACTGATATGATGATTAATTTGCAACCTGCTAATGCTTAAAGAAATGCTTAA 1560
DB 1501 ACTGATATGATGATTAATTTGCAACCTGCTAATGCTTAAAGAAATGCTTAA 1560
QY 1561 ATGGAATATGTTTCCGAGTCAATTAAGAAATGCTGATTAAGAAATGCTTAA 1620
DB 1561 ATGGAATATGTTTCCGAGTCAATTAAGAAATGCTGATTAAGAAATGCTTAA 1620
QY 1621 ATTAGTGAATGATTAATGATGCTGCTGAATGATTAAGAAATGCTTAA 1680
DB 1621 ATTAGTGAATGATTAATGATGCTGCTGAATGATTAAGAAATGCTTAA 1680
QY 1681 TCGATGTTGAAAAACATAGATTTTATTTAG 1713
DB 1681 TCGATGTTGAAAAACATAGATTTTATTTAG 1713

RESULT 8
US-09-068-960-14
Sequence 14, Application US/09068960A
Patent No. 623515
GENERAL INFORMATION:
APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.
TITLE OF INVENTION: MALATHION CARBOXYL ESTERASE
FILE REFERENCE: Attorney Docket No. 623515 50179-051
CURRENT APPLICATION NUMBER: US/09/068,960A
EARLIER FILING DATE: 1998-05-20
EARLIER APPLICATION NUMBER: PCT/AU96/00746
EARLIER FILING DATE: 1996-11-22
EARLIER APPLICATION NUMBER: AU 6751
EARLIER FILING DATE: 1995-11-23
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentl Ver. 2.0
SEQ ID NO 14
LENGTH: 1710
TYPE: DNA
ORGANISM: Musca domestica
US-09-068-960-14

QY	596	AAATTAATTCGCCCAACTTTGGTGGCAATCCCGATATATATACAGCTTTGGGGAAGTG	655
Db	1082	AAACAATATATTCATCCCTTTGGTGGTACCCCAACAATGAGACTATTTTGGGGAATCAG	102
QY	656	CCGATGCGCTCATCCCACTACATGATGTATTAACGACAACACGCGGCTTTTCCATC	715
Db	1022	CAGGTGGTGCAGAGTTCATATTATTTGATGTTATCAGATCTTTCCAAAGGACTTTTCATA	963
QY	716	GTGTATTAATGTGCGGTATGCTATTTGTCCATTGGC	755
Db	962	AAGCATCTCACAAGTGAGAGTCTTTTAATCCTTGGGC	923

```

1      RESULT 11 051-51
2      US-09-005-051-51
3      : Sequence 51, Application US/09005051
4      : Patent No. 6291222
5      :
6      : GENERAL INFORMATION:
7      : APPLICANT: Silver, Gary W.
8      : APPLICANT: Wisniewski, Nancy
9      : TITLE OF INVENTION: No. 6291222e1 Carboxylesterase Nucleic Acid
10     : TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
11     : NUMBER OF SEQUENCES: 66
12     : CORRESPONDENCE ADDRESS:
13     : ADDRESSEE: Carol Talkington Verser, Ph.D.
14     : ADDRESSEE: Heska Corporation
15     : STREET: 1825 Sharp Point Drive
16     : CITY: Fort Collins
17     : STATE: Colorado
18     : COUNTRY: USA
19     : ZIP: 80525
20     : COMPUTER READABLE FORM:
21     : MEDIUM TYPE: Floppy disk
22     : COMPUTER: IBM PC compatible
23     : OPERATING SYSTEM: Windows 95
24     : SOFTWARE: Wordperfect for Windows, Version 7.0
25     : CURRENT APPLICATION DATA:
26     : APPLICATION NUMBER: US/09/005,051
27     : FILING DATE:
28     : CLASSIFICATION:
29     : PRIOR APPLICATION DATA:
30     : APPLICATION NUMBER: 08/747,221
31     : FILING DATE: No. 6291222ember 12, 1996
32     : ATTORNEY/AGENT INFORMATION:
33     : NAME: Verser, Carol Talkington
34     : REGISTRATION NUMBER: 37,459
35     : REFERENCE/DOCKET NUMBER: FC-1
36     : TELECOMMUNICATION INFORMATION:
37     : TELEPHONE: 970/493-7272
38     : TELEFAX: 970/484-9505
39     : INFORMATION FOR SEQ ID NO: 51:
40     : SEQUENCE CHARACTERISTICS:
41     : LENGTH: 1584 nucleotides
42     : TYPE: nucleic acid
43     : STRANDEDNESS: single
44     : TOPOLOGY: linear
45     : MOLECULE TYPE: cDNA
46     : FEATURE:
47     : NAME/KEY: CDS
48     : LOCATION: 1..1584
49     :
50     : US-09-005-051-51

```

Query Match	10.5%;	Score 179.6;	DB 4;	Length 1584;
Best Local Similarity	56.2%;	Pred. No. 2.5e-42;		
Matches 360;	Conservative	0;	Mismatches 274;	Indels 6;
				Gaps 11

OY 176 AGGTTATACCGTACGCCAACGGCCAGTGGGGTAGCTGATTAAAGCACCACCGAC 235
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 89 CTGAATTTCATATGCACAACCTCCTTAGTGATCTAAGATTAAAGCACCACTCAACTG 148

[illegible]

RESULT 12
 US-09-005-051-52/c
 ; Sequence 52, Application us/09005051
 ; Patent No. 6291222
 ; GENERAL INFORMATION:
 APPLICANT: Silver, Gary W.
 APPLICANT: Wisniewski, Nancy
 TITLE OF INVENTION: No. 6291222el Carboxylesterase Nucleic Acid
 TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
 NUMBER OF SEQUENCES: 66
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Carol Talkington Verser, Ph.D.
 ADDRESSEE: Heska Corporation
 STREET: 1825 Sharp Point Drive
 CITY: Fort Collins
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80525
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: Wordperfect for Windows, Version 7.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/005,051
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/747,221
 FILING DATE: No. 6291222eember 12, 1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Verser, Carol Talkington
 REGISTRATION NUMBER: 37,459
 REFERENCE/DOCKET NUMBER: FC-1
 TELECOMMUNICATION INFORMATION:

TELEPHONE: 970/493-7272
 TELEFAX: 970/484-9505
 INFORMATION FOR SEQ ID NO: 52:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1584 nucleotides
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-09-005-051-52

Query Match 10.5%; Score 179.6; DB 4; Length 1584;
 Best Local Similarity 56.2%; Pred. No. 2.5e-42;
 Matches 360; Conservative 0; Mismatches 274; Indels 6; Gaps 1;

QY 116 ATGGCAAGTAAAGCGCTTAAAGCTTTAACTGTACGTACGTATCTCTACAGTTTG 175
 DB 1556 AAGTACTTTAAAGGAAAAGCAATTAAGTAAAGAAATGCTCCATAGTTATT 1497
 QY 176 AGGTATACCGTACGCCCAACCGCCAGTGGGTAGCTGAGTTTAAAGCAACCCAGCGAC 235
 DB 1496 CTGGAAATTCATATGCAAACTCTGTAGTGTAGTAAAGTAAAGCAACCTG 1437
 QY 236 CAACACCTGGGATGGTGGTGGCTGATTTGAATCATAAAGTAAAGTACAGTCAAGTTG 295
 DB 1436 CAAACCTTGGTCAAGTGTCTTGTAGTCTAGTAAAGAGGAATAGTTAGATCAGTAC 1377
 QY 296 ATTTTAAACGGGCAAGTGTGTGCTCAGAGGATTTCTATACCTAAAGTCTATACGA 355
 DB 1376 ATTTTAAAGAAATTAAGTAGAGGGCTGAAAGATTTGTTATACCTCAATGCTATGAC 1317
 QY 356 ATATCTAATATCCCGAAGTAAAGCTCCCGTTTATGATATCATATCAATAGTGTGTTTGA 415
 DB 1316 CAAAAACATCAGAGAACTACTTCTCCAGTAAATGATATGATATGAGAGAGCTTCT 1257
 QY 416 TTAATCGTAAATCATCTGATATGATAGTCTGATATTTTCAATTTAAAGAGATGG 475
 DB 1256 TCATGGATCTGGAATATGATATGATATGATATGATATGATATGATATGATATG 1197
 QY 476 TGTGATTAACATCAATATCTGTTGGAGCTCTAGCTTTTCAATTTAAATTCAGAG 535
 DB 1196 TTTCTGATCTTCAATATTCATATGATATGATATGATATGATATGATATGATATG 1137
 QY 536 ACCTTAATGTGCGGCTATGCGGCTTAAAGTCAATGATGCTGCTGCTGCTGATTA 595
 DB 1136 AA-----CGCGCTGGCAATGTTGGTTGATGAGCAGAGTGAAGCTTAATGGTAA 1083
 QY 596 AAAATATTTGGCCCACTTTTGTGCAATCCCGATATATTAACAGTCTTTGTGCAAGTG 655
 DB 1082 AAAACAATATTCATCTTTGTGCTGAGCCCAACATGATGATATTTTGGAGAAATCAG 1023
 QY 656 CCGGTGCTGCTCTACCACTACATGATGTTAACGAAACAACTGCGGCTTTTCCATC 715
 DB 1022 CAGGTGTCGAAGTGTATTTATTTGATGATATTCAGATCTTTCCAAAGACTTTTTCATA 963
 QY 716 GTGATATCAATATGCTGGGTAATGCTATTTGCTATTTGCTG 755
 DB 962 AAGCATCTCAAAAGTGAAGTGTATTATTCCTTGGGC 923

RESULT 13

US-08-747-221B-36
 Sequence 36, Application US/08747221B
 Patent No. 6063610
 GENERAL INFORMATION:
 APPLICANT: Silver, Gary W.
 APPLICANT: Wisniewski, Nancy
 TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid
 TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
 NUMBER OF SEQUENCES: 66
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Carol Talkington Verseer, Ph. D.
 ADDRESSEE: Heska Corporation

STREET: 1825 Sharp Point Drive
 CITY: Fort Collins
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80525
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: WordPerfect for Windows, Version 7.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/747,221B
 FILING DATE: No. 6063610emher 12, 1996
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: Verseer, Carol Talkington
 REGISTRATION NUMBER: 37,459
 REFERENCE/DOCKET NUMBER: FC-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 970/493-7272
 TELEFAX: 970/484-9505
 INFORMATION FOR SEQ ID NO: 36:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2007 nucleotides
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA

FEATURE:
 NAME/KEY: CDS
 LOCATION: 11..1594
 US-08-747-221B-36

Query Match 10.5%; Score 179.6; DB 3; Length 2007;
 Best Local Similarity 56.2%; Pred. No. 2.8e-42;
 Matches 360; Conservative 0; Mismatches 274; Indels 6; Gaps 1;

QY 116 ATGGCAAGTAAAGCGCTTAAAGCTTTAACTGTACGTACGTATCTCTACAGTTTG 175
 DB 39 AAGTACTTTAAAGGAAAAGCAATTAAGTAAAGAAATGCTCCATAGTTATT 98
 QY 176 AGGTATACCGTACGCCCAACCGCCAGTGGGTAGCTGAGATTTAAAGCAACCCAGCGAC 235
 DB 99 CTGGAAATTCATATGCAAACTCTGTAGTGTATGATATTTAAAGCAACCTCAACCTG 158
 QY 236 CAACACCTGGGATGGTGGTGGCTGATTTGCAATCATAAAGATTAAGTCAAGTCAAGTTG 295
 DB 159 CAGAACCTGCTCAGGCTCTTGTAGTCTAGTAAAGAGGATATGTTAGATCAGTAC 218
 QY 296 ATTTTAAACGGGCAAGTGTGCTCAGAGGATTTGCTATACCTAAGTGTCTATACGA 355
 DB 219 ATTTTAAATTAATAAATTAAGTGAAGGCTGAAAGATTTTAACTCAATGCTATGATAC 278
 QY 356 ATATCTAATATCCCGAAGTAAAGCTCCGCTTAAAGTCAATGATGCTGCTGCTGATTA 415
 DB 279 CAAAAACATAGAAATCTCTTCCAGTAAATGATATGATATGAGAGAGAGCTTCT 338
 QY 416 TTAATCGTAAATCATCTGATATGATAGTCTGATATTTTCAATTTAAAGAGATGTTG 475
 DB 339 TCATGGATCTGGAATATGATATGATATGATATGATATGATATGATATGATATG 398
 QY 476 TGTGATTAACATCAATATCTGTTGGAGCTCTAGCTTTTCAATTTAAATTCAGAG 535
 DB 399 TTTCTGATCTTCAATATTCATATGATATGATATGATATGATATGATATGATATG 458
 QY 536 ACCTTAATGTGCGGCTATGCGGCTTAAAGTCAATGATGCTGCTGCTGCTGATTA 595
 DB 459 AA-----CGCGCTGGCAATGTTGGTTGATGATGACAGGTTGAAGTCTTAATGGTAA 512
 QY 596 AAAATATTTGGCCCACTTTTGTGCAATCCCGATATATTAACAGTCTTTGTGCAAGTG 655
 DB 513 AAAACAATATTCATCTTTGTGCTGAGCCCAACATGATGATATTTTGGAGAAATCAG 572

```

SEQUENCE CHARACTERISTICS:
LENGTH: 2007 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:

```

NAME/KEY: CDS
LOCATION: 11..1594
US-09-005-051-36

Query Match 10.5%; Score 179.6; DB 4; Length 2007;
Best Local Similarity 56.2%; Pred No. 2.8e-42;
Matches 360; Conservative 0; Mismatches 274; Indels 6; Gaps 1;

```

OY 116 ATGGCAAGTGAAGCGCTTAACGTTTACTGTGTACGATGATTCCTCTACAGTTTG 175
DB 39 AAGGTACTTTAAAGAAAGAAAGCAAAATAGTGAAGAAAGAAATGTTCCATATT 98
OY 176 AAGGTATACCGTACCGCCAGCGGAGTGAAGATTAAAGCACCAGCAG 235
DB 99 CTGGATTTCATATGCCAAACCTCGTGTAGTATTAAGATTAAAGCACCAGCAG 158
OY 236 CACACACCTGGATGGTGTGCTGATTTGTGCATTAAGATTAAGTCAAGTCAAGT 295
DB 159 CAGAACCTGGTGTGCTGATTTGTGCATTAAGATTAAGTCAAGTCAAGT 218
OY 296 ATTTTAAAGGCGCAAGTGTGCTGATTTGTGCATTAAGATTAAGTCAAGT 355
DB 219 ATTTTAAAGGCGCAAGTGTGCTGATTTGTGCATTAAGATTAAGTCAAGT 278
OY 356 ATATCTAATCCGGAACCTAAGCTCCGTTTATATACATACATGATGTTT 415
DB 279 CAAAAACATAGAAATATCTCTTCCATATGATGATGATGATGATGATGATG 338
OY 416 TTATCGGTGAAAATCATCGTATATGATGCTCTCATTTTCAATTAAGATG 475
DB 339 TCATGGATCTGAAATAGTATGATGATGATGATGATGATGATGATGATGATG 398
OY 476 TGTGATTAACATACATATGATGATGATGATGATGATGATGATGATGATG 535
DB 399 TCTGTTACTTCAATATATGATGATGATGATGATGATGATGATGATGATGATG 458
OY 536 ACCTTAATGACCGGTAATGCGGCTTAAGATCAAGTCAAGTCAAGTCAAGT 595
DB 459 AA-----GCGCCTGGCAATGTTGTTGATGACCAAGTGAAGCTTAATG 512
OY 596 AAAATATATGCGCAACTTTGGTGGCAATCGATTAATATATACAGTCTTTG 655
DB 513 AAAACAATATGCAATCTTTGGTGGCAATCGATTAATATATACAGTCTTTG 572
OY 656 CCGGTGCTGCTTACCCATACATGATGATGATGATGATGATGATGATGATG 715
DB 573 CAGGTGCTGCAAGTGTATATGATGATGATGATGATGATGATGATGATGATG 632
OY 716 GTGATATATATGATGATGATGATGATGATGATGATGATGATGATGATG 755
DB 633 AAGCATCTCAAAAGTGAAGTGTCTTTAATCCTTGSGG 672

```

Search completed: April 11, 2003, 08:51:35
Job time : 47.518 secs

GenCore version 5.1.4-p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 11, 2003, 01:07:17 ; Search time 94.5276 Seconds
(without alignments)
15895.765 Million cell updates/sec

Title: US-09-776-910-9
Perfect score: 1713
Sequence: 1 atgaattcaacgttagttl.....aacatagagattatttttag 1713

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapept 1.0

Searched: 593429 seqs, 438583890 residues

Total number of hits satisfying chosen parameters: 1186858

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Published Applications, NA.*

1: /cgn2_6/prodata/2/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/prodata/2/pubpna/US06_PUB_PUB.seq.*
3: /cgn2_6/prodata/2/pubpna/US06_PUBCOMB.seq.*
4: /cgn2_6/prodata/2/pubpna/US07_PUBCOMB.seq.*
5: /cgn2_6/prodata/2/pubpna/US07_PUB_PUB.seq.*
6: /cgn2_6/prodata/2/pubpna/US08_PUBCOMB.seq.*
7: /cgn2_6/prodata/2/pubpna/US08_PUB_PUB.seq.*
8: /cgn2_6/prodata/2/pubpna/US09_PUBCOMB.seq.*
9: /cgn2_6/prodata/2/pubpna/US09_PUB_PUB.seq.*
10: /cgn2_6/prodata/2/pubpna/US10_PUBCOMB.seq.*
11: /cgn2_6/prodata/2/pubpna/US10_PUB_PUB.seq.*
12: /cgn2_6/prodata/2/pubpna/US10_PUBCOMB.seq.*
13: /cgn2_6/prodata/2/pubpna/US60_PUB_PUB.seq.*
14: /cgn2_6/prodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	88.8	5.2	1691	9 US-10-083-590-13	Sequence 13, Appl
2	77.2	4.5	1611	9 US-09-738-626-1254	Sequence 1254, Ap
3	62.2	3.6	1967	10 US-09-748-739A-1	Sequence 1, Appl
4	62.2	3.6	2381	10 US-09-880-107-2271	Sequence 2271, Ap
5	62.2	3.6	2416	10 US-09-748-739A-3	Sequence 3, Appl
6	62.2	3.6	2416	10 US-09-748-739A-5	Sequence 5, Appl
7	62.2	3.6	2416	10 US-09-748-739A-7	Sequence 7, Appl
8	62.2	3.6	2416	10 US-09-748-739A-16	Sequence 16, Appl
9	62.2	3.6	2444	9 US-09-893-519A-112	Sequence 112, App
10	57.8	3.4	657	10 US-09-974-300-1107	Sequence 1107, Ap
11	57.6	3.4	2508	10 US-09-934-323-3	Sequence 3, Appl
12	57.6	3.4	4667	10 US-09-934-323-1	Sequence 1038, Ap
13	56.8	3.3	2191	9 US-09-954-531-1038	Sequence 3854, Ap
14	56.8	3.3	2191	10 US-09-880-107-3854	Sequence 3854, Ap
15	56.8	3.3	2484	9 US-10-102-806-271	Sequence 271, Appl
16	55.4	3.2	1641	10 US-09-895-860-3	Sequence 3, Appl
17	55.4	3.2	2087	10 US-09-895-860-1	Sequence 1, Appl
18	55.4	3.2	2428	9 US-09-418-176-1	Sequence 1, Appl
19	55.4	3.2	2428	10 US-09-969-347-220	Sequence 220, App

20	55.4	3.2	3824	9 US-10-036-041-22	Sequence 22, Appl
21	55.4	3.2	3824	9 US-10-028-072-541	Sequence 541, Appl
22	55.4	3.2	3824	9 US-10-035-855-22	Sequence 22, Appl
23	55.4	3.2	3824	9 US-10-121-049-541	Sequence 541, Appl
24	55.4	3.2	3824	9 US-10-123-904-541	Sequence 541, Appl
25	55.4	3.2	3824	9 US-10-140-470-541	Sequence 541, Appl
26	55.4	3.2	3824	9 US-09-931-836-22	Sequence 22, Appl
27	55.4	3.2	3824	9 US-10-175-746-541	Sequence 541, Appl
28	55.4	3.2	3824	9 US-10-176-918-541	Sequence 541, Appl
29	55.4	3.2	3824	9 US-10-176-921-541	Sequence 541, Appl
30	55.4	3.2	3824	9 US-10-227-884-209	Sequence 209, Appl
31	55.4	3.2	3824	9 US-10-036-214-22	Sequence 22, Appl
32	55.4	3.2	3824	9 US-10-137-865-541	Sequence 541, Appl
33	55.4	3.2	3824	9 US-10-140-474-541	Sequence 541, Appl
34	55.4	3.2	3824	9 US-10-035-719-22	Sequence 22, Appl
35	55.4	3.2	3824	9 US-10-143-431-541	Sequence 541, Appl
36	55.4	3.2	3824	9 US-10-143-114-541	Sequence 209, Appl
37	55.4	3.2	3824	9 US-10-230-163-209	Sequence 541, Appl
38	55.4	3.2	3824	9 US-10-140-002-541	Sequence 541, Appl
39	55.4	3.2	3824	9 US-10-036-160-22	Sequence 22, Appl
40	55.4	3.2	3824	9 US-10-142-419-541	Sequence 541, Appl
41	55.4	3.2	3824	9 US-10-218-631-209	Sequence 209, Appl
42	55.4	3.2	3824	9 US-10-230-338-209	Sequence 209, Appl
43	55.4	3.2	3824	9 US-10-035-958-22	Sequence 22, Appl
44	55.4	3.2	3824	9 US-10-036-150-22	Sequence 22, Appl
45	55.4	3.2	3824	9 US-10-123-262-541	Sequence 541, Appl

ALIGNMENTS

RESULT 1
US-10-083-590-13
Sequence 13, Application US/10083590
Publication NO. US20030027257A1
GENERAL INFORMATION:
APPLICANT: IATROU, Kostas
APPLICANT: FARRELL, Patrick J.
TITLE OF INVENTION: SEQUENCES FOR IMPROVING THE EFFICIENCY OF SECRETION OF
TITLE OF INVENTION: NON-SECRETED PROTEINS FROM MAMMALIAN AND INSECT CELLS
FILE REFERENCE: 028722-207
CURRENT APPLICATION NUMBER: US/10/083.590
CURRENT FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/256,694
PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-24
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/136,421
PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-20
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/056,871
PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
LENGTH: 1691
TYPE: DNA
ORGANISM: Heliothis virescens
US-10-083-590-13

Query Match 5.2%, Score 88.8, DB 9, Length 1691;
Best local similarity 53.6%, Pred. No. 6.4e-13;
Matches 211: Conservative 0; Mismatches 177; Indels 6; Gaps 1;
DB 368 CCGAAGCTAAAGCTCCCGTTAGTATACATACAGTGGTGGTTATATCGGTAAAA 427
DB 380 CCACACCTTACGGCTATCCCGTGGTTCATACATGCTGGAGATTTGCTTGGCTCCG 439
DB 428 ATCATCGTATGATGATGCTGCTGATTTATTCATTAAGAGATGCTGTTGATTACA 487
DB 440 GCACAGGACGCCACACGACGACGATATTTGCTACATAAAGTCTATCTCATCGT 499
DB 488 TACATATGTTGGAGCTCTAGGTTTCTTATAGTTTAATTCGAAGACCTTATGTCG 547
DB 500 TTATTTACAGATTGAACGCTTCTGCTTCTGCTCATGACACACACA-----AAATCC 553

QY 548 CCGTAATGCCGCGCTTAAAGATCAAGTCAATGGCTTGGCTGATTAATAATATTCG 607
Db 554 CCGGAATGCCGCTCGGATAGTAACCCCTGGCTGGTCCAAAGAGAGGCCA 613
QY 608 CCAATTTGGGCAATCCGATATATTTACACTTTGGTGAAGTCCGCTGCTGCT 667
Db 614 AGAATTTGGAG 673
QY 668 CTACCCATCAATGATGTTTAAACGAAACAGAGAGAGAGAGAGAGAGAGAG 727
Db 674 CTGGGATCTAGTACCTTTCTAAAGCTACGAGAGAGAGAGAGAGAGAGAG 733
QY 728 TGTGGGTATGCTATTTTGTCCATTTGCTATATAC 761
Db 734 TGAGCGGAACAGAGATGAGCTACTTCTTACTAC 767

RESULT 2

US-09-738-626-1254
Sequence 1254, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 1254
LENGTH: 1611
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
US-09-738-626-1254

Query Match 4.5%; Score 77.2; DB 9; Length 1611;
Best Local Similarity 50.2%; Pred. No. 6.4e-10;
Matches 277; Conservative 0; Mismatches 263; Indels 12; Gaps 3;

QY 177 GGGTATACCGTACCCCAACCGCCAGTGGTGAAGTATTAAGACCCCGAGC 236
Db 78 GGGATTCCTACGCGGCAACACTGGGGAATATCCCTCGCGGACCCCGCCG 137
QY 237 AACCCCTGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 293
Db 138 CAGAAATGGAGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 197
QY 294 TGATTTTATACGGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 353
Db 198 GTACTCTGAGCAGATTAAGATGCGGTTTGAAGAGTCTGCTTAACTGATGCT 257
QY 354 GAATATCTAATCCGAAATCAACGCTGCTTGAATATACATACATGCTGCTG 413
Db 258 G-----CTGATTCGCAAGAAAGCTTCTGTTGCTATCTCCAGCGGCTTCT 311
QY 414 TATATGCGTGA---AATCATGCTGATATGATGCTGCTGCTGCTGCTGCTGCT 470

Db 312 CATCATGGGCTCATCAGAGGAAAAAGCGCTGCGGATATATACCTCTGCACAAACATGA 371
QY 471 TGTGCTGTTGATTAACATATCAATATGCTTGGAGCTCTAGCTTTTCTAATTAATTC 530
Db 372 TGTGCTGTTGATTAACATATCAATATGCTTGGAGCTCTAGCTTTTCTAATTAATTC 530
QY 531 AGAAGACCTTATGTCGCGGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 590
Db 432 CGTGGGAGAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 491
QY 591 GATTAATAATTAATTTGCGCACTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 650
Db 492 GGTGAGCGGCTATATGCAAGCATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 551
QY 651 AAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 710
Db 552 ATCCGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 611
QY 711 CCATGCTGCTAT 722
Db 612 CCACCGCGCCCAT 623

RESULT 3

US-09-748-739A-1
Sequence 1, Application US/09748739A
Patent No. US20020119489A1
GENERAL INFORMATION:
APPLICANT: Lockridge, Oksana
APPLICANT: Watkins, Jeffrey D.
TITLE OF INVENTION: Butyrylcholinesterase Variants and
METHODS OF USE
FILE REFERENCE: P-IX 4143
CURRENT APPLICATION NUMBER: US/09/748,739A
CURRENT FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1967
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Human Butyrylcholinesterase variant
FEATURE:
NAME/KEY: CDS
LOCATION: (86)...(1891)
US-09-748-739A-1

Query Match 3.6%; Score 62.2; DB 10; Length 1967;
Best Local Similarity 54.8%; Pred. No. 5.6e-06;
Matches 190; Conservative 0; Mismatches 148; Indels 9; Gaps 3;

QY 325 GAGGATGCTATACCTAGTGTGCTATACGATTAATCTAATCCGAACTAAAGCTCC 384
Db 437 GAGGATGCTATATATCTAATATGATGATTCAGACACTAAAC---AAAAATCCACT 493
QY 385 GTTTAGTATACATACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 444
Db 494 GATGATATGATGATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 553
QY 445 GGTCCGATTAATTCATTAAGAAAG---TGTGCTGCTGCTGCTGCTGCTGCTGCT 501
Db 554 GATGCAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 613
QY 502 GAGCTCTAGGTTTCTTAAGTTTAATTCAGAGAGCTTAATGCTGCTGCTGCTGCTG 561
Db 614 GGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 670
QY 671 TTTATTTGATCAACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 730
Db 622 AATCCGATTAATTAACAGTCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 668

Db 731 AATCCTAAAGTGTACTCTCTTTGGAGAAAGTGCAGGACAGCTTC 777

RESULT 4

US-09-880-107-2271

Sequence 2271, Application US/09880107

Patent No. US20020142981A1

GENERAL INFORMATION:

APPLICANT: Horne, Darci T.

APPLICANT: Vockley, Joseph G.

APPLICANT: Scherf, Uwe

APPLICANT: Gene Logic, Inc.

TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer

FILE REFERENCE: 44921-5028-WO

CURRENT APPLICATION NUMBER: US/09/880,107

CURRENT FILING DATE: 2001-06-14

PRIOR APPLICATION NUMBER: US 60/211,379

PRIOR FILING DATE: 2000-06-14

PRIOR APPLICATION NUMBER: US 60/237,054

PRIOR FILING DATE: 2000-10-02

NUMBER OF SEQ ID NOS: 3950

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2271

LENGTH: 2381

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: Genbank Accession No. US20020142981A1 M16474

US-09-880-107-2271

Query Match 3.6%; Score 62.2; DB 10; Length 2381;
Best Local Similarity 54.8%; Pred. No. 6.2e-06;
Matches 190; Conservative 0; Mismatches 148; Indels 9; Gaps 3;

QY 325 GAGGATGCTATACCTAGCTGTATACGAATATCTAAATCCGAACTAAACGTC 384
Db 427 GAAGACTGTTATATCTAAATGATGATCCAGACCTAAACC---AAAAATGCCACT 483
QY 385 GTTTAGTATACATACATGCTGCTTTATATATCGGTCAAAATCATCTGATGTAT 444
Db 484 GTATTGATGATGATGATGCTGCTTTCAACATGCAACATCTTTCATGTTTAT 543
QY 445 GGTCCGATATATTCATTAATAAGAA---TGCTGCTGATTAATACATATCTTTG 501
Db 544 GATGGCAAGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 603
QY 502 GAGCTCTAGCTTTCTAGCTTTAAATTCAGAACTTAATGCTGCTGCTGCTGCTG 561
Db 604 GGTCCCTAGGATTTCTAGCTTT---GCCAGAAATCCTGAGCTCCAGGAGCATGCT 660
QY 562 CTAAAGATCAAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 621
Db 661 TTATTGATCAACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
QY 622 AATCCGATATATATACAGTCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 668
Db 721 AATCCTAAAGTGTACTCTCTTTGGAGAAAGTGCAGGACAGCTTC 767

RESULT 5

US-09-748-739A-3

Sequence 3, Application US/09748739A

Patent No. US20020119489A1

GENERAL INFORMATION:

APPLICANT: Lockridge, Oksana

APPLICANT: Watkins, Jeffrey D.

TITLE OF INVENTION: Butyrylcholinesterase Variants and

FILE REFERENCE: P-IX 4143

CURRENT APPLICATION NUMBER: US/09/748,739A

CURRENT FILING DATE: 2000-12-06

NUMBER OF SEQ ID NOS: 31

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 3

LENGTH: 2416

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Human Butyrylcholinesterase variant

NAME/KEY: CDS

LOCATION: (214)...(1935)

US-09-748-739A-3

Query Match 3.6%; Score 62.2; DB 10; Length 2416;
Best Local Similarity 54.8%; Pred. No. 6.3e-06;
Matches 190; Conservative 0; Mismatches 148; Indels 9; Gaps 3;

QY 325 GAGGATGCTATACCTAGCTGTATACGAATATCTAAATCCGAACTAAACGTC 384
Db 481 GAAGACTGTTATATCTAAATGATGATCCAGACCTAAACC---AAAAATGCCACT 537
QY 385 GTTTAGTATACATACATGCTGCTTTATATCGGTCAAAATCATCTGATGTAT 444
Db 538 GTATTGATGATGATGATGCTGCTTTCAACATGCAACATCATCTTTCATGTTAT 597
QY 445 GGTCCGATATATTCATTAATAAGAA---TGCTGCTGATTAATACATATCTTTG 501
Db 598 GATGGCAAGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 657
QY 502 GAGCTCTAGCTTTCTAGCTTTAAATTCAGAACTTAATGCTGCTGCTGCTGCTG 561
Db 658 GGTCCCTAGGATTTCTAGCTTT---GCCAGAAATCCTGAGCTCCAGGAGCATGCT 714
QY 562 CTAAAGATCAAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 621
Db 715 TTATTGATCAACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 774
QY 622 AATCCGATATATATACAGTCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 668
Db 775 AATCCTAAAGTGTACTCTCTTTGGAGAAAGTGCAGGACAGCTTC 821

RESULT 6

US-09-748-739A-5

Sequence 5, Application US/09748739A

Patent No. US20020119489A1

GENERAL INFORMATION:

APPLICANT: Lockridge, Oksana

APPLICANT: Watkins, Jeffrey D.

TITLE OF INVENTION: Butyrylcholinesterase Variants and

FILE REFERENCE: P-IX 4143

CURRENT APPLICATION NUMBER: US/09/748,739A

CURRENT FILING DATE: 2000-12-06

NUMBER OF SEQ ID NOS: 31

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 5

LENGTH: 2416

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Human Butyrylcholinesterase variant

NAME/KEY: CDS

LOCATION: (214)...(1935)

US-09-748-739A-5

Query Match 3.6%; Score 62.2; DB 10; Length 2416;
Best Local Similarity 54.8%; Pred. No. 6.3e-06;
Matches 190; Conservative 0; Mismatches 148; Indels 9; Gaps 3;

QY 325 GAGGATGCTATACCTAGCTGTATACGAATATCTAAATCCGAACTAAACGTC 384
Db 481 GAAGACTGTTATATCTAAATGATGATCCAGACCTAAACC---AAAAATGCCACT 537

QY 385 GTTTTACTATACATACATGCTGCTTTTATATATCGTGAAATCATCGTATATGAT 444
DB 538 GTATTGATATGATTTATGCTGCTTTTCAACTGGAACATCATCTTACATGTTAT 597
QY 445 GGTCCTGATTTTTCATTTAAAAAGA---TGTGCTGTTGATTAACATCATATCGTTG 501
DB 598 GATGGCAAGTTTCTGGCTCGGGTGAAGAAGATTTAGTGTCAAGTCAATAGGGTG 657
QY 502 GGACCTCTAGGTTTCTTAAGTTTAAATTCAGAACCTTAATGCGCCGTAATGCCGGC 561
DB 658 GTGCGCCCTAGATTTCTTACGTTT---GCCAGGAATCTCTAGGCTCCAGGCAACATGGGT 714
QY 562 CTTAAGATCAAGTCATGCGCTTCTGCTGATTAATAAATTCGCCCAACTTTGGTGGC 621
DB 715 TTATTTGATCAACAGTTGGCTCTTCAGTGGGTCAAAAAATATAGCAGCCTTTGGTGA 774
QY 622 AATCCCATATATATACAGTCTTTGGTGAAGTCCCGTCTGCTC 668
DB 775 AATCCTAAAGTGTACTCTCTTTGGAGAAAGTGCAGGAGCAGCTTC 821

RESULT 7

US-09-748-739A-7
; Sequence 7, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
; APPLICANT: Lockridge, Oksana
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: P-IX 4143
; CURRENT APPLICATION NUMBER: US/09/748,739A
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 2416
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human Butyrylcholinesterase variant
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (214)...(1935)
US-09-748-739A-7

Query Match 3.6%; Score 62.2; DB 10; Length 2416;
Best Local Similarity 54.8%; Pred. No. 6.3e-06;
Matches 190; Conservative 0; Mismatches 148; Indels 9; Gaps 3;

QY 325 GAGGATTGCTATACATAGTCTATAGCATATATCTAAATCCGAACTAAAGCTGCC 384
DB 481 GAGAGCTGTTATATCTAAATGATGATTCACAGACCTTAACCC---AAAAATGCCACT 537
QY 385 GTTTTACTATACATACATGCTGCTTTTATATGCGTAATAATCATCTGATATGAT 444
DB 538 GTATTGATATGATTTATGCTGCTTTTCAACTGGAACATCATCTTACATGTTAT 597
QY 445 GGTCCTGATTTTTCATTTAAAAAGA---TGTGCTGTTGATTAACATCATATCGTTG 501
DB 598 GATGGCAAGTTTCTGGCTCGGGTGAAGAAGTATGATGATGATGATGATGATGATG 657
QY 502 GGACCTCTAGGTTTCTTAAGTTTAAATTCAGAACCTTAATGCGCCGTAATGCCGGC 561
DB 658 GTGCGCCCTAGATTTCTTACGTTT---GCCAGGAATCTCTAGGCTCCAGGCAACATGGGT 714
QY 562 CTTAAGATCAAGTCATGCGCTTCTGCTGATTAATAAATTCGCCCAACTTTGGTGGC 621
DB 715 TTATTTGATCAACAGTTGGCTCTTCAGTGGGTCAAAAAATATAGCAGCCTTTGGTGA 774
QY 622 AATCCCATATATATACAGTCTTTGGTGAAGTCCCGTCTGCTC 668
DB 775 AATCCTAAAGTGTACTCTCTTTGGAGAAAGTGCAGGAGCAGCTTC 821

DB 775 AATCCTAAAGTGTACTCTCTTTGGAGAAAGTGCAGGAGCAGCTTC 821

RESULT 8

US-09-748-739A-16
; Sequence 16, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
; APPLICANT: Lockridge, Oksana
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: P-IX 4143
; CURRENT APPLICATION NUMBER: US/09/748,739A
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 2416
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-748-739A-16

Query Match 3.6%; Score 62.2; DB 10; Length 2416;
Best Local Similarity 54.8%; Pred. No. 6.3e-06;
Matches 190; Conservative 0; Mismatches 148; Indels 9; Gaps 3;

QY 325 GAGGATTGCTATACATAGTCTATAGCATATATCTAAATCCGAACTAAAGCTGCC 384
DB 481 GAGAGCTGTTATATCTAAATGATGATTCACAGACCTTAACCC---AAAAATGCCACT 537
QY 385 GTTTTACTATACATACATGCTGCTTTTATATGCGTAATAATCATCTGATATGAT 444
DB 538 GTATTGATATGATTTATGCTGCTTTTCAACTGGAACATCATCTTACATGTTAT 597
QY 445 GGTCCTGATTTTTCATTTAAAAAGA---TGTGCTGTTGATTAACATCATATCGTTG 501
DB 598 GATGGCAAGTTTCTGGCTCGGGTGAAGAAGTATGATGATGATGATGATGATGATG 657
QY 502 GGACCTCTAGGTTTCTTAAGTTTAAATTCAGAACCTTAATGCGCCGTAATGCCGGC 561
DB 658 GTGCGCCCTAGATTTCTTACGTTT---GCCAGGAATCTCTAGGCTCCAGGCAACATGGGT 714
QY 562 CTTAAGATCAAGTCATGCGCTTCTGCTGATTAATAAATTCGCCCAACTTTGGTGGC 621
DB 715 TTATTTGATCAACAGTTGGCTCTTCAGTGGGTCAAAAAATATAGCAGCCTTTGGTGA 774
QY 622 AATCCCATATATATACAGTCTTTGGTGAAGTCCCGTCTGCTC 668
DB 775 AATCCTAAAGTGTACTCTCTTTGGAGAAAGTGCAGGAGCAGCTTC 821

RESULT 9

US-09-893-519A-112
; Sequence 112, Application US/09893519A
; Publication No. US20030027243A1
; GENERAL INFORMATION:
; APPLICANT: ANADYS PHARMACEUTICALS, INC.
; APPLICANT: THOMPSON, Craig
; APPLICANT: MOORE, Jeffrey
; APPLICANT: BURMAN, Ed T.
; APPLICANT: BRADLEY, John
; APPLICANT: DESTIVA, Thameira
; APPLICANT: HARRIS, Sandra
; APPLICANT: KOMARNITSKY, Svetlana
; APPLICANT: MENDILLO, Marc
; APPLICANT: MOORE, Daniel
; APPLICANT: MCCOY, Melissa
; APPLICANT: SANDERSON, Karen
; APPLICANT: HAO, Jariq
; APPLICANT: ZHU, Shuhao
; APPLICANT: LONG, Fan
; APPLICANT: DAVIDOV, Eugene

;; TITLE OF INVENTION: ANTIFUNGAL COMPOUNDS AND METHODS OF USE
;; FILE REFERENCE: 0342/1G548-US2
;; CURRENT APPLICATION NUMBER: US/09/893,519A
;; CURRENT FILING DATE: 2001-06-28
;; PRIOR APPLICATION NUMBER: US 60/215,164
;; PRIOR FILING DATE: 2000-06-29
;; PRIOR APPLICATION NUMBER: US 60/224,457
;; PRIOR FILING DATE: 2000-08-10
;; NUMBER OF SEQ ID NOS: 146
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 112
;; LENGTH: 2444
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; PUBLICATION INFORMATION:
;; DATABASE ACCESSION NUMBER: Human Genbank/NM_000055
;; DATABASE ENTRY DATE: 2001-02-03
;; RELEVANT RESIDUES: (1)..(2444)
US-09-893-519A-112

Query Match 3.6%; Score 62.2; DB 9; Length 2444;
Best Local Similarity 54.8%; Pred. No. 6.3e-06;
Matches 190; Conservative 0; Mismatches 148; Indels 9; Gaps 3;

QY 325 GAGGATGCTATACCTAAGTGTCTATACGAATATCTAAATCCCGAACTAAACGTCC 384
DB 509 GAAAGACTGTTATATCTAATGATGATTCACACCTTAACCC---AAAAATGCCACT 565
QY 385 GTTATATACATACATACATGCGTGTGTTATATGCGTGAATATCATCTGATATGTAT 444
DB 566 GTATTGATATGATTTATGATGCGTGTGTTTCAAACTGAAACATCATCTTACATGTTAT 625
QY 445 GGTCCGATATATTCATTAATAAAGA---GTGCGTGTGTTAATACATCAATATCGTTTG 501
DB 626 GATGCAAGTTTCGGTGGTGGTGAAGAGTATTTAGTGTCAATGATATAGGCTG 685
QY 502 GGAAGCTAGTGTTCATGATTAATTCAGAAAGACCTTAATGCGCGTAAATGCGCGC 561
DB 686 GTGCGCCCTGATCTTCTAGCTTT---GCCAGGAATCTCTAGCGCTCAGGGAACATGCGT 742
QY 562 CTTAAGATGATGATGATGCGTGTGATTAATAATATGCGCACTTGTGCGC 621
DB 743 TTATTTATATCAACAGTTGGCTCTTCAGTGGTTCATAAAATATATAGAGCTTTGCTGA 802
QY 622 AATCCGATATATATACAGTCTTTGTAAGAGCCGCGTCTGCTGCTG 668
DB 803 AATCTTAAGATGATCTCTTTGGAGAAAGTGCAGAGACAGCTTC 849

RESULT 10
US-09-974-300-1107
;; Sequence 1107, Application US/09974300
;; Patent No. US20020146721A1
;; GENERAL INFORMATION:
;; APPLICANT: Berka, Randy M.
;; APPLICANT: Clausen, Ib Groth
;; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
;; FILE REFERENCE: 10085-500-US
;; CURRENT APPLICATION NUMBER: US/09/974,300
;; CURRENT FILING DATE: 2001-10-05
;; PRIOR APPLICATION NUMBER: 09/680,598
;; PRIOR FILING DATE: 2000-10-06
;; PRIOR APPLICATION NUMBER: 60/219,526
;; PRIOR FILING DATE: 2001-03-27
;; NUMBER OF SEQ ID NOS: 8481
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 1107
;; LENGTH: 657
;; TYPE: DNA
;; ORGANISM: Bacillus licheniformis
US-09-974-300-1107

Query Match 3.4%; Score 57.8; DB 10; Length 657;
Best Local Similarity 49.9%; Pred. No. 4.2e-05;
Matches 174; Conservative 0; Mismatches 172; Indels 3; Gaps 1;

QY 377 AACGTCCGTTTATGATACATACATGCTGTTTATATTCGCG---TGAAATATATC 433
DB 30 ATCTGCTGTATGATGCTGATTCATGAGGGCGCTTTTATGCGCGCGGCAATGAGAC 89
QY 434 GTGATATGATGCTGCTGATTTATTCATTAATAAAGATGCTGCTGATTAATACATACAT 493
DB 90 CGCTATATACGAGGACTGCTGCTGCAAGACAGGAAGATGATCTGCTGATCATCATATT 149
QY 494 ATCGTTTGGAGCTCTAGGTTTCTAAGTTTAATTCAGAAAGACCTTAATGTCGCCGGA 553
DB 150 ATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 209
QY 554 ATGCGCGCTTAAAGATCAAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 613
DB 210 ATCTTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 269
QY 614 TTGTCGCAATCCCGATATATATACAGTCTTTGTTGTTGAAGTCCGCGTCTGCTTACCC 673
DB 270 TTGGCGGAGACGCTCATCATATACAGTCTTTTGGAGAGTCCGCGGATGATGACATCG 329
QY 674 ACTACATGATGTTAACCGAAACAACTCGCGCTCTTTCCATCGTGTAT 722
DB 330 CTTCGCTTTTGGGAGTCCGGAAGAGGCGCTTTTCAACAGGCGCAT 378

RESULT 11
US-09-934-323-3
;; Sequence 3, Application US/09934323
;; Patent No. US20020150910A1
;; GENERAL INFORMATION:
;; APPLICANT: Cirlis, Roy A. J.
;; TITLE OF INVENTION: 33410, A NOVEL HUMAN CARBOXYESTERASE
;; FILE REFERENCE: 10448-081001
;; CURRENT APPLICATION NUMBER: US/09/934,323
;; CURRENT FILING DATE: 2001-08-21
;; PRIOR APPLICATION NUMBER: US 60/726,774
;; PRIOR FILING DATE: 2000-08-21
;; NUMBER OF SEQ ID NOS: 8
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 3
;; LENGTH: 2508
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-934-323-3

Query Match 3.4%; Score 57.6; DB 10; Length 2508;
Best Local Similarity 54.2%; Pred. No. 0.0001;
Matches 117; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 530 CAGAAAGCTTAATGTCGCGGTAATGCGGCTTAAGATGAATGATGATGCTTGCCTT 589
DB 671 CCGGGAGCAGGCTGGAAGAAAGCAATATGAGCTCTGACAGATCCAGGCGCTGCGCT 730
QY 590 GGATTAATAAATAATGCGCAACTTTGTTGTCGAATCCGATATATTAATCACTTTGCTG 649
DB 731 GGTCTAGTGAATAACATCGCCACTTTGGGGGCGACCCGAGGATGATCAATCTTTGGTT 790
QY 650 AAGTGGCGTCTGCTTACCCACTACATGATGTTAAGCAAGAAACTGCGGCTCTT 709
DB 791 CCGGGGAGGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 850
QY 710 TCCATGCTGATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 745
DB 851 TCCAGAGGCCATCGCCGAGAGTGGCAGCCGCAATTT 886

RESULT 12
US-09-934-323-1

Sequence 1, Application US/09934323
Patent No. US20020150910A1
GENERAL INFORMATION:
APPLICANT: Curtis, Roy A. J.
TITLE OF INVENTION: 33410, A NOVEL HUMAN CARBOXYLESTERASE
FILE REFERENCE: 10448-081001
CURRENT APPLICATION NUMBER: US/09/934,323
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/226,774
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 4667
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (420)...(2924)
US-09-934-323-1

Query Match 3.4%; Score 57.6; DB 10; Length 4667;
Best Local Similarity 54.2%; Pred. No. 0.00014;
Matches 117; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 530 CAGAACCTTAATGTCGGGCTTAATGCGGCTTAAGATCAAGTCAATGCGCTTGGCTT 589
DB 1090 CCGGGACCAAGCTCAAAAGGCACTATGGCTCTGACCAATCCAGGCCCTGGCTT 1149
QY 590 GATTAATAATATGTCGCACTTGTGCAATCCGATATATTAATTAAGTCTTGGTG 649
DB 1150 GGCTAGGAAACATGCGCCACTTTGGGGGAGACCCGAGGATATCAATCTTGGTT 1209
QY 650 AAGTCCGCTGCTCTCTCAACCACTACATGATGTTAACGACAACTCGGCTCTT 709
DB 1210 CCGGGGACGGGCTCTCTCAACCTCTGATCTCTCCACCATTCAGAAAGGGCTGT 1269
QY 710 TCCATGCTGATTAATGTCGGGCTTAATGCTATTT 745
DB 1270 TCCAGAGGCGCATGCGCCAGAGTGGACCGCCCATTT 1305

RESULT 13
US-09-954-531-1038

Sequence 1038, Application US/09954531
Patent No. US2002015180A1
GENERAL INFORMATION:
APPLICANT: Weaver, Zoe
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cand
FILE REFERENCE: 689290-77
CURRENT APPLICATION NUMBER: US/09/954,531
CURRENT FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: US/60/233,133
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/234,009
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,034
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,509
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: US/60/234,567
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 1392
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1038
LENGTH: 2191
TYPE: DNA
ORGANISM: Homo sapiens
US-09-954-531-1038

Query Match 3.3%; Score 56.8; DB 9; Length 2191;

Best Local Similarity 53.2%; Pred. No. 0.00015;
Matches 215; Conservative 0; Mismatches 177; Indels 12; Gaps 4;

QY 322 TCAGAGAGTGTCTATACCTAAGTGTCTATACGATATATCTAATCCGAA--ACTAAA 378
DB 436 TCTGAGAGACTGCTGTACCTACACATCTACACGCGCCCATAGCCATGAGCTCTAAC 495
QY 379 CGTCCGTTTATATACATACATGAGTGGGTTTATTATGCGTAATCATGCTGAT 438
DB 496 CTGCGGATGATGCTGTGATCCAGGCTGGTGGCTGTTTGG--GCATGGCTTCTTGT 553
QY 439 ATGTATGCTCTGATTAATTTCAATTAAGAGATGCTGTTGATTAATACATATGCT 498
DB 554 ATGATGTTTCAATGCTGGCTGCT--TGAGAAAGCTGGTGGTGTATCATACAGTACCC 612
QY 499 TTGGAGCTCTAGCTTTTCTAATTAATTCAGAGACCTTAATGTCGCCGATATGCC 558
DB 613 CTGGGTCTCTGGGCTT-----CTTACGACATGAGACAGACGCAACGCGCACTTGG 666
QY 559 GGCCTTAAGATCAAGTCAATGCTGCTGCTGATTAATAATTAATGCGCAACTTGGT 618
DB 667 GGCTACCTGACCAAGTGGCTGCTACAGCTGGCTCCAGACGATATCCGCACTTGGTA 726
QY 619 GCGAATCCGATATATATTAACAGTCTTGGTGAAGTCCGGTCTGCTTACCCACTAC 678
DB 727 GCGAACCCTGACGCTGACCATTTTGGGAGTCTGCGGGTGGCAGAGTGTCTTGG 786
QY 679 ATGATGTTAACGACAACTCGGCTTTTCCATGCTGAT 722
DB 787 CTGTGTGTGTCCTATCCAGGACTCTTCCAGGAGCCAT 830

RESULT 14
US-09-880-107-3854

Sequence 3854, Application US/09880107
Patent No. US20020142981A1
GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3854
LENGTH: 2191
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20020142981A1 Y09616
US-09-880-107-3854

Query Match 3.3%; Score 56.8; DB 10; Length 2191;
Best Local Similarity 53.2%; Pred. No. 0.00015;
Matches 215; Conservative 0; Mismatches 177; Indels 12; Gaps 4;

QY 322 TCAGAGAGTGTCTATACCTAAGTGTCTATACGATATATCTAATCCGAA--ACTAAA 378
DB 436 TCTGAGAGACTGCTGTACCTACACATCTACACGCGCCCATAGCCATGAGCTCTAAC 495
QY 379 CGTCCGTTTATATACATACATGAGTGGGTTTATTATGCGTAATCATGCTGAT 438
DB 496 CTGCGGATGATGCTGTGATCCAGGCTGGTGGCTGTTTGG--GCATGGCTTCTTGT 553
QY 439 ATGTATGCTCTGATTAATTTCAATTAAGAGATGCTGTTGATTAATACATATGCT 498

Db 554 ATGATGCTTCATGCTGGCTGCT-76GAGAACGTGGTGGTGCATCATCAGTACCGC 612
QY 499 TTGGAGCTCTAGCTTTTCTTAAGTTAAATTCAGAGACCTTAATGTCGGGTAATGCC 558
Db 613 CTGGGTGCTCGGGCTT-----CTTCAGCACTGAGACACAGCAGACCGGGAACCTGG 666
QY 559 GGCCTTAAAGATCAATGATGAGCGCTTGGATTAATAATTAATTCGCAACTTTGGT 618
Db 667 GGCTACCTGACCAAGGCTGCTACGCTGGGTCAGAGAAATATGCGCACTTTGGA 726
QY 619 GGCATCCCGATATATTAAGTCTTTGGTGAAGTCCGCTGCTTACCCACTAC 678
Db 727 GGCACACCTGACCGTGCACATTTTGGGAGTGTGCGGAGTGCAGAGTGTCTTGG 786
QY 679 ATGATGTTAACCGAACACTCGCGCTTTTCCATGCTGTAT 722
Db 787 CTGTGTGTGTCCTCCCATATCCCAAGGACTCTTCCACGAGCCAT 830

RESULT 15

US-10-102-806-271
; Sequence 271, Application US/10102806
; Publication No. US20030054421A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: P103P1C1
; CURRENT APPLICATION NUMBER: US/10/102,806
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/925,298
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 271
; LENGTH: 2484
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (194)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (623)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (2396)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (2484)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-102-806-271

Query Match 3.3%; Score 56.8; DB 9; Length 2484;
Best Local Similarity 53.2%; Pred. No. 0.00016;
Matches 215; Conservative 0; Mismatches 177; Indels 12; Gaps 4;

QY 322 TCAGAGGATTTCTAATCTAGTGTCTTACGATATCTAATCCGAA--ACTAAA 378
Db 950 TCTGAGAGATGCTGCTTACCTCAGACTACACGCGCCCATGAGCCATGAGCTCTAAC 1009
QY 379 GCTCCGTTTATATACATACATGATGATGATGATGATGATGATGATGATGATGAT 438
Db 1010 CTGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1067
QY 439 ATGATGCTCTGATATTTCTAATAAAGATGATGATGATGATGATGATGATGATGAT 498
Db 1068 ATGATGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1126
QY 499 TTGGAGCTCTAGTTTCTAAGTTTAAATTCAGAACCTTAATGTCGGGTAATGCC 558

Db 1127 CTGGGTGCTCGGGCTT-----CTTCAGCACTGAGACACAGCAGACCGGCAACTGG 1180
QY 559 GGCCTTAAAGATCAATGATGAGCGCTTGGATTAATAATTAATTCGCAACTTTGGT 618
Db 1181 GGCTACCTGAGACCAAGTGGCTGCTACGCTGGGTCAGAGAAATATGCGCACTTTGGA 1240
QY 619 GGCATCCCGATATATTTACAGCTTTTGGTGAAGTCCGCTGCTTACCCACTAC 678
Db 1241 GGCATCCCGATATATTTACAGCTTTTGGTGAAGTCCGCTGCTTACCCACTAC 1300
QY 679 ATGATGTTAACCGAACACTCGCGCTTTTCCATGCTGTAT 722
Db 1301 CTGTGTGTGTCCTCCCATATCCCAAGGACTCTTCCACGAGCCAT 1344

Search completed: April 11, 2003, 13:24:04
Job time : 105.528 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2003, 09:08:22 ; Search time 44.0154 Seconds

(without alignments)
1725.596 Million cell updates/sec

Title: US-09-776-910-13

Perfect score: 3045
Sequence: 1 MFRLKQFIRLKLCKVCNVN.....PEMDKIKGASIFDKKLEF 570

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A_Geneseq_101002.*
1: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3017	99.1	570	18	AAW17767	Md-alpha-E7 malath
2	2348	77.1	570	16	AAW17767	OP-sensitive ester
3	2348	77.1	570	18	AAW17765	Lc-alpha-E7 malath
4	2335	76.7	570	18	AAW17768	Malathion carboxyl
5	2335	76.7	570	18	AAW17768	Malathion carboxyl
6	1844.5	60.6	572	22	ABBS7850	Drosophila melanog
7	1330	43.1	554	22	ABBS7866	Drosophila melanog
8	1311	43.1	572	22	ABBS7867	Drosophila melanog
9	1298.5	42.6	567	22	ABBS7857	Drosophila melanog
10	1277.5	42.0	554	22	ABBS9161	Drosophila melanog

11	1267.5	41.6	566	22	ABBS1983	Drosophila melanog
12	1236.5	40.6	565	22	ABBS7746	Drosophila melanog
13	1217	40.0	530	22	ABBS7868	Drosophila melanog
14	1204	39.5	542	22	ABBS7790	Drosophila melanog
15	1194.5	39.2	602	23	AAW47598	Drosophila cell cy
16	994	32.6	551	22	ABBS7788	Drosophila melanog
17	948.5	31.1	541	22	ABBS7789	Drosophila melanog
18	899	29.5	568	22	ABBS7831	Drosophila melanog
19	795	26.1	528	22	AAW57862	C. felis esterase,
20	795	26.1	528	22	AAE12916	C. felis esterase,
21	793	26.0	513	19	AAW57863	C. felis esterase,
22	741.5	24.4	562	22	ABBS7808	Drosophila melanog
23	735.5	24.2	550	19	AAW57864	C. felis esterase,
24	735.5	24.2	550	19	AAW57865	C. felis esterase,
25	735.5	24.2	550	19	AAW57853	C. felis esterase,
26	735.5	24.2	550	19	AAW57854	C. felis esterase,
27	735.5	24.2	550	22	AAE12910	Ctenocephalides fe
28	735.5	24.2	550	22	AAE12923	Ctenocephalides fe
29	733.5	24.1	530	19	AAW57855	C. felis esterase,
30	733.5	24.1	530	19	AAW57857	C. felis esterase,
31	733.5	24.1	530	22	AAE12911	Ctenocephalides fe
32	723.5	23.8	505	19	AAW57851	C. felis esterase,
33	722.5	23.7	505	19	AAW57852	C. felis esterase,
34	722.5	23.7	505	22	AAE12909	Ctenocephalides fe
35	721.5	23.7	495	19	AAW57869	C. felis esterase,
36	693	22.8	530	19	AAW57866	C. felis esterase,
37	693	22.8	530	19	AAW57867	C. felis esterase,
38	690.5	22.7	527	22	ABBS64915	Drosophila melanog
39	662	21.7	527	22	ABBS6353	Drosophila melanog
40	641.5	21.1	584	23	ABBS7676	Carboxylesterase d
41	635	20.9	575	23	ABBS79538	Carboxylesterase c
42	624	20.5	570	19	AAW57860	C. felis esterase,
43	624	20.5	570	19	AAW57879	C. felis esterase,
44	624	20.5	570	22	AAE12915	Ctenocephalides fe
45	624	20.5	595	19	AAW57859	C. felis esterase,

ALIGNMENTS

RESULT 1	AAW17767	
ID	AAW17767 standard; Protein; 570 AA.	
XX		
AC	AAW17767:	
XX		
DT	08-AUG-1997 (first entry)	
XX		
DE	Md-alpha-E7 malathion resistant mutant.	
XX		
KW	Malathion carboxylesterase; organophosphate; insecticide;	
KW	pesticide; remediation; bioremediation; decontamination.	
XX		
OS	Musca domestica Rutgers strain.	
XX		
EH	Key	Location/Qualifiers
FT	Misc-difference 251	
FT	/note= "Ser-251 is tryptophan in the susceptible	
FT	allele expression product"	
XX		
PN	WO9719176-A1.	
XX		
PD	29-MAY-1997.	
XX		
PF	22-NOV-1996; 96MO-AU00746.	
XX		
PR	23-NOV-1995; 95AU-0006751.	
XX		
PA	(CSIR) COMMONWEALTH SCI & IND RES ORG.	
XX		
PI	Boyce T, Brownlie JC, Campbell PM, Claudianos C;	
XX	Newcomb RD, Oakshott JC, Robin GC, Russell RJ, Smyth K;	

DR WPI; 1997-298113/27.
 DR N-PSDB; AAT68597.
 XX DNA encoding enzyme that degrades organophosphate pesticides -
 PT useful for decontamination of soil, water, food etc
 XX
 XX Disclosure: Fig 3; 52pp; English.
 XX
 CC A polypeptide (AAW17767) is the expression product of a malathion
 CC resistant allele of the *Musca domestica* Md-alpha-E7 gene, and
 CC contains a Ser for Trp substn. at amino acid position 251. The
 CC enzyme is capable of hydrolysing carboxylester and/or
 CC diethylloxon organophosphates and can be formulated for use
 CC in bioremediation strategies for treatment of soil or water.
 CC
 XX
 XX Sequence 570 AA;
 SQ

Query Match 99.1%; Score 3017; DB 18; Length 570;
 Best Local Similarity 99.3%; Pred. No. 6.8e-276;
 Matches 566; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MPELKFIFRLKCYKCMVNTYNTRLSTNETQIIDTEYGOIKGYKRMVYDSDSYSPES 60
 DB 1 MPELKFIFRLKCYKCMVNTYNTRLSTNETQIIDTEYGOIKGYKRMVYDSDSYSPES 60
 QY 61 IPYAKPPVGELEFKAPQRPVPEWEGVRDCCGPANRSVQTDFTSGKPTGSEDCLYLVNTND 120
 DB 61 IPYAKPPVGELEFKAPQRPVPEWEGVRDCCGPANRSVQTDFTSGKPTGSEDCLYLVNTND 120
 QY 121 LNPDKRRPVYVFIHGGDFIFGEANRNMFGPDYFMKRPVLYVYQRLVGLFLSLKSEN 180
 DB 121 LNPDKRRPVYVFIHGGDFIFGEANRNMFGPDYFMKRPVLYVYQRLVGLFLSLKSEN 180
 QY 181 NVPGNAGLKDOYVALRWKSNIAIFGSDVNTITVFGESAGASTHYMMITEQTRGLFHRG 240
 DB 181 NVPGNAGLKDOYVALRWKSNIAIFGSDVNTITVFGESAGASTHYMMITEQTRGLFHRG 240
 QY 241 IMMSGNSMCWASTECOSRALTMARVGYKGEDNEKDILEFLMKANPYDLIKEBPQVLT 300
 DB 241 IMMSGNSMCWASTECOSRALTMARVGYKGEDNEKDILEFLMKANPYDLIKEBPQVLT 300
 QY 301 ERMQNVMPFGPTVEPYOTADCVKPIREKWSAMGNSIPTLIGNSYGGLSLKSTAK 360
 DB 301 ERMQNVMPFGPTVEPYOTADCVKPIREKWSAMGNSIPTLIGNSYGGLSLKSTAK 360
 QY 361 QYPEVVKELKESCVNYVPELADSEKAPETLERAAIVKKAHVDEGPTPLDNFMELCSYFY 420
 DB 361 QYPEVVKELKESCVNYVPELADSEKAPETLERAAIVKKAHVDEGPTPLDNFMELCSYFY 420
 QY 421 FLFPMHRLQLRFNHTAGTPILYLYRFEDFSEELINPYRIMRFGKGVKGVSHADELYLFW 480
 DB 421 FLFPMHRLQLRFNHTAGTPILYLYRFEDFSEELINPYRIMRFGKGVKGVSHADELYLFW 480
 QY 481 NILSKRLPKESREYKTIERMVGIWTEFATGKPSNDIAGMENLTWPIKSDVYKCLN 540
 DB 481 NILSKRLPKESREYKTIERMVGIWTEFATGKPSNDIAGMENLTWPIKSDVYKCLN 540
 QY 541 IGDELKVMDEPMKIKOGASIFDKKELF 570
 DB 541 IGDELKVMDEPMKIKOGASIFDKKELF 570

RESULT 2
 AAR78142
 ID AAR78142 standard; Protein: 570 AA.
 XX
 AC AAR78142;
 XX
 XX 22-DEC-1995 (first entry)
 DT
 XX OP-sensitive esterase E3.
 DE
 XX Esterase; E3; bioremediation; organophosphate; carbamate;
 KW

KW Insecticide; pesticide; water decontamination; meat decontamination.
 XX
 XX *Lucilia cuprina*.
 OS
 PN W09519440-A1.
 XX
 XX 20-JUL-1995.
 PD
 XX
 PF 13-JAN-1995; 95MO-AU00016.
 XX
 PK 13-JAN-1994; 94AU-0003347.
 XX
 PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
 XX
 PI Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;
 PI Parker AG, Robin GC, Russell RJ, Smyth K;
 DR N-PSDB; AAQ91561.
 DR WPI; 1995-263870/34.
 XX
 XX Pure E3 esterase from *Lucilia cuprina* and related DNA - used to
 PT eliminate residues of organo:phosphate and carbamate pesticides from
 PT water, meat etc.
 XX
 PS Example 3; Page 12-17; 38pp; English.
 XX
 CC cDNA from organophosphate (OP)-sensitive *L. cuprina* pupa cDNA
 CC library was amplified using cluster-specific esterase primers.
 CC Isolated clone lc743, a probable full-length cDNA, was expressed
 CC using a baculovirus vector in insect cells and shown to encode
 CC an OP-susceptible E3 esterase useful in bioremediation.
 CC
 XX
 XX Sequence 570 AA;
 SQ

Query Match 77.1%; Score 2348; DB 16; Length 570;
 Best Local Similarity 74.2%; Pred. No. 1.1e-212;
 Matches 423; Conservative 73; Mismatches 74; Indels 0; Gaps 0;

QY 1 MPELKFIFRLKCYKCMVNTYNTRLSTNETQIIDTEYGOIKGYKRMVYDSDSYSPES 60
 DB 1 MPELKFIFRLKCYKCMVNTYNTRLSTNETQIIDTEYGOIKGYKRMVYDSDSYSPES 60
 QY 61 IPYAKPPVGELEFKAPQRPVPEWEGVRDCCGPANRSVQTDFTSGKPTGSEDCLYLVNTND 120
 DB 61 IPYAKPPVGELEFKAPQRPVPEWEGVRDCCGPANRSVQTDFTSGKPTGSEDCLYLVNTND 120
 QY 121 LNPDKRRPVYVFIHGGDFIFGEANRNMFGPDYFMKRPVLYVYQRLVGLFLSLKSEN 180
 DB 121 LNPDKRRPVYVFIHGGDFIFGEANRNMFGPDYFMKRPVLYVYQRLVGLFLSLKSEN 180
 QY 181 NVPGNAGLKDOYVALRWKSNIAIFGSDVNTITVFGESAGASTHYMMITEQTRGLFHRG 240
 DB 181 NVPGNAGLKDOYVALRWKSNIAIFGSDVNTITVFGESAGASTHYMMITEQTRGLFHRG 240
 QY 241 IMMSGNSMCWASTECOSRALTMARVGYKGEDNEKDILEFLMKANPYDLIKEBPQVLT 300
 DB 241 IMMSGNSMCWASTECOSRALTMARVGYKGEDNEKDILEFLMKANPYDLIKEBPQVLT 300
 QY 301 ERMQNVMPFGPTVEPYOTADCVKPIREKWSAMGNSIPTLIGNSYGGLSLKSTAK 360
 DB 301 ERMQNVMPFGPTVEPYOTADCVKPIREKWSAMGNSIPTLIGNSYGGLSLKSTAK 360
 QY 361 QYPEVVKELKESCVNYVPELADSEKAPETLERAAIVKKAHVDEGPTPLDNFMELCSYFY 420
 DB 361 QYPEVVKELKESCVNYVPELADSEKAPETLERAAIVKKAHVDEGPTPLDNFMELCSYFY 420
 QY 421 FLFPMHRLQLRFNHTAGTPILYLYRFEDFSEELINPYRIMRFGKGVKGVSHADELYLFW 480
 DB 421 FLFPMHRLQLRFNHTAGTPILYLYRFEDFSEELINPYRIMRFGKGVKGVSHADELYLFW 480
 QY 481 NILSKRLPKESREYKTIERMVGIWTEFATGKPSNDIAGMENLTWPIKSDVYKCLN 540
 DB 481 NILSKRLPKESREYKTIERMVGIWTEFATGKPSNDIAGMENLTWPIKSDVYKCLN 540

[illegible]XX
XX
A malathion carboxylester

XX A malathion carboxylesterase (AAW17766) differs from the esterase
CC (AAW17765) of a malathion susceptible clone of *Lucilia cuprina* by
CC

CC a substr. of the tryptophan residue at amino acid position 251.
 CC The enzyme is capable of hydrolysing carboxylester and/or
 CC dimethylloxon organophosphates and can be formulated for use in
 CC bioremediation strategies for treating soil or water.

SO Sequence 570 AA;

Query Match 76.7%; Score 2335; DB 18; Length 570;
 Best Local Similarity 74.0%; Pred. No. 1.9e-211;
 Matches 422; Conservative 73; Mismatches 75; Indels 0; Gaps 0;

```

QY 1 MTFLEKQFIRLKLCKVCKVNTYNTSTNETQIITDEYGOIKGKRYVYDSDYSFES 60
DB 1 MNFNLSLMKRLKWKIKCIENKFLNRLTNETVVAETEGYKVGKRLTYDSDYSFEG 60
QY 61 IPYAKPPVGELEFRKAPQRPVMEGVDRCCGPNARSVOTDFISGPTSECDLYNTND 120
DB 61 IPYAPPPVGELEFRKAPQRPVMEGVDRCCGPNARSVOTDFISGPTSECDLYNTND 120
QY 121 LNPDKRRPVMEVETIHGGDFIFGEANRNMFGPDYPMKKRPVLYVYRGLVGLSLKSENL 180
DB 121 LNPDKRRPVLYIHGGDFIFGEANRNMFGPDYPMKKRPVLYVYRGLVGLSLKSENL 180
QY 181 NVPGNAGLKDOVMALRMVKSNIATFGGDVNTIVFEGSAGASTHYMMITEQTRGLFHNG 240
DB 181 NVPGNAGLKDOVMALRMVKSNIATFGGDVNTIVFEGSAGASTHYMMITEQTRGLFHNG 240
QY 241 IMMSGNSMCWASTECOSRALYMAKRVYKGEDENEKDLLEFLMKANPYDLIKEEPOVLT 300
DB 241 IMMSGNSMCWASTECOSRALYMAKRVYKGEDENEKDLLEFLMKANPYDLIKEEPOVLT 300
QY 301 ERMOKNMPFPGPTVEPYQADCVKPRPREMVKSAWNSIPTLIGNTSYEGILSKSVAK 360
DB 301 EERTNKVMPFPGPTVEPYQADCVKPRPREMVKSAWNSIPTLIGNTSYEGILSKSVAK 360
QY 361 QYEVYKELSCVNYVPELADSERAPETLERAAIVKKAHVDGETPTLDMFELCSYFY 420
DB 361 QMPLVLEKELSCVNYVPELADSERAPETLERAAIVKKAHVDGETPTLDMFELCSYFY 420
QY 421 FLFPMHRLQLRNHTAGPITLYLRDPDSEELINPYRIMRGKGVKGVSHADELTLYFEW 480
DB 421 FLFPMHRLQLRNHTAGPITLYLRDPDSEELINPYRIMRGKGVKGVSHADELTLYFEW 480
QY 481 NILSKRLPKESREYKTIETRMVGIWTEFATTKGPKYSNDIAGENLTPDIKKSDDVYKCLN 540
DB 481 NOLAKRMPKESREYKTIETRMVGIWTEFATTKGPKYSNDIAGENLTPDIKKSDDVYKCLN 540
QY 541 IGDELKYMDELPMDDIKOGASIFDKKLEF 570
DB 541 ISDELKIMDIVPEMDKIKOWESMEKHRDLF 570

```

RESULT 5
 AAM17768
 ID AAM17768 standard; Protein; 570 AA.

AC AAM17768;

DT 08-AUG-1997 (first entry)

DE Malathion carboxylesterase RM8Con.

KW Malathion carboxylesterase; organophosphate; insecticide;
 pesticide; remediation; bioremediation; decontamination; esterase;

KW Lucilia cuprina.

XX Lucilia cuprina.

XX OS

XX PN

XX PD

XX PF

22-NOV-1996; 96WO-AU00746.

XX 23-NOV-1995; 95AU-0006751.
 PR (CSIR) COMMONWEALTH SCI & IND RES ORG.
 PA Boyce T, Brownlie JC, Campbell PM, Claudianos C;
 PI Newcomb RD, Oakeshott JG, Robin GC, Russell RJ, Smyth K;
 DR WPI: 1997-298113/27.

XX DNA encoding enzyme that degrades organophosphate pesticides -
 PT useful for decontamination of soil, water, food etc
 PS Claim 6; Fig 1; 52pp; English.

CC A malathion carboxylesterase (AAM17768), designated RM-8Con, differs
 CC from the esterase (AAM17765) of a malathion susceptible clone of
 CC Lucilia cuprina by a substr. of the tryptophan residue at amino
 CC acid position 251 by a leucine residue. This mutation is situated
 CC at the base of the active site gorge, 6.5 Angstroms from the active
 CC site serine. The RM8Con amino acid sequence is a consensus deduced
 CC from the DNA sequences of 3 resistant clones (RM8 A-C) and their
 CC comparison to reference susceptible clone Lc743 (AAR68596) of
 CC Lc-alpha-E7. The enzyme is capable of hydrolysing carboxylester
 CC and/or dimethylloxon organophosphates and can be formulated for use
 CC in bioremediation strategies for treatment of soil or water.

SO Sequence 570 AA;

Query Match 76.7%; Score 2335; DB 18; Length 570;
 Best Local Similarity 74.0%; Pred. No. 1.9e-211;
 Matches 422; Conservative 73; Mismatches 75; Indels 0; Gaps 0;

```

QY 1 MTFLEKQFIRLKLCKVCKVNTYNTSTNETQIITDEYGOIKGKRYVYDSDYSFES 60
DB 1 MNFNLSLMKRLKWKIKCIENKFLNRLTNETVVAETEGYKVGKRLTYDSDYSFEG 60
QY 61 IPYAKPPVGELEFRKAPQRPVMEGVDRCCGPNARSVOTDFISGPTSECDLYNTND 120
DB 61 IPYAPPPVGELEFRKAPQRPVMEGVDRCCGPNARSVOTDFISGPTSECDLYNTND 120
QY 121 LNPDKRRPVMEVETIHGGDFIFGEANRNMFGPDYPMKKRPVLYVYRGLVGLSLKSENL 180
DB 121 LNPDKRRPVLYIHGGDFIFGEANRNMFGPDYPMKKRPVLYVYRGLVGLSLKSENL 180
QY 181 NVPGNAGLKDOVMALRMVKSNIATFGGDVNTIVFEGSAGASTHYMMITEQTRGLFHNG 240
DB 181 NVPGNAGLKDOVMALRMVKSNIATFGGDVNTIVFEGSAGASTHYMMITEQTRGLFHNG 240
QY 241 IMMSGNSMCWASTECOSRALYMAKRVYKGEDENEKDLLEFLMKANPYDLIKEEPOVLT 300
DB 241 IMMSGNSMCWASTECOSRALYMAKRVYKGEDENEKDLLEFLMKANPYDLIKEEPOVLT 300
QY 301 ERMOKNMPFPGPTVEPYQADCVKPRPREMVKSAWNSIPTLIGNTSYEGILSKSVAK 360
DB 301 EERTNKVMPFPGPTVEPYQADCVKPRPREMVKSAWNSIPTLIGNTSYEGILSKSVAK 360
QY 361 QYEVYKELSCVNYVPELADSERAPETLERAAIVKKAHVDGETPTLDMFELCSYFY 420
DB 361 QMPLVLEKELSCVNYVPELADSERAPETLERAAIVKKAHVDGETPTLDMFELCSYFY 420
QY 421 FLFPMHRLQLRNHTAGPITLYLRDPDSEELINPYRIMRGKGVKGVSHADELTLYFEW 480
DB 421 FLFPMHRLQLRNHTAGPITLYLRDPDSEELINPYRIMRGKGVKGVSHADELTLYFEW 480
QY 481 NILSKRLPKESREYKTIETRMVGIWTEFATTKGPKYSNDIAGENLTPDIKKSDDVYKCLN 540
DB 481 NOLAKRMPKESREYKTIETRMVGIWTEFATTKGPKYSNDIAGENLTPDIKKSDDVYKCLN 540
QY 541 IGDELKYMDELPMDDIKOGASIFDKKLEF 570
DB 541 ISDELKIMDIVPEMDKIKOWESMEKHRDLF 570

```

[illegible]

Db 247 AICPMALNGDITNHPYIAKLVGKGEDNDKDVLEFLQWAKADLRDENAVLTIEEKN 306
Qy 306 KVMFEPGPEVPEYQIADCVVPKPIREMYVSAMGNSIPTLLGNTSYEGLLSKVAQYREV 365
Db 307 KIMFAPGSPLEPSTPECVSKPKPKEMKMTAMGNSIPMETGNTSYEGLLMDEVKLMPOV 366
Qy 366 VKLESCVNVYPMFLADSESAPELTERRAIYVKAHVDEFTPLDNEFMELCSYFFFLPMP 425
Db 367 LQQLDAQGTPELPKLLATPEPSKKEKLSMSAQINDVHRTSESTPDMYDLCIYFVPPA 426
Qy 426 HRFQLPFPNTAGPIPLVYRFPDSEETIIMPRIMFPGGVGVSHADELTFLFNNITSK 485
Db 427 LRVVSHKHAAGAAGPVYFYRYDPDSEELLIPYIMLGGVGVSHADLTSTQPSLLAR 486
Qy 486 RLPESEBEYKTIERMVGIWTEFATFGKPYSNDIAGMENTWDPRIKSDDYVKCLNIGDEL 545
Db 487 RLPESEBEYRIERTVGIWTFQATGNPYSEKINGMDTLTIDPVKRKSDVICKLNIISDL 546
Qy 546 KVMFLPEMDKIKQGSIFPDKKEL 569
Db 547 KEIDLPEWPKLKWESLIDPNKDL 570
RESULT 7
ABB57866
ID ABB57866 standard; Protein; 554 AA.
XX
AC ABB57866;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 390.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical.
XX Drosophila melanogaster.
OS
XX WO200171042-A2.
PN
XX 27-SEP-2001.
PD
XX 23-MAR-2001; 2001WO-US09231.
PF
XX 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NY.
XX
P1 Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI: 2001-656860/75.
XX
DR N-PSDB; ABL01969.
PT
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
PS Disclosure; SEQ ID NO 390; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX

Seq	Sequence	554 AA;	43.7%;	Score 1330;	DB 22;	Length 554;
Query Match			47.6%;	Pred. No. 1.7e-116;		
Best Local Similarity			95;	Mismatches 184;	Indels 12;	Gaps
Matches 264;						
OY	1 KVTNRSTLNENQIIDTEGQIKGVKRMIVYDSDYSFSEFIPYAKRPVVELRFAKAPQRPV	80				
Db	5 KVOQRKRYRTSEKTVSTTYTGPIKGVKRSIKYSQSFSEFIRIFANRPVVELRFAKAPQRPV	64				
OY	81 FMEGVRCDCGPGANRSVQDFJISGKFTGSEDCILYLVNITNDLPDKRPVPMVFIHGDETE	140				
Db	65 VTEVRSTCSOGPKPLQKHFEVEMEDGSDSDCYLVNVTNKLPTKPMVPMVVIYGGEGEF	124				
OY	141 GEANNWNGPDPFMKRPVLIVYQYRLGVLFSLIKSENLANYPGNAGLKIDQYMALRWVMS	200				
Db	125 GPASKECTSPDILIEDVYVVISINRLQPLGLCLDDPELDVPGNAGLKIDQYVALRWYKA	184				
OY	201 NIAIFGVDNITVGESEAGASTHYMMITEQTRGLFHRIKMSGNSMCSMASTECQSR	260				
Db	185 NCSRFSGDSANITTINGDSAGSASVHYMMITEQTHGIFHKAICMSGNTLSLPMVAVTPOQRMP	244				
OY	261 LTMAKRVQYKSGDNKKDILEFLMKANRPVDLKEEQQVILPREMOKVMPEGPTEPYOT	320				
Db	245 YRLAVQAGIAGENNRDWEFLKNAKGESEILANGSLCIDEEKKEKIGTSFGVLEPIYT	304				
OY	321 ADCVAPKPIRENVKSKAMGNSIPTLLIGNTSYEGILSKSVAKQYPEVVKELSCVNYVPMEL	380				
Db	305 SHCVAPKPIREMKRTPAMSNIPDLIIIGVSNEGILLYSEKTKNPCKLNEIDDCRFVPIEL	364				
OY	381 ADSEMSAETLERALIVKKAHYDGETPTID---NEMELCSYTYFLFPMRIEQLQRLNHTA	437				
Db	365 -NMDEESALCRGYDQLRCQYGGDTPPSLDTHLEYLQWVSHYFWEPPIYRTVLSRLQYAR	423				
OY	438 GTPILYLFDFDSEELINPYRIMRFGRGVGVSHADELYLEFMINLISKRLPKESREYKTI	497				
Db	424 SAPFLYLRFDPEPSKH-FNHLRLISGCKKVRGCHODDLSYLEYNSLARLKNHTREYKCI	482				
OY	498 ERMVGIWTEFATYTGKPYNSNDIAGMENTLV---DPIKSSDYVKKCLNIGDELKVMIDLPEKD	554				
Db	483 ERLVGLMTWFFAACGNP--NFDEPEQEDL-WQVPDPAVEKHKOLCLNISPDELKVIDVBDLK	539				
OY	555 KIKGASIFDKKKEI 569					
Db	540 KLMWSEFP-RDEL 553					
RESULT 8						
ABB57867						
ID	ABB57867	standard; Protein; 572 AA.				
XX	AC	ABB57867;				
XX	DT	26-MAR-2002 (first entry)				
XX	DE	Drosophila melanogaster polypeptide SEQ ID NO 393.				
XX	KW	Drosophila: developmental biology; cell signalling; insecticide;				
XX	OS	pharmaceutical.				
XX	PN	Drosophila melanogaster.				
XX	PD	W0200171042-A2.				
XX	PE	27-SEP-2001.				
XX	PF	23-MAR-2001; 2001WO-US09231.				
XX	PR	23-MAR-2000; 2000US-191637P.				
XX	RA	11-JUL-2000; 2000US-0614150.				
XX	PE	(PEKE) PE CORP NY.				

Query Match	43.1%	Score 1311	DB 22	Length 572
Best Local Similarity	46.1%	Pred. No. 1.1e-14		
Matches 264	Conservative 95	Matches 184	Indels 30	Gaps 8
21 KTYNRLSTNENQIIDTEGQIKGYKRMVYDDSYSPFSIFPAKPPVGLRFAKAPQRY 80	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :			
5 KYQQRRTTSEVTVTGPIKGYKRSIYQSFSFRIFPAKPPVGLRFAKAPQRY 64	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :			
81 PWEVGDDCCGPAKNSVQTDIFSGKPTGSDCLYLVNTDLPDKRPVAFIHGGDTF 140	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :			
65 VTEVRSCTSGGPKPLOKHFFEMEDGSDCLYLVNTKLTPTKPMVWVIYGGGQF 124	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :			
141 GEAANNMGPDVFEMKKPVLYLVQYRLGLV-----GELSKSENLV 182	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :			
125 GGAESRECSPTDLLDEDVVISINIRLGLPGTNDTQKKHIFNISLPGLCLDDBEL 184	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :			
183 PENAGLKQDVALLRWVKSIAIFGDDVDNITYFGESAGASTHYMNTBOTRGLFHRGIM 242	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :			
185 PENAGLKQDVALLRWVKAANSRFGGSANITIFGDSAGASVHYMNTBOTRGLFHRKIC 244	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :			
243 MSGNSMCSASTIECOSRALTMAKRGVKGEDNEKILFELMANPDIKKEPQVITPER 302	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :			
245 MSGNTLSPAAVYDPRMWPYRLAVQGYAENNTROWELFKNAKGSSEITKANGELOCIDE 304	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :			
303 MONKNAFPGFVPEYQOTADCVPRPIREMYVSANGNSIPTLTIGNTSYEGLLSKSVAKQY 362	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :			
305 KKERIGFSGPIEPIFYVISHCVAPKPIEMMTAMSNINPILIGVSNBGLLYSETKTN 364	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :			
363 PEVVAELESQVNVVPEMLADRSAPETIERAALYKKAHVDEPTPLD--NFMELCSYF 419	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :			
365 PCLNELLEDRCRVVPIEL--NMDRESALCREYDQLOCYGQKGTBPLDLHEYLQVSH 423	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :			
420 YLFPMHPRFLQRFNHTACTPIYLRFPEDSEIINPYRIMFGRGVKGVSHADELTLYF 479	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :			
424 YWFPIRYLRVLSLOYARAPYIYLRFPEDSKH--FNHLRLISCGKKVYRGTCHGDDLSYLF 482	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :			
480 WNLISRLPKRESREYKTIERWVGIVTEFAATGKPYSNDIAGMENTLV--DPIKASDVIY 536	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :			
483 YNSLARKLKLNHTRKYCIERLGLVMTHEAACNP--NFPEQEDL--WQVYDPAVAEKHOL 539	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :			
537 KCLNTGDELKAVDLPBMDKIKOGASLFDKREL 569	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :			
540 KCLNISDELKVIDVPLKLIWSEFF--RDEL 571	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :			

XX ABB57857;
 XX 26-MAR-2002 (first entry)
 DT Drosophila melanogaster polypeptide SEQ ID NO 363.
 XX Drosophila melanogaster polypeptide SEQ ID NO 363.
 DE Drosophila melanogaster polypeptide SEQ ID NO 363.
 XX Drosophila melanogaster polypeptide SEQ ID NO 363.
 KM Drosophila melanogaster polypeptide SEQ ID NO 363.
 OS Drosophila melanogaster.
 XX WO200171042-A2.
 XX 27-SEP-2001.
 PD 23-MAR-2001: 2001WO-US09231.
 PF 23-MAR-2000: 2000US-191637P.
 XX 11-JUL-2000: 2000US-0614150.
 PR (PEKE) PE CORP NY.
 PA Venter JC, Adams M, Li PMD, Myers EW;
 PI WPI: 2001-656860/75.
 XX N-PSDB: ABL01960.
 DR New isolated nucleic acid detection reagent for detecting 1000 or more
 XX genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 PS Disclosure: SEQ ID NO 363; 21pp + Sequence Listing; English.
 XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
 CC sequences (AB101840-AB16175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX Sequence 567 AA:
 SQ
 Query Match 42.6%; Score 1298.5; DB 22; Length 567;
 Best Local Similarity 46.8%; Pred. No. 1.7e-113;
 Matches 261; Conservative 91; Mismatches 187; Indels 19; Gaps 7;

DB 314 LTPHCYIPKSPLEMMRDGMSIPWVIGNSPGLMPPEVNMKPELCOJGDENLAPQ 373
 QY 379 ELADSERAPETLERAAVKA---HVDGEP---TLDNFMELCSYFELFPMRFLQLR 432
 DB 374 DAHDEQ-----QRKAFKKVRELFPGRPTILEYSDLSYKFEWGHRTLSR 427
 QY 433 FNTACTPIYLVRFPDSEELINPYRIMFGRGVSHADELYLEFNMILSKRLPRESR 492
 DB 428 AHHAPLAPFLIRFPDSSKH-FNIMRLITCGKRVGCTCHADLSLYFNAAKRLKRTA 486
 QY 493 EYKTIEMVGIWTEFATGKP---YSNDIAGMENIWDPIKSDVYKCLINDELAKYM 548
 DB 487 EFKTIKRLVSMVHFALISDPNIPMWCODEKOPRGAWLPIKDDKVRQCLINSHDHYI 546
 QY 549 DLEPMKIKOGASIFDKK 566
 DB 547 DLPEAEKRLIMDCTYDRE 564

RESULT 10
 ID ABB59161 standard; Protein; 554 AA.
 XX ABB59161;
 AC 26-MAR-2002 (first entry)
 DT Drosophila melanogaster polypeptide SEQ ID NO 4275.
 XX Drosophila melanogaster polypeptide SEQ ID NO 4275.
 DE Drosophila melanogaster polypeptide SEQ ID NO 4275.
 KM Drosophila melanogaster polypeptide SEQ ID NO 4275.
 OS Drosophila melanogaster.
 XX WO200171042-A2.
 XX 27-SEP-2001.
 PD 23-MAR-2001: 2001WO-US09231.
 PF 23-MAR-2000: 2000US-191637P.
 XX 11-JUL-2000: 2000US-0614150.
 PR (PEKE) PE CORP NY.
 PA Venter JC, Adams M, Li PMD, Myers EW;
 PI WPI: 2001-656860/75.
 XX N-PSDB: ABL03264.
 DR New isolated nucleic acid detection reagent for detecting 1000 or more
 XX genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 PS Disclosure: SEQ ID NO 4275; 21pp + Sequence Listing; English.
 XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
 CC sequences (AB101840-AB16175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX Sequence 554 AA:
 SQ
 Query Match 42.0%; Score 1277.5; DB 22; Length 554;
 Best Local Similarity 46.2%; Pred. No. 1.5e-111;

Matches	250;	Conservative	106;	Mismatches	170;	Indels	15;	Gaps	9;
---------	------	--------------	------	------------	------	--------	-----	------	----

OY	20	NKTYNVLSTNEQIIDITEVGOIKGVRKMTYVD-DSYISFESIPAKPVGELRFKAQR	78
Db	8	HKKOQVYLSTGHIVYLDITKGQVRGLQRTKYDKEEFAFEIGIPYAKPPYVDLFRFAQP	67
OY	79	PVEEGVRCDCGPANNSVOPTDFISGKPTSGEDCLVNTNDLNDRKRPVVFTHGDF	138
Db	68	PEWOGVLNCTTKRSKPMORNMILGIVEGSEDLHLNVYALKSEKPLPIVIMLYGGGF	127
OY	139	IPEANRNMFGPYFPFKRPVLYTVQYRLGVLGFLTSSENLTNPGNAGLDQVALRW	198
Db	128	QKEASNDIISPDIYFMKKPVYVAINTYLAALGFLSLDKDPKLDVPGNAGLDQVALRW	187
OY	199	KSNIAIFGGDVNDITVESGASGASTHYMMITEOTRGLEFHRIIMSGSMCSMASTECOS	256
Db	188	SOMIAHFNDPNNTILMGESASASYHVMATTEQTRGLEFHRAIMOGCALSEWESEDNN	247
OY	259	RALTMAKRYGKGEDENKEKILEFLKANPDYDLKEEPQVLTPEKQNKMPFFGTVEPY	318
Db	248	MARLAKNLGYKDEKDADLVFLSKVCAROTAIDQVINLMDEVSRFLFAFGVLEPY	307
OY	319	QTADCVPRPIREMYKSANGSIPTLLGNTSYEGLSLSKSAKOYPEVKLESCVNYPW	378
Db	308	EFDHCVPRRHRKDLLSEAMGNDIPVIYVGSNGEFLSYQLRKDPMLKNH---NILPR	364
OY	379	ETLAD--SERAPETLERAAIVKKAHVDGE--TPTLNF--MELCSFYTLFFMHRLQLREN	434
Db	365	EYREHSLSLEGOLLVR--LKQLYINNMQSMEFEALNTFSHQIWDHTHPILAROS	422
OY	435	HTAGPIPIYLRPFDESEETINPYRIRMRGRGVKGVSHADELYLFWMNLSKRLPKESREY	494
Db	423	VAPKPPTLYLRPDFDSPPH-FNQFRLYCGDRIRGVAHADELSYLFYNITASIKDKSSMEY	481
OY	495	KTIEMVGIWTFEATGTGPKPSYNDIAGMENLFWDPK-KSDQVYKCLNISGELYMDLPEM	553
Db	482	KTIEMVGMWITSFASGPNCEPELSAK--WEAVQLKENAVECFENISHLEMDIPES	538
OY	554	D 554	
Db	539	D 539	
RESULT	11		
ID	ABB61983		
ID	ABB61983 standard; Protein; 566 AA.		
XX	AC	ABB61983;	
XX	DT	26-MAR-2002 (first entry)	
XX	DE	Drosophila melanogaster polypeptide seq ID NO 12741.	
XX	KW	Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.	
XX	OS	Drosophila melanogaster.	
XX	PN	MO200171042-A2.	
XX	PD	27-SEP-2001.	
XX	PF	23-MAR-2001; 2001MO-US09231.	
XX	PR	23-MAR-2000; 2000US-191637P.	
XX	PR	11-JUL-2000; 2000US-0614150.	
PA	(PEKE) PE CORP NY.		
PI	Venter JC, Adams M, Li PWD, Myers EW;		
XX	WPI; 2001-656860/75.		
XX	N-PDB; ABL06086.		
NR			

XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from *Drosophila* and for elucidating cell signalling and cell-cell
XX interactions -
PT
PS Disclosure; SEQ ID NO 12741; 21bp + Sequence listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from *Drosophila*. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB101840-AB161575), expressed DNA
CC sequences (AB101840-AB161575) and the encoded proteins
CC (BAB57737-ABR20272).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at http://wipo.int/pub/published_pct_sequences.
XX
XX Sequence 566 AA;
XQ

Query Match	41.6%;	Score 1267.5;	DB 22;	Length 566;
Best Local Similarity	47.0%;	Pred. No. 1.4e-110;		
Matches 259;	Conservative 92;	Mismatches 187;	Indels 13;	Gaps 8.

QY	7	FIRLRLCYKCMVKNYUJRLSTJNETJOTIDPEGOLKGVKMYRUV--DSYVFESEIPAK	65
Dd	7	FSDKRLGAKIIGHKHVVYQKXJGTQGTQETELATKTKYQOLKGGORRLXIDGEPYISFSEBIPRAQ	66
QY	66	PRVGEIRFAAPRPRVMEGVNDCCGPRANRSVQDFTISGRPTSGEDCLVLYNTYDNLNDK	122
Dd	67	PRVGEIRFAAPRPSMVGVDCTYAREKPMORSNITMAEGSEDCDLYLVYAKRLSEBPK	126
QY	126	RRVWVFINGDGTIFGEANRMWFGPDYFEMKKPVYLTVOYRGVYGFSLKSEMLNPNGN	185
Dd	127	PLPVWVWINGGGFGYCGASRRELYGPDYFEMKHDLITVITKRVGYLGFSLKDEKLEKTPGN	186
QY	186	AGKROOVALMKRVYSNLAIEGGVDNITTVYGSBAGASATHYMMITEDQRTGLFPHRGIMMSG	245
Dd	187	AGKRODLOALRMVKNENIASFNGDEISTYVGEBSAGASATHIMQTEOARGLFHNAIYOSG	246
QY	246	NSMCSMASTECOSRALTMIAKAVYKGE--DNERKILEFLMKANPYULKEEPQVLTPEPMO	304
Dd	247	SALCMATQOPRRKMPORLREKELGYAGNLESEKELLEFPQIPASKLADYCMSYTTQEBOR	306
QY	305	NKVMPEPGTEYEPQIADCVVYKPIRBMKYSAMGNSIPLLIGNTSYEBGLSKSVAKOYPE	364
Dd	307	DEYILAFVPIEYVGDVCYIPKSOQEOJSSAAGNSIPWITIGTSFEBGLFYSRTTLDDP--	365
QY	365	VKELDESCVNVPEMLDSDRSAPETLEERAIYKKAHVNG--EPTPLDNMELCSYFYF	421
Dd	366	-LYMSAEALITPROVDA--IDKEELAEWVRRLKSSYEDDDPRASMELEYECHELITLSIKNF	423
QY	422	LEPMHREIQLRHNITAGTPIYLIRPFDSDEELINPRIMRFRGVKGYSHADELTYYLFWN	481
Dd	424	WHDHTRILALALATNLPYLIRFMDSPH--FMYRILIKGGKKVGRGCHADISTYWFYG	482
QY	482	ILSKRLPESREXYTIERMGIWTEPATGKPYSDNDIGMENTLWTPPKKSDVOYKCLNT	541
Dd	483	ILSSLDKNSEYRTIERLVGMWTSFATIGDNCELTAPVK---WDLPRFG--GVENCLNT	538
QY	542	GDELKVDNDEP	552
Dd	539	ADGLEFIPLDEP	549

RESULT12
ABB57746
ID ABB57746 standard; Protein; 565 AA.
XX
AC ABB57746;
XX
DT 26-MAR-2002 (first entry)

XX Drosophila melanogaster polypeptide SEQ ID NO 30.
 DE
 XX Drosophila: developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 KW
 XX Drosophila melanogaster.
 OS
 XX WO200171042-A2.
 PN
 XX 27-SEP-2001.
 PD
 XX 23-MAR-2001; 2001WO-US09231.
 PF
 XX 23-MAR-2000; 2000US-191637P.
 PR
 XX 11-JUL-2000; 2000US-0614150.
 PA
 XX (PEKE) PE CORP NY.
 PI
 XX Venter JC, Adams M, Li PWD, Myers EW;
 PI
 XX WPI; 2001-656860/75.
 DR
 XX N-PSDB; ABL01849.
 PT
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 PS
 XX Disclosure; SEQ ID NO 30; 21pp + Sequence Listing; English.
 PS
 XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
 CC sequences (AB101840-AB16175) and the encoded proteins
 CC (AB57737-AB572072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX
 XX Sequence 565 AA;
 SQ
 Query Match 40.6%; Score 1236.5; DB 22; Length 565;
 Best Local Similarity 44.3%; Pred. No. 1.2e-107;
 Matches 253; Conservative 103; Mismatches 188; Indels 27; Gaps 10;

DB 365 EHMSAFEVLPRRI--REKSTQSHLK--DLLRQFVDNEDDATRGMEFNECLHLSVK 420
 QY 420 YFLPMPHRLQLRNNHAGPIYLYRDPDSEELINRYIMRGRGVKSHADELTLYF 479
 DB 421 FHWGHIHRYTLARLSHAPAPPYLYRDPDSPH-FNHFROVCGKHVGVSHADLSTYLF 479
 QY 480 WNLTKRLPKESREYKTIERNVGIWTFEATGKPYSDIAGMNLWDPYIKSDDYKCL 539
 DB 480 YHILANKVDKSSMETQITQRLVGMVAFARNDNPCQIG---PTTWALDEKGP-QMCL 535
 QY 540 NIGDELKVMDLPEMDKIKOGASIFDKRKELF 570
 DB 536 NIGKLEFIYLPESKONRIMDRLYD-KNDLF 565
 RESULT 13
 ABB57868
 ID ABB57868 standard; Protein; 530 AA.
 XX
 XX ABB57868;
 AC
 XX 26-MAR-2002 (first entry)
 DT
 XX Drosophila melanogaster polypeptide SEQ ID NO 396.
 DE
 XX Drosophila: developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 KW
 XX Drosophila melanogaster.
 OS
 XX WO200171042-A2.
 PN
 XX 27-SEP-2001.
 PD
 XX 23-MAR-2001; 2001WO-US09231.
 PF
 XX 23-MAR-2000; 2000US-191637P.
 PR
 XX 11-JUL-2000; 2000US-0614150.
 PA
 XX (PEKE) PE CORP NY.
 PI
 XX Venter JC, Adams M, Li PWD, Myers EW;
 PI
 XX WPI; 2001-656860/75.
 DR
 XX N-PSDB; ABL01971.
 PT
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 PS
 XX Disclosure; SEQ ID NO 396; 21pp + Sequence Listing; English.
 PS
 XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
 CC sequences (AB101840-AB16175) and the encoded proteins
 CC (AB57737-AB572072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX
 XX Sequence 530 AA;
 SQ
 Query Match 40.0%; Score 1217; DB 22; Length 530;
 Best Local Similarity 46.3%; Pred. No. 7.5e-106;
 Matches 242; Conservative 98; Mismatches 169; Indels 14; Gaps 8;

Db 5 GPARGVKRNITMGSGVSPFEKIPFAKPPVLDLRFKAPVDELEPMDQELDTSPADKPLQGN 64
 QY 100 FISKPTGSDCLYLYNYNDLNDKRRPVVFIHGDDIFFGANRNWPCDPYFMKKPV 159
 Db 65 MFRKRYAGSDCLYLYNYNDLNDKRRPVVFIHGDDIFFGANRNWPCDPYFMKKPV 124
 QY 160 LTVVQRLVGLSLKSENLVPGNAGLKDQVMAALRWKSNIAIFGCDNITVFGESA 219
 Db 125 IIVVAVRLGALGSLDDPOLNVPNGNAGLKDQVMAALRWKSNIAIFGCDNITVFGESA 184
 QY 220 GGAETHMTTEQTRGIFHFGIMSGNSKMSASTECOSALTMARVKGEDNCKDL 279
 Db 185 GGAETHMTTEQTRGIFHFGIMSGNSKMSASTECOSALTMARVKGEDNCKDL 244
 QY 280 EFLMKANPYDLKEEPOVLTPERMOKNMFPEGPVEPYQADCVKPKIREVKSAMGN 339
 Db 245 EFLRMSGGEIVKATATVLSNDEKHRIILFAFGPVVEPTTEHTVYAKQPHLMQNSWH 304
 QY 340 SIPTLGNISYEGLLSKSAKQVPEVVKELSCVNTVPELADSESADETLERAT-VK 398
 Db 305 RITPMFGGTSFEGLLPEVSRPRLDEVGCKNLPSDL--GLNLDKRLRENYGLQLK 362
 QY 399 KAHVDETP---TLDFMELCSYFFFLPMPHRLQLRFNHTAGRPILYRFDPDSEII 454
 Db 363 KAYF-GDEPCONQNMKFLFELCSYRFEMPIRYAALNRVQSS-APTYLRFDDHS-KLC 419
 QY 455 NPYRIRFGRGVKGVSHADELYLEWNLISKRLPKESREYKTERVWGIWTEFATGKPY 514
 Db 420 NAIKYLCHOMGVCHGDLCTIFHSMLSHOSAPSPBKHVITGVWVTSFAHGDPN 479
 QY 515 SNDIAGENLWDPITKSDVYKCLINIGDELVMGLPEMDKIK 557
 Db 480 CEST---KSLKRAPIENVTN-FKCLNTIGDFEVMALPELQKTE 518

RESULT 14
 ABB57790
 ID ABB57790 standard; Protein; 542 AA.
 AC ABB57790;
 DT 26-MAR-2002 (first entry)
 DE Drosophila melanogaster polypeptide SEQ ID NO 162.
 KW Drosophila: developmental biology; cell signalling; insecticide; pharmaceutical.
 OS Drosophila melanogaster.
 PN WO2001/1042-A2.
 PD 27-SEP-2001.
 PF 23-MAR-2001; 2001WO-US09231.
 PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 PA (PEKE) PE CORP NY.
 PI Venter JC, Adams M, Li PMD, Myers EW;
 DR WPI: 2001-656860/75.
 DR N-PSDB: ABL01893.
 XX
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 PS Disclosure: SEQ ID NO 162; 21pp + Sequence Listing; English.
 XX The invention relates to an isolated nucleic acid detection reagent
 CC

CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB116176-AB130511), expressed DNA
 CC sequences (AB101840-AB116175) and the encoded proteins
 CC (AB57737-AB572072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.
 CC
 SO Sequence 542 AA;
 Query: Match 39.5%; Score 1204; DB 22; Length 542;
 Best Local Similarity 47.5%; Pred. No. 1.3e-104;
 Matches 257; Conservative 79; Mismatches 179; Indels 26; Gaps 11;
 QY 28 STNETQIIDTEYGOIKGVKRMVYDSDSYSPESIPYAKPPVGELEFRKAPQRPVMEGVAD 87
 Db 5 SSIETCELLPVGOIKGVKRLSLYDDPYFSEKIPFAKPLGELRFRAPVADPWSGVLD 64
 QY 88 CCGPANKRVQDFISGKPTGSDCLYLYNYNDLNDKRRPVVFIHGDDIFFGANRNW 147
 Db 65 CTHAEKPTQGLLTRELEGEDCLYLYNSKOLSKSEKPLPVVVIYIGAFVGEATREL 124
 QY 148 FGPDYFMKKPVVLYTVQVRLGLFLSLKSENLVPGNAGLKDQVMAALRWKSNIAIFG 207
 Db 125 XGPYFPMKDVVLYTVLNRVDCGLFSLKDPSLKVPONAGLKDQVLAALWVQYISFNG 184
 QY 208 DVNITVFGESAGASTHYMMITEQTRGILFHRGIMSGNSKMSASTECOSALTMARV 267
 Db 185 DDSNITVFGESAGGCGSTHFMWCTEQTRGILFHKALPMGCTVHANNPAPDFAFLAQN 244
 QY 268 GYKGEDNEKDLFELMKANPYDLKEEPOVLTPERMOKNMFPEGPVEPYQADCVK 327
 Db 245 GFTGENDAKVLEYLQGVPAADLVNH--NLTPHRRNGLLFAFGPVVEAYVGEDCVPR 302
 QY 328 PIREVKSAMGNSIPTLIGNTSYEGLLSKSAKQVPEV---VALESC---VNYVPWET 380
 Db 303 PVEVMDAWMSNNPVMVLAGTSFEGLE-----MYPAVSANLALDLSODPTRLVPDV 356
 QY 381 ADSEKSAPELTERAALYKKAHVGEPT---LNFMEELCSYFFFLPMPHRLQLRFNHTA 437
 Db 357 R-TVSSSEKENLEYEQRLMAKAFGYSPPSELLNMDFYSKLFMGGFNTFNARLTLY-A 414
 QY 438 GTPYLYRFPDSEELINPRIMRFGGVK-GVSHADELYLEWNLISKRLPKESREYK 496
 Db 415 KAPTYRRFPDSDPN-FNFRAKFCGDKIKTGAHADDLSYLFNAGSMKLDKTSAEVKT 473
 QY 497 IERNVGIWTEFATGKPYSDIAGMENLWDPITKSDVYKCLINIGDELVMGLPEMDKI 556
 Db 474 IERNVGIWTEFATGKPYSDIAGMENLWDPITKSDVYKCLINIGDELVMGLPEMDKI 529
 QY 557 K 557
 Db 530 Q 530

RESULT 15
 AAM47598
 ID AAM47598 standard; Protein; 602 AA.
 AC AAM47598;
 DT 12-FEB-2002 (first entry)
 DE Drosophila cell cycle progression protein #27.
 KW Antiproliferative; cytosolic; cardiac; immunosuppressive; meiosis;
 KW antiinflammatory; antiparasitic; dermatological; antifungal; mitosis;
 KW antiparasitic; antimalarial; antirheumatic; antidiabetic; cell division;
 KW cell cycle progression protein; tumour; proliferative disorder;
 KW cardiovascular; autoimmune; dermatological disorder.
 CC

XX Drosophila sp.
 OS
 XX
 PN W020017274-A2.
 XX
 PD 04-OCT-2001.
 XX
 PF 23-MAR-2001; 2001WO-GB01297.
 XX
 PR 24-MAR-2000; 2000GB-0007268.
 XX
 PA (CYCL-) CYCLACEL LTD.
 XX
 PI Deak P, Glover DM, Midgley C;
 XX
 DR WPI: 2002-055132/07.
 XX
 PT Polynucleotides encoding cell cycle progression proteins, useful for
 XX treating a tumor or a proliferative disorder -
 XX
 PS Claim 8; Page 164; 213pp; English.
 XX
 CC The present invention relates to Drosophila cell cycle progression
 CC proteins (AAM47572-AAM47608) and their coding sequences
 CC (ABA90366-ABA90520). The coding sequences and proteins are useful for
 CC identifying a substance capable of affecting the function of the
 CC corresponding gene, a substance capable of inhibiting the cell division
 CC cycle, or capable of inhibiting mitosis and/or meiosis. They can also be
 CC used in a method for treating a tumor or proliferative disorder,
 CC cardiovascular disorders (such as restenosis and cardiomyopathy),
 CC autoimmune disorders such as (glomerulonephritis and rheumatoid
 CC arthritis), dermatological disorders (such as psoriasis),
 CC antiinflammatory, antifungal and antiparasitic disorders (such as
 CC malaria).
 CC
 SQ Sequence 602 AA:
 Query Match 39 2%; Score 1194.5; DB 23; Length 602;
 Best Local Similarity 45.4%; Pred. No. 1.2e-103;
 Matches 246; Conservative 98; Mismatches 175; Indels 23; Gaps 10;
 QY 21 KYNVRLSTNENQIIDTEYGQIKGVKMTVYDSDYSPESIPYAKPPVGLRFAQRPV 80
 DB 67 KYEQRSLTAIYVITKSGPVAGVKNMTIMGSGYFSEKIPFAKPPVGLRFAQRPV 126
 QY 81 PHEGVDCGCPANKSVQTDPIFGSGEDCLYNTNDLNPKRRPVMVFIHGDFIF 140
 DB 127 PMQDELCTSPADKPLQTHMFFRKVAGSEDCILNVYKDLQDKLRPVAMWLYGGGYOY 186
 QY 141 GEANRMWFGPDYFMKPPVVLVTVQYRGLVGEFLSKSENLNPGNAGLKDQVVALRMVKS 200
 DB 187 GEASR-----VAVTVAYRIGALGFLSLDDPOLNVPNGNLKQOIMALRMVOO 237
 QY 201 NIAIFGGDVNITVEGESAGCSTHYMTTEQTRGLFHRGIMSGNSMCWMASTECOSRA 260
 DB 238 NIEAFGGDSNNITLFGESAGASTHFLALSPQTEGLIKHAIWMSGVLCPTQPPRNMA 297
 QY 261 LTMARRGYGENENKILFEIKKANPYDLIKEPVLTEPERMOKVMFPFGPTVEPYOT 320
 DB 298 YRLAQKLGTYGDNKKAIFELNSMGCEYKATAYLSNDEKHHRIELFAFGPVVEPYTT 357
 QY 321 ADCVVPKIREMWSKANSIPLTIGNTSYEGLLSKSVAKOYBEVYKELESCVNVYPMEL 380
 DB 358 EHTVYAKOPHELMQNSHRIIPMMFGTSEGLLFYEVSRBPATLDEVGNCKNLIPSDL 417
 QY 381 ADSERSAPETLERAAI-VKKAHVDETP-----TIDNFMELCSYFELFPMHFLQLEFNH 435
 DB 418 --GLNLPKLENGYGLQKAYF-GDEPCNANMKFLELCSTREHNPITYRAALNVRQ 474
 QY 436 TAGTPYLYRDFDSEETINPYRIMRFRGVKGVSHADELYTLFWNTLSKRLPKESREYK 495
 DB 475 SS-APTYLYRDFDHS-KLCNARIYVLCGHQMRGVCHGDLDLCYIFHSMLSHOSAPDSPEHK 532

QY 496 TIERMGTIERFATGKPYSDIAGMENLTWDPKSDPDVYKCLNIGDELKVMYDLPEMDK 555
 DB 533 VITGAVDWNTSFAAHQDPNCEST---KSLKFAPIENVTN-FKCLNIGDQFVYMALPELOK 588
 QY 556 IK 557
 DB 589 IE 590
 Search completed: April 4, 2003, 09:13:01
 Job time : 45.0154 secs

1
 2
 3
 4
 5
 6
 7
 8
 9
 10
 11
 12
 13
 14
 15
 16
 17
 18
 19
 20
 21
 22
 23
 24
 25
 26
 27
 28
 29
 30
 31
 32
 33
 34
 35
 36
 37
 38
 39
 40
 41
 42
 43
 44
 45
 46
 47
 48
 49
 50
 51
 52
 53
 54
 55
 56
 57
 58
 59
 60
 61
 62
 63
 64
 65
 66
 67
 68
 69
 70
 71
 72
 73
 74
 75
 76
 77
 78
 79
 80
 81
 82
 83
 84
 85
 86
 87
 88
 89
 90
 91
 92
 93
 94
 95
 96
 97
 98
 99
 100
 101
 102
 103
 104
 105
 106
 107
 108
 109
 110
 111
 112
 113
 114
 115
 116
 117
 118
 119
 120
 121
 122
 123
 124
 125
 126
 127
 128
 129
 130
 131
 132
 133
 134
 135
 136
 137
 138
 139
 140
 141
 142
 143
 144
 145
 146
 147
 148
 149
 150
 151
 152
 153
 154
 155
 156
 157
 158
 159
 160
 161
 162
 163
 164
 165
 166
 167
 168
 169
 170
 171
 172
 173
 174
 175
 176
 177
 178
 179
 180
 181
 182
 183
 184
 185
 186
 187
 188
 189
 190
 191
 192
 193
 194
 195
 196
 197
 198
 199
 200
 201
 202
 203
 204
 205
 206
 207
 208
 209
 210
 211
 212
 213
 214
 215
 216
 217
 218
 219
 220
 221
 222
 223
 224
 225
 226
 227
 228
 229
 230
 231
 232
 233
 234
 235
 236
 237
 238
 239
 240
 241
 242
 243
 244
 245
 246
 247
 248
 249
 250
 251
 252
 253
 254
 255
 256
 257
 258
 259
 260
 261
 262
 263
 264
 265
 266
 267
 268
 269
 270
 271
 272
 273
 274
 275
 276
 277
 278
 279
 280
 281
 282
 283
 284
 285
 286
 287
 288
 289
 290
 291
 292
 293
 294
 295
 296
 297
 298
 299
 300
 301
 302
 303
 304
 305
 306
 307
 308
 309
 310
 311
 312
 313
 314
 315
 316
 317
 318
 319
 320
 321
 322
 323
 324
 325
 326
 327
 328
 329
 330
 331
 332
 333
 334
 335
 336
 337
 338
 339
 340
 341
 342
 343
 344
 345
 346
 347
 348
 349
 350
 351
 352
 353
 354
 355
 356
 357
 358
 359
 360
 361
 362
 363
 364
 365
 366
 367
 368
 369
 370
 371
 372
 373
 374
 375
 376
 377
 378
 379
 380
 381
 382
 383
 384
 385
 386
 387
 388
 389
 390
 391
 392
 393
 394
 395
 396
 397
 398
 399
 400
 401
 402
 403
 404
 405
 406
 407
 408
 409
 410
 411
 412
 413
 414
 415
 416
 417
 418
 419
 420
 421
 422
 423
 424
 425
 426
 427
 428
 429
 430
 431
 432
 433
 434
 435
 436
 437
 438
 439
 440
 441
 442
 443
 444
 445
 446
 447
 448
 449
 450
 451
 452
 453
 454
 455
 456
 457
 458
 459
 460
 461
 462
 463
 464
 465
 466
 467
 468
 469
 470
 471
 472
 473
 474
 475
 476
 477
 478
 479
 480
 481
 482
 483
 484
 485
 486
 487
 488
 489
 490
 491
 492
 493
 494
 495
 496
 497
 498
 499
 500
 501
 502
 503
 504
 505
 506
 507
 508
 509
 510
 511
 512
 513
 514
 515
 516
 517
 518
 519
 520
 521
 522
 523
 524
 525

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2003, 09:10:33 ; Search time 19.0734 seconds
(without alignments)
2872.940 Million cell updates/sec

Title: US-09-776-910-13

Perfect score: 3045
Sequence: 1 MTFIKQPIFKLKVCVMVN.....PEMDKIKOGASTFDKKELF 570

Scoring table: BLOSUM62
Gapop 10.0, Gapept 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: PIR 73:***
1: p1r1:***
2: p1r2:***
3: p1r3:***
4: p1r4:***

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	959.5	31.5	540	2 S53370	carboxylesterase (
2	954.5	31.3	540	2 A35986	esterase B1 - sout
3	945.5	31.1	540	2 S53371	carboxylesterase (
4	861.5	28.3	503	2 S53372	carboxylesterase (
5	607	19.9	578	2 F89068	protein T28C12.4b
6	607	19.9	658	2 T32053	hypothetical prote
7	602.5	19.8	489	2 A43325	juvenile-hormone e
8	575	18.9	489	2 B68680	para-nitrobenzyl e
9	553.5	18.2	547	2 S36787	carboxylesterase (
10	545	17.9	547	2 S55233	juvenile hormone e-
11	544	17.9	583	2 T25690	hypothetical prote
12	544	17.9	552	2 S36786	carboxylesterase (
13	542	17.8	548	2 S47655	carboxylesterase (
14	529	17.4	561	2 T32907	hypothetical prote
15	523	17.2	597	2 A33668	sterol esterase (e
16	518	16.9	602	1 ACH014	cholinesterase (EC
17	515.5	16.9	614	2 JH0314	acetylcholinestera
18	512.5	16.8	581	2 C39768	cholinesterase (EC
19	512	16.8	562	2 S27782	acetylcholinestera
20	511	16.8	596	1 ACRYE	acetylcholinestera
21	508.5	16.7	603	2 S70849	cholinesterase (EC
22	507.5	16.7	545	2 S58980	carboxylesterase (
23	505.5	16.6	545	2 S58979	carboxylesterase (
24	505.5	16.6	545	2 S58972	carboxylesterase (
25	505.5	16.6	545	2 S58982	carboxylesterase (
26	505.5	16.6	545	2 S58983	carboxylesterase (
27	505.5	16.6	545	2 S58977	carboxylesterase (
28	504.5	16.6	545	2 S58973	carboxylesterase (
29	504.5	16.6	614	2 JH0811	acetylcholinestera

30	503.5	16.5	545	2 S58975	carboxylesterase (
31	501.5	16.5	545	2 S58970	carboxylesterase (
32	500.5	16.4	511	2 D70944	probable lipi prot
33	500.5	16.4	545	2 S58976	carboxylesterase (
34	500	16.4	559	1 JC5408	carboxylesterase (
35	500	16.4	561	2 S71597	carboxylesterase (
36	499.5	16.4	545	2 S58981	carboxylesterase (
37	499.5	16.4	557	2 A47162	thiolesterase B (e
38	499	16.4	562	2 S27800	elastase precursor
39	498.5	16.4	539	2 T32052	hypothetical prote
40	498.5	16.4	545	2 S58978	carboxylesterase (
41	498.5	16.4	545	2 S10367	carboxylesterase (
42	497.5	16.3	545	2 S58974	carboxylesterase (
43	497.5	16.3	545	2 S58971	carboxylesterase (
44	496.5	16.3	545	2 S58969	carboxylesterase (
45	495.5	16.3	545	2 S58968	carboxylesterase (

ALIGNMENTS

RESULT 1

S53370
carboxylesterase (EC 3.1.1.1) B2 - southern house mosquito
C:Species: Culex pipiens quinquefasciatus (southern house mosquito)
C:Date: 15-Jul-1995 #sequence: 08-Sep-1995 #text: change 21-Jul-2000
C:Accession: S53370; S44211
R:Vaughan, A.; Rodriguez, M.; Hemingway, J.
Biochem. J. 305, 651-658, 1995
A:Title: The independent gene amplification of electrophoretically indistinguishable
A:Reference number: S53370; MUID:95134253; PMID:7530448
A:Accession: S53370
A:Molecule type: mRNA
A:Residues: 1-540 <NA>
A:Cross-references: EMBL:Z3694; NID:9475067; PIDD:CAAB3643.1; PID:9475068
A:Experimental source: strain PeIR
C:Superfamily: Cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase

Query Match 31.5%; Score 959.5; DB 2; Length 540;
Best Local Similarity 37.3%; Pred. No. 1.3e-65;
Matches 205; Conservative 111; Mismatches 211; Indels 23; Gaps 10;

QY	31	ETQIIDTEYQIKVGRMTVYDSDSYSESTIYAKPPYGGELRFKAPQRPVMEGRDC--	88
DB	4	ESLTVQTKYKVPGRKRSVSLGQEVYFQGIYARAPBGLRFKAPVPPQWTFELDCSQ	63
QY	89	-CGPA---NSVQTFDISCKPTGSEDCILINYYTNDLNDKRRPYVFIHGDFIFGEAN	144
DB	64	QCEPCYHRRLO-----KIYGCEDSLKINVPKAKINSKPLPYMLYIYGGEFTGSG	117
QY	145	RNMFGPDYFMKPYVLTVOYRGLVGLFSLKSENLNVGNGMGLDOYVALRWYKSNIAI	204
DB	118	TELYGPDPLVQKDIYLVFNRIAGLGLCCSEQGVGNGKADONAIWVLENTAA	177
QY	205	FGVDYNTITVGEASGAGSTHYMTIETQRLGFRHGMNSGNSWASWTEQSRALIMA	264
DB	178	FGGDKRRTVLGHSAGAAVYHILSDASNDLRFALVMSGSYNSWSTLRRNVEKIA	237
QY	265	KRVGYKGEDNEKDLLEFLKAPNPDYLIKEPOVLTPEBMONKVMFPGFTVEPYQADCV	324
DB	238	KALGMGQGESGALRFLKAKPBDIVANOKELTLDQDDIFTPRGPFVEVYEQCM	297
QY	325	VKRPTEEMVKSAMGNSIPTLIGTSEGLILSKSAKQYEVVKELESCVNYVWELADSE	384
DB	298	IKPEPEMKATMGKIDIMIGTSEGLILKIKLOPBLISHPILFLNVPNNL---K	354
QY	385	RSAPETLERAIVKKAHDGERTPTLDN---FMELCSYVYFLFPMHRLQIRFHTATPI	441
DB	355	ISMEKRIEFAKIKORYPPDSSPMENNIQYHMSDVFVHGHRTLIARAASRAR-T	413
QY	442	YLVRFDDSEILNPRIMRFGVGVSHADELYLFWNILSKRLPRESEVYTIIRAV	501

Db 414 FVYRICLOS-EFYNHYRIMIDPKLRGTAHADELSTYLFNSFQVPEKTEFEYRIGLQTLV 472
 QY 502 GIWTEFATGKPYSDIAGMENLWDPKRSKSDVYKCLNI-GDELKVMDLPEMDKIKOGA 560
 Db 473 DVFATFVINGDP-NCGMTAKSGVFEFPAQTKPTFKCLNTANDGVAFVDYDPADRLDMMD 531
 QY 561 SIFDKKLEF 570
 Db 532 AMY-VNDEL 540

RESULT 2

A35986
 esterace B1 - southern house mosquito
 C:Species: Culex pipiens quinquefasciatus (southern house mosquito)
 C:Date: 16-Nov-1990 #sequence_revision 13-Jan-1993 #text_change 21-Jul-2000
 R:Accession: A35986
 Proc. Natl. Acad. Sci. U.S.A. 87, 2574-2578, 1990
 A:Title: Characterization of amplification core and esterace B1 gene responsible for ins
 A:Reference number: A35986; MUID:90207238; PMID:2320576
 A:Accession: A35986
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-540 <MOU>
 A:Cross references: GB:M32328; NID:9156687; PIDN:AAA28289.1; PID:9156688
 A>Note: the authors translated the codon CGT for residue 213 as Ala, and CGT for residue
 C:Superfamily: cholinesterase; cholinesterase homology

Query Match 31.38; Score 954.5; DB 2; Length 540;
 Best Local Similarity 36.98; Pred. No. 3.1e-65;
 Matches 203; Conservative 113; Mismatches 211; Indels 23; Gaps 10;

QY 31 ETQIDITEYQIKGKRMVYDSDYSEFISIPYAKPVEELRPAQRFPVMEGVDC-- 88
 Db 4 ESLVOTKRYGVGRKRNVSLLGOEYVSPGIPYARABGELRFAKVPPOKMTETLDCQ 63
 QY 89 -CGPA---NRSVQDPFISGKPTGSEDCILVNTYNDLNDPKRRPWFVHGGDFJFGEAN 144
 Db 64 OCEPCYHFRRLQ-----KIVGCEDSLKINFAKEINSPPLVMLYIGGFTGSG 117
 QY 145 RNMFGPDYFMKRPVVLVYVYRIGVGLSKSENLNVPNAGLKQVMAIRWYKSNIAI 204
 Db 118 TELYGDPLVOKDVLVSFNYRIGALGFLCCQSDQDGVPGNGLKQDOLARVLENTIA 177
 QY 205 FCGDVNDITVFESAGASTHYMTTEOTRGLHRGIMSGNSMCSWASTECQSRALTM 264
 Db 178 FGDDPKRYTLVAGHSGAASVQYHLISDASKDLFORIYVSGSYSSMLRQNRWVEKLA 237
 QY 265 KRVGYGEDNEKDLLEFLKAPYDLKEEPOVLTPEMQNKVFPFGPTVEPYQTADCV 324
 Db 238 KAIGMDGGGSGALRFLRAKPEDIVAHQKLLTDQMDODITFPFGPTVEPYLTQCI 297
 QY 325 VKPRIREWKSAMGNSIPTLLIGNTSYEGLSKSVAKQYEVVKELESCVNVPELADSE 384
 Db 298 IKRPFEMARTAMGDKIDIMIGTSEGLLQKIKLPELLSHPLFLGNVPPNL--K 354
 QY 385 RSAPETLERAAIVKKAHVDETPILDN--FMELCSYFVFLPMHRLQLRNTACTPI 441
 Db 355 ISMEKRIEFAKLRKORYPDPSPSMENNLGYHMSDRVFWHGLHRTILARAARSRAR-T 413
 QY 442 YLYRFDSEELINPYRIRFGKGVSHADELYLFWNLSKRLPKRESREYKTERMV 501
 Db 414 FVYRICLOS-EFYNHYRIMIDPKLRGTAHADELSTYLFNSFQVPEKTEFEYRIGLQTLV 472
 QY 502 GIWTEFATGKPYSDIAGMENLWDPKRSKSDVYKCLNI-GDELKVMDLPEMDKIKOGA 560
 Db 473 DVFATFVINGDP-NCGMTAKSGVFEFPAQTKPTFKCLNTANDGVAFVDYDPADRLDMMD 531
 QY 561 SIFDKKLEF 570
 Db 532 AMY-VNDEL 540

RESULT 3

S53371
 carboxylesterase (EC 3.1.1.1) B1 - southern house mosquito
 C:Species: Culex pipiens quinquefasciatus (southern house mosquito)
 C:Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jul-2000
 R:Accession: S53371
 Biochem. J. 305, 651-658, 1995
 A:Title: The independent gene amplification of electrophoretically indistinguishable
 A:Reference number: S53370; MUID:95134253; PMID:7530448
 A:Accession: S53371
 A:Molecule type: mRNA
 A:Residues: 1-540 <YAU>
 A:Cross references: EMBL:222695; NID:9475069; PIDN:CAA83644.1; PID:9780238
 A:Experimental source: Strain MRES
 C:Superfamily: cholinesterase; cholinesterase homology
 C:Keywords: carboxylic ester hydrolase

Query Match 31.18; Score 945.5; DB 2; Length 540;
 Best Local Similarity 36.78; Pred. No. 1.5e-64;
 Matches 202; Conservative 112; Mismatches 213; Indels 23; Gaps 10;

QY 31 ETQIDITEYQIKGKRMVYDSDYSEFISIPYAKPVEELRPAQRFPVMEGVDC-- 88
 Db 4 ESLVOTKRYGVGRKRNVSLLGOEYVSPGIPYARABGELRFAKVPPOKMTETLDCQ 63
 QY 89 -CGPA---NRSVQDPFISGKPTGSEDCILVNTYNDLNDPKRRPWFVHGGDFJFGEAN 144
 Db 64 OCEPCYHFRRLQ-----KIVGCEDSLKINFAKEINSPPLVMLYIGGFTGSG 117
 QY 145 RNMFGPDYFMKRPVVLVYVYRIGVGLSKSENLNVPNAGLKQVMAIRWYKSNIAI 204
 Db 118 TELYGDPLVOKDVLVSFNYRIGALGFLCCQSDQDGVPGNGLKQDOLARVLENTIA 177
 QY 205 FCGDVNDITVFESAGASTHYMTTEOTRGLHRGIMSGNSMCSWASTECQSRALTM 264
 Db 178 FGDDPKRYTLVAGHSGAASVQYHLISDASKDLFORIYVSGSYSSMLRQNRWVEKLA 237
 QY 265 KRVGYGEDNEKDLLEFLKAPYDLKEEPOVLTPEMQNKVFPFGPTVEPYQTADCV 324
 Db 238 KAIGMDGGGSGALRFLRAKPEDIVAHQKLLTDQMDODITFPFGPTVEPYLTQCI 297
 QY 325 VKPRIREWKSAMGNSIPTLLIGNTSYEGLSKSVAKQYEVVKELESCVNVPELADSE 384
 Db 298 IKRPFEMARTAMGDKIDIMIGTSEGLLQKIKLPELLSHPLFLGNVPPNL--K 354
 QY 385 RSAPETLERAAIVKKAHVDETPILDN--FMELCSYFVFLPMHRLQLRNTACTPI 441
 Db 355 ISMEKRIEFAKLRKORYPDPSPSMENNLGYHMSDRVFWHGLHRTILARAARSRAR-T 413
 QY 442 YLYRFDSEELINPYRIRFGKGVSHADELYLFWNLSKRLPKRESREYKTERMV 501
 Db 414 FVYRICLOS-EFYNHYRIMIDPKLRGTAHADELSTYLFNSFQVPEKTEFEYRIGLQTLV 472
 QY 502 GIWTEFATGKPYSDIAGMENLWDPKRSKSDVYKCLNI-GDELKVMDLPEMDKIKOGA 560
 Db 473 DVFATFVINGDP-NCGMTAKSGVFEFPAQTKPTFKCLNTANDGVAFVDYDPADRLDMMD 531
 QY 561 SIFDKKLEF 570
 Db 532 AMY-VNDEL 540

RESULT 4

S53372
 carboxylesterase (EC 3.1.1.1) B - southern house mosquito (fragment)
 C:Species: Culex pipiens quinquefasciatus (southern house mosquito)
 C:Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 20-Sep-1999
 R:Accession: S53372; S44212
 R:Vaughan, A.; Rodriguez, M.; Hemingway, J.
 Biochem. J. 305, 651-658, 1995
 A:Title: The independent gene amplification of electrophoretically indistinguishable

A:Title: The independent gene amplification of electrophoretically indistinguishable

A:Experimental source: strain Bristol N2; clone T28C12
 C:Genetics:
 A:Gene: T28C12.4a; CESP:T28C12.4b
 A:Map position: 5
 A:Introns: 70/1; 96/3; 137/3; 192/3; 366/2; 423/1; 480/3; 573/2
 C:Superfamily: cholinesterase; cholinesterase homology

Query Match 19.9%; Score 607; DB 2; Length 658;
 Best Local Similarity 30.2%; Pred. No. 2e-38;
 Matches 172; Conservative 98; Mismatches 214; Indels 86; Gaps 23;

QY 22 YTNVYLSNENQIIDTEVGQIKGVKRMVYDSSYSESIYAPRPVGLKAPQRPV 81
 DB 85 FSNLKSSENAIVYQGGLEGFRVKTAKGDLCDVFGHGYAPPELREKOPKOPKA 144
 QY 82 WGVVDCGCPANRSVQDIFSGK--PTG--SEDCLYLVYNTNDLPKRRVYVFIHGG 137
 DB 145 WEGIKCKKRYPRSIHKEMPDKALPSANOSDCLYLVPAPKIREDKKYVLYIHGG 204
 QY 138 FIFGAPNRMFGPDYFKM-----KPVLVYVQYRLGVGLFSLKSENLVPGMGLK 189
 DB 205 YVMSAER-----YTAKNICKLVSRRIIVTFHYRLGFLSTGDD--VCGNGYGLF 256
 QY 190 DOVALRMVKSNIATFEGDVNTIFEGSAGASTHYMTIETQRLGFRHGMGNSMC 249
 DB 257 DMLEAMRVYANISFGGDPENITLSGAGAAADLISFSLPKGLFKRKIVMGNSYC 316
 QY 250 SWAST---ECOSRALTYMAKRVYKGE-----DNEKDILEFLKAPYDLIKEEPVLT 299
 DB 317 HMAVTSNHDIREYCKKNAKRLGKMPQNLVANKRESDIINF--NGLPSTKIGMFMF 373
 QY 300 PERQNKVMPFPGVPEVYQTAQCVKPKIREMKSAMGNSIPPLIGNTSEGLSKSVA 359
 DB 374 SNTJFKEGQLPLAVIDGE---ILPHDKLVLETO--ELVPSLVGGEYEAALLFCAIG 426
 QY 360 KQPEVYKELSCVNYVPMELADSESAPELERAIVYKAHVGEPTLT--DN----- 411
 DB 427 ---LRGTEKEINSAIDVLSRKNRLSRKIE--AMTEKY--GDSPALRADSKAKMF 477
 QY 412 FMEICSTFYFLFPMHRLQLRFNHTACTPIYLYRFDSEBI-----INPYRIMRGRG 465
 DB 478 FVQLISIFANYGNVYR--MRDCCQGVCEGYSFDSQKQMGWLOHVVPF----- 527
 QY 466 VKGSVHDELTYLFL--WMILSRKLPKESREKTIEMVG--IMTEPATGKRYNDIAGMEN 523
 DB 528 -TGCTHSELSYLDPCVYMSAPLAKMTD--KVSGMADYFTVNFKFTDNG--PNSQL 582
 QY 524 LTMWPIKSDVDYKCLNIGDELKVMPLPEM 553
 DB 583 PKMERISPDDEHMKLISIKPE-----PEM 606

RESULT 7

A:Juvenile-hormone esterase (EC 3.1.1.59) precursor - tobacco budworm
 C:Species: Heliothis virescens (tobacco budworm)
 C>Date: 22-Jun-1990 #sequence_revision 25-Sep-1992 #text_change 13-Sep-1998
 R:Accession: A34325
 R:Hanzlik, T.N.; Abdel-Aal, Y.A.I.; Harshman, L.G.; Hammock, B.D.
 J. Biol. Chem. 264, 12419-12425, 1989
 A>Title: Isolation and sequencing of cDNA clones coding for juvenile hormone esterase fr
 of the serine proteases.
 A:Reference number: A34325; MUID:89308671; PMID:2745451
 A:Accession: A34325
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-564 <HAN>
 A:Cross-references: GB:J04955; NID:9159222; PID:9159223
 C:Superfamily: juvenile-hormone esterase
 C:Keywords: carboxylic ester hydrolase

Query Match 19.8%; Score 602.5; DB 2; Length 564;
 Best Local Similarity 32.0%; Pred. No. 3.5e-38;

Matches 166; Conservative 96; Mismatches 211; Indels 45; Gaps 19;

QY 29 TNEQOII-DTEYQIKVAKMTYDSSYSESIYAPKPPVGLRKAPQRPVMEGYD 87
 DB 23 TNSRVVAHLDSGITRKVPVPR-SADGIRFASFLGVAPKQPVGLRREKLELEPPWNIIN 81
 QY 88 CCGPANKSVQDTEISGKPTG---SEDCLYLVYNTNDLPKRRVYVFIHGG 132
 DB 82 ATNMGPICTQDVLVGLMAASEMSACIYANIHVMQSLPRKGTPL-----RPIVLF 136
 QY 133 IHGGDIFEGANRMFGPDYFKMPPVLTVOYRLGVGLFSLKSENLVPGNAGLKDV 192
 DB 137 IHGGGFAFGSGHDLGPELVYKLVNIVTFNRLVNFVGLSMNT--TKIPNAGLRDQV 194
 QY 193 MALRWKSNIAITGSDVNTIVGCSAGASTHYMTIETQRLGFRHGMGNSCMSA 252
 DB 195 TLIRWQNRANKNGGSDPTITAGQSAHAHLTLTKATGGLFRALITMSTGTSYFF 254
 QY 253 STECOSRALTYMAKRVYKGE--EDNEKDILEFLKAPYDLIKEEPVLTPEKQKVMFP 310
 DB 255 TTSPLFAAYISKQLDILGNORGSEIHRQLDL-PAKLEANNVL-----IEQIGLTT 309
 QY 311 EGPVVE-PIQTADCVKPKIREMKSAMGNSIPPLIGNTSEGLSKSVAKQYPEVVEL 369
 DB 310 FLPVESPPLVGVTTIIDDPPEILIEGRGKNVPLLIGFTSSCEFTFRNLLNFDVKIKQ 369
 QY 370 ESCVNYVPMELADSESAPEL--ERAIVYKAHVGEPTLTNDMEICSYFELPMHRF 428
 DB 370 DNTFTIIPKRL--FWTPPELLMELAKTIERKTYNG--TISDNFVKSQSDGYEYPAKL 426
 QY 429 LQRFNHTAGTPIYLYRFDSEBIINPYRIMRFGVYSHADELYLFL--WMILSRK 487
 DB 427 AQKR-AETGAPLYLYRFAYEGONSLIK--KVM--GLNHGVGHIDLYVFKVMSMAL 482
 QY 488 ---PKSREKTIEMVGIMTEPATGKRYNDIAGME 522
 DB 483 HASPSEN-DVKMKNTGTGFLNFICSOPTCEDNNSLE 519

RESULT 8

A:para-nitrobenzyl esterase (EC 3.1.1.-) - Bacillus subtilis
 C:Species: Bacillus subtilis
 C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
 R:Accession: B69680; I40510
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
 C.; Bron, S.; Brouillette, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
 A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
 Nature 390, 249-256, 1997
 A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fuma, S.; Galiszl, A.; Gal
 lech, J.; Harwood, C.R.; Henault, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M
 Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino
 A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Men
 Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portee
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scall
 A:Authors: Schleich, S.; Schroeder, R.; Scottone, F.; Sekiguchi, J.; Sekowska, A.; Se
 tteuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpiltra, P.; Tognoni, A.; Tosato, V.; Uchiya
 A:Authors: Yoshikawa, H.F.; Zunsstein, E.; Yoshikawa, H.; Danilich, A.
 A>Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis
 A:Reference number: A69580; MUID:96044033; PMID:9384377
 A:Accession: B69680
 A>Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-489 <KUN>
 A:Cross-references: GB:Z99121; GB:AL009126; NID:92635827; PIDN:CAB15444.1; PID:926359
 A:Experimental source: strain 168
 R:Zook, J.; Cantwell, C.; Swartling, J.; Hodges, R.; Pohl, T.; Sutton, K.; Rosteck, P
 Gene 151, 37-43, 1994
 A>Title: The Bacillus subtilis pnda gene encoding p-nitrobenzyl esterase: cloning, se
 A:Reference number: I40510; MUID:95129891; PMID:7828995
 A:Accession: I40510
 A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-58, 'P', '60-94', 'O', '96-149', 'D', '151-229', 'A', '231-241', 'S', '243-245', 'R', '247-250', 'T'
A:Cross-references: EMBL:U06089; NTD:9468045; PIDN:AAA81915.1; PID:9468046
A:Experimental source: strain NRRL B8079
C:Genetics:
A:Gene: *pnba*
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase
F:24-476/Domain: cholinesterase homology <CHE>

Query Match	18.9%;	Score 575;	DB 2;	Length 489;
Best Local Similarity	30.7%;	Pred. No. 3.7e-36;		
Matches 170;	Conservative 90;	Mismatches 209;	Indels 84;	Gaps 23

[illegible]

RESULT 9
S36787
carboxylesterase (EC 3.1.1.1) F&A precursor - green peach aphid
C:Species: Myzus persicae (green peach aphid)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S36787
R:Field, L.M.; Williamson, M.S.; Moores, G.D.; Devonshire, A.L.
Biochem. J. 294, 569-574, 1993
A:Title: Cloning and analysis of the esterase genes conferring insecticide resistance in
A:Reference number: S36786; MUID:93384534; PMID:8373371
A:Accession: S36787
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-564 <PE>
A:Cross-references: EMBL:X74555; NID:g397512; PION:GAA5649.1; PID:g397513
C:Superfamily: cholinesterase, cholinesterase homology
C:Keywords: carboxylic ester hydrolase
F:52-352/Domain: cholinesterase homology <CH>

Query Match	18.2%;	Score 553.5;	DB 1;	Length 564;
Best Local Similarity	31.5%;	Pred. No. 2e-34;		
Matches 178;	Conservative 81;	Mismatches 231;	Indels 75;	Gaps 26;

```

0Y      8  IFKKLCVCKMVKNTYNTLSTJETEQI IDREYQOLGVMKMTIYDDSYSEFISYAPR  67
Db      8  LNLFLTLGCFLT-----CSASNTKRVQYHSEIANGGEFTYTYNGRKIYSFLGIPYASP  61

0Y      68  VGLERFAPORPYPMWEGVRCCGCPANKRSVQDEISG-KPTGSEDCLYLNVYNTDINPDKR  126
Db      62  VQNNRFEPQPYQVQWMLQVMNATVPGSACGIEFGSSKIIGEDCLFLNVTPKPLQENS  121

0Y      127  ----RPMWFTHGCDLTFEGEANKRMGPRDYFM-KKRVVLYTQYRLGVGLFSLKSEMLN  181
Db      122  AGDLMNVIYVHIGGGYFEGEG-ILGYPHLLDNNDFYVYSINYRLGVGFASGDGYL-  178

0Y      182  VPGNAGIKDOVMALRWKXSNIAIFGSGVNDITVFGESAGASTHYMMKITEQGRJLFHRGI  241
Db      179  -PGNGLKDOYAAKMTIQONIVAFEGDPNSVYITTHGSAGASSVHNHLISPMKGLFENRI  237

0Y      242  MMSGSMCSMASTECOSRALTMAKRVYKGE-----DNEKDLFEFLMKANDYDLIKEEP  295
Db      238  IQSGGAFCHMSTAE-----NVAQKTYILNLCPTNNSVEIETCL-RSPRAKAIAMSY  290

0Y      236  OVLIPERNQNKVMPPEGEPTYB-PLYQADCVNFKPIREMKXSMGSIPTLLGNSTYESTL  353
Db      231  LNFMPWR-NNEPFPFGFTEVAGYE-----KFLPEIDPEKVLPHDIPVLLISTADBSGL  341

0Y      354  LKSAVAKQYEVVKELESCVY-VYPMELADSEBSAPETL--EBAIVYKKAHDYGETP--  407
Db      342  IF-STFELGLENGFMDLNNNNNEHILPHLLDYNTIISNENLFRKAQDIKEFYF-GDKPISK  399

0Y      408  -TLDNFMELCSEFYFLPMPHRLQLRNNHAG--PPIYLRFDDESEELINDYIRMRP-  462
Db      400  EKSLSLKMISIDRSPGYCTSAAG-----HIAAKWTAPVYEEFGYSGN-----YSYVAF  450

0Y      463  ----GRGVKQVSHADELTYLFNMLLSKRLPKSEREKTERTERVQVWTEPATQGRKYSND  517
Db      451  DPKYSYRG-SSPTJHDEFTNYVL-KVDGFTYADNEEDKRMKTYVNWATFATIKSGVP--D  505

0Y      518  IAGMENLWMDPIKSD-DVYKCLMI  541
Db      506  TENSE--TWLPSKMPADLEFPTXI  528

```

RESULT 10
S55233
juvenile hormone esterase-related protein - cabbage looper
C:Species: Trichoplusia ni (cabbage looper)
C:Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 07-May-1999
C:Accession: S55233
R:Jones, G.; Venkataraman, V.; Ridley, B.; O'Mahony, P.; Turner, H.
Biochem. J. 302: 827-835, 1994
A:Title: Structure, expression and gene sequence of a juvenile hormone esterase-related protein from the cabbage looper, *Trichoplusia ni*
A:Reference number: S55233; MUID:95031924; PMID:7945209
A:Accession: S55233
A:Status: preliminary
A:molecule type: mRNA
A:Residues: 1-547 <ON>
C:Superfamily: juvenile-hormone esterase

[illegible][illegible]

QY 120 DLNPKRRPVVFIHGDFIEGEANRMWFGPDYEMKRPVLTVOYRLGLGLSLKSEN 179
 DB 127 YNQTANYLPILVFIHGDFIEGSSGSDIHGEYLMKSKVIYITFHRLNIVGYLSLNS-- 194
 QY 180 LNVPCNAGLKDOVALRWKSNIAIEGDDVNTIVFESAGASTHYMMITEQTRGLFHR 239
 DB 195 TKIPNNLRRAITLTKLVORNAVFEGDPDNNVLIGQSCGAVAAHLISLSKASGJFKR 254
 QY 240 GIMSGNCSMWASTE---COSRALTMAKRVYKGEDEKXILEFLMKANPYDLIKEPQ 296
 DB 255 LILMSGVATAGFYTTSPSYTQVNAOMFLGNVINSTDAV-ELHDLQVOM-PLEKIMEANR 312
 QY 297 VLTPEPMONKV-MEPFEGTVEPYOT-ADCVYKPKIREMKSAMGNSIPTLIGNTSYEGL 354
 DB 313 I-----YOFKTVISFAVESEELTGVSRILDDPANLIKQGRGDLPMIIGSTTKCEEF 367
 QY 355 SKS-----YAKQYEVYKLESCVNYVPWELADSEKAPETLERAAIVKAAHYDGE 405
 DB 368 FKNRIIYDLIGLIKENSVA-----LPVMSYSV-SAKRSFDLYOMISDRYFOGN 417
 QY 406 TPTLDNFMELCSYFELPFRHFLQLRPNHTAGTPRIYLRFPDSEELINFRIMRFRG 465
 DB 418 L-TYENYLPYCADSEFTIRPAIKVAMRAS-LGAPVRYEPEFNS-----TFNVYKFTLM 470
 QY 466 V---KGVSHADELYLF-----WNLSKRLPKESREKKTERRVNGIWTEPATTKP 513
 DB 471 LHYSEGAHVHEDMTFVFERTNSMGADKESFPPTRRDLMKSMTSFVNFMRCSQP 526

RESULT 11

225690
 hypothetical protein F15A8.6 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
 C:Accession: T25690
 R:Miller, N.
 submitted to the EMBL Data Library, April 1997
 A:Description: The sequence of C. elegans cosmid f15a8.
 A:Reference number: 220069
 A:Accession: T25690
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-583 <MIL>
 A:Cross-references: EMBL:U97549; PIDN:AA52848.1; GSPDB:GN00028; CESP:F15A8.6
 A:Experimental source: strain Bristol N2; clone F15A8
 C:Genetics:
 A:Gene: CESP:F15A8.6
 A:Map position: X
 A:Introns: 23/3: 165/2: 247/1: 432/3: 481/1: 524/2
 C:Superfamily: cholinesterase; cholinesterase homology

Query Match

17.9%; Score 545; DB 2; Length 583;
 Best local similarity 28.1%; Pred. No. 9.6e-34;
 Matches 160; Conservative 100; Mismatches 209; Indels 100; Gaps 23;

QY 30 NENQI-----IDTEYQIKYKRTVYDDSYYS-FESIPYAKPVGELRPAQRPVWE 83
 DB 14 NESNLTPSKOYRTFNGLVEGF-RIKIDDDREVDMLGIPPAKAPVGDRLRKNPEHEDMD 72
 QY 84 GVRCGCCPANRSVOTDFISGKPT-----GSEDCILYLVNTDNLMPD----- 124
 DB 73 GYKCAVFGFRAPADFEWERFLIGVKSSEDCLILNVFSPTWKAEEVSNVSGVFFKPICGK 132
 QY 125 ----KRRPVVFIHGDFIEGEANRMWFGPD---YFMKRPVLTVOYRLGLGLSLK 176
 DB 133 IELFOLHPVAVYVYGGGFLIDSAVK--YDGEGLAKYLCRHGGVAVVLTQYRLGLGFFSNG 190
 QY 177 SENLVNAGNLKDOVALRWKSNIAIEGDDVNTIVFESAGASTHYMMITEQTRGL 236
 DB 191 DQ---VCGNGNLGMDMTALQVNRDVAHAFGSDPRKTYVFGQSAGVSDLSLSPHSRDL 248
 QY 237 FHHGIMMSGMSMWASTEGOSRALTMKRVYK-----GEDEKXILEFLMK 284

DB 249 FHQVVPWAGGEDEW-STVGKNRLVACBFAARKCWDEKQARGNENASMEFLPT 307
 QY 285 ANPYDLIKEPVOYLTPERMQ-NKVMFPFGTVEPYOTADCVYKPKIREMKSAMGNSIPT 343
 DB 308 RKEBEF---EKRLITRRKGVDSKIGDLAPVIGS-KPSD-FLPKSIIEELRKAAPKNI-- 360
 QY 344 LIGNTSYEGLSKSVA-----KQYEVYKLESCVNYVPWELADSEKAPETLERAAIV 397
 DB 361 MVGTCEHEGLIFSLGPSNFDKGTDLALALITTEHEDFEALKEE-----AKMYL 413
 QY 398 KKAHYDGEPTL-----DNFMELCSYFELPFRHFLQLRPNHTAGTPRIYLRPD 447
 DB 414 KKLSDDEDKEVAARGYIQLYSLDFVNGNYN---AEKMKRL-----GAKVFMYSPD 463
 QY 448 FDEBEIINP--YIMFPGKGVKSHADELYLFMWILSKRLPKESREKKTERRVNGIWT 505
 DB 464 Y-----CNPRSFGLSLRAFPRAATHTCLAYIFGVSYFNRYNESDRAMLDMTKMT 518
 QY 506 EFATTKPYSN-DIAGENLTPDKSD 533
 DB 519 NFAKYNPNQYEDSTVPPDKMEPTSKEE 547

RESULT 12

536786
 carboxylesterase (EC 3.1.1.1) E4 - green peach aphid
 C:Species: Myzus persicae (green peach aphid)
 C>Date: 09-Jun-1994 #sequence_revision 01-Dec-1995 #text_change 18-Jun-1999
 C:Accession: S36786
 R:Field, L.M.; Williamson, M.S.; Moores, G.D.; Devonshire, A.L.
 Biochem. J. 294, 569-574, 1993
 A:Title: Cloning and analysis of the esterase genes conferring insecticide resistance
 A:Reference number: S36786; MUID:93384534; PMID:8373371
 A:Accession: S36786
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-552 <FTE>
 A:Cross-references: EMBL:X74554; NID:q397510; PIDN:CA52648.1; PID:q397511
 C:Superfamily: cholinesterase; cholinesterase homology
 C:Keywords: carboxylic ester hydrolase
 F:52-552/Domain: cholinesterase homology <CHE>

Query Match

17.9%; Score 544; DB 2; Length 552;
 Best local similarity 31.4%; Pred. No. 1.1e-33;
 Matches 176; Conservative 79; Mismatches 221; Indels 84; Gaps 26;

QY 8 IFRLKLCVCMNNKYNLTNLTNEQIIDTEYQIKYKRTVYDDSYYSFESIPYAKP 67
 DB 8 LNLFLFICGFLT-----CSASNTPKVOVHSGELAGFEYTYNGRKLYSFLGIPYASP 61
 QY 68 VGLRFAKAPORVPWEGVRCGCCPANRSVOTDFISG-KPTSEDCILYLVNTDNLMPDKR 126
 DB 62 YONNRKEQPQVPMGLGVNNAIVPSAGLIGFEGSGKIIIOEDCLFNVYTPKLPQENS 121
 QY 127 ----RPVWFIHGDFIEGEANRMWFGPDYEM-KRPVLTVOYRLGLGLSLKSEN 181
 DB 122 AGDLNMAVIVIHGGVYEGEG--ILYGRHYLLDNNDFFVYINRYLGLVGAISGDDVLT 179
 QY 182 VPGNAGLKDOVALRWKSNIAIEGDDVNTIVFESAGASTHYMMITEQTRGLFHRGI 241
 DB 180 --GNGNLKDOVALRWKSNIAIEGDDVNTIVFESAGASTHYMMITEQTRGLFHRGI 241
 QY 242 MMSGMSMWASTEGOSRALTMKRVYKGE-----DNEKXILEFLMKANPYDLIKEP 295
 DB 238 IQSGSAFCHWSIAE-----NVAQTKRIANLMDGPTNNSVEIYECI-RSPRAAIAKSY 290
 QY 296 QYLTPEPMONKVMEPFEGTVE--PYQADCVYKPKIREMKSAMGNSIPTLIGNTSYEGL 353
 DB 291 INFMFWR--NEPFTFGTVEVAGYE-----KFLPDIPKLVPHDIPVLTISIAQDEGL 341
 QY 354 LSKSVAKQYEVYKLESCVNYVPWELADSEKAPETL--ERAAIVKKAHYDGEPT--- 407

Db 342 IF-STFLGLENGENELNNMNEHLPHILDYNTISNENLRFKAQDIKEEYF-GDKRISK 399
QY 408 -TLDNFMELCSYFFLPFMRPFLQLRNFHAG---TPIYLRDPDSEELINRYMRP- 462
Db 400 ETKSNLSKMTSDSFGYTSKAAO---HIAAKNTAPVYFEGYSGN---YSYVAF 450
QY 463 -GGVGVGSHADLFYLF---FMNLSKRLPKESREYVGTMTFPAATTK 512
Db 451 DPKSYSG-SSPHGDETSYVLKMDGY-----VYDNEDRKMTKTMVIMATFIKSGV 503
QY 513 PYSNDIAGMENTLWDPKRS 532
Db 504 P---DTENSE--IWLPSKN 518

RESULT 13

S47655
carboxylesterase (EC 3.1.1.1) precursor - golden hamster
C:Species: Mesocricetus auratus (golden hamster)
C>Date: 26-Dec-1994 #sequence_revision 03-Aug-1995 #text_change 20-Jun-2000
C:Accession: S47655
R:Gene, T.: Isobe, M.; Takabatake, E.; Wang, C.Y.
Biochim. Biophys. Acta 1207, 138-142, 1994
A:Title: Cloning and sequence analysis of a hamster liver cDNA encoding a novel putative
A:Reference number: S47655; MUID:94318665; PMID:8043605
A:Accession: S47655
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-561 <SON>
A:Cross-references: EMBL:D28566; NID:9531238; PIDN:BA05913.1; PID:9531239
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase
F:58-546/Domain: cholinesterase homology <CHE>
F:227,459/Active site: Ser, His status predicted

Query Match 17.8%; Score 542; DB 2; Length 561;

Best Local Similarity 30.4%; Pred. No. 1.5e-33;
Matches 173; Conservative 87; Mismatches 204; Indels 106; Gaps 25;

QY 34 IITDEYQIQVKRMITYD--DSTYSSESTPYAKPYGELFRKAPQRPVMEGVRDCCGP 91
Db 33 IRTHTQVVRG-KLVYVEGVTVYAFGLIPFAKRPVGPPLFAPPEPESGVRDTS 91
QY 92 ANRSVQTFDTSK-----PT--GSECLYLVNVT--NDLNPDKRRPVVFTHGDFI 139
Db 92 PAKCLQIDFKMPQTSKERTIILPTISSECLYINITYTPRAHAGSMLPVMWTHGALV 151
QY 140 FGEANRMWFGPDYMKRPVVLVYQYRLGVGLSLKSENLNVPNGNLKDYVALRMVK 199
Db 152 MGNMAMN-DGSLAATEDIYIVSIYRLGILGFSTGDEHAR--GNMGYLDQVALHMQ 208
QY 200 SNIAIFGSDVNTVFGESAGASTHYMTTEQRLGFLFHGIMMSGMSKMSASTECOSR 259
Db 209 QNIAISFGNPOVYIFGVSAGTSVSLVSPMSKGLFHGAIMOSGVALLPDLISDTPEA 268
QY 260 ALT--MAKRVGYKEDNEKOLIEFLMKANPYDLIKEEPOVLTPEPMONKVMFPFGVPEP 317
Db 269 VYTPVAVANQSCSEAKDSFA-LVHCLRE-----KTEAEILIA-----INQVFI-----MTP 311
QY 318 YQTADCVVPRKPIREMYKSAWNSIPTLIGNTSYE-----GL--LSNSVAKQ--PPEV 365
Db 312 GVNQGIPLRPRQELLASVDHPVPSIIGVSDCGMGPFLFMGLDHYIKITRETLPAF 371
QY 366 VKELESCVNYVPELAD-----SESAPELTERALIVKKAHVDGELPILDNFMELCSY 418
Db 372 LKSRAEHM-MLRPPCSDLMLQYMGVDEDPQTQA-----QERLEMKD 413
QY 419 FYFLPRMRPFLQLRNFHAGTPIYLRDPDSEELIN---PYRIMRFGKGVKGVSHADE 474
Db 414 PMFVTPA---LKAVAFQSHAPVYFEPQHOSSFIKKNDARPSHYR-----ADHGCH 462
QY 475 LTYL---FMNLSKRLPKESREYKTIERNVGIWTEFATTKPYSNDIAGMENTLWDPK 530

Db 463 VAFVSGDSFWSL--KIDLTREEKLLNRMKMYANFARHGNPNS-----EGLPWDEL 513
QY 531 KSDDYKCLNTI-----GDELKVMIDLPEMDKI 556
Db 514 VHDQTLKIDLPANVGRALKSKLHFWIKI 543

RESULT 14

T32907

hypothetical protein F56C11.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 31-Jan-2000
C:Accession: T32907

R:Fin-Wollam, A.; Wohlmann, P.; Morris, M.
submitted to the EMBL Data Library, January 1998

A:Description: The sequence of C. elegans cosmid F56C11.

A:Reference number: 221244

A:Accession: T32907

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-548 <TIN>

A:Cross-references: EMBL:AF043697; PIDN:AMB97558.1; GSPDB:GN00019; CESP:F56C11.6

A:Experimental source: strain Bristol N2; clone F56C11

C:Gene(s):

A:Gene: CESP:F56C11.6

A:Map position: 1

A:Introns: 29/3; 84/3; 264/1; 340/1; 398/3; 447/1; 490/2

C:Superfamily: cholinesterase; cholinesterase homology

Query Match 17.4%; Score 529; DB 2; Length 548;

Best Local Similarity 29.8%; Pred. No. 1.5e-32;
Matches 177; Conservative 91; Mismatches 207; Indels 118; Gaps 28;

QY 32 TQITDEYQIQVKRMITYDSDYSSESTPYAKPYGELFRKAPQRPVMEGVRDCCGP 91
Db 12 TAVHDTGCPKIGVGYEQEDGSVBSGLPIPAEPGLARKKAYAHKKTPELDCYRF 71
QY 92 ANRSVQTFDTSK-----FISGKPTGSEDCLYLVNVT-----NDLNPDKRRPVVFTHGDFI--- 139
Db 72 GPRSPONDELQFGVTVTKSEHCLSLNVFTPKMESNMPD--GFPVVFTHGGEFAVHS 130
QY 140 ---FGEAN--RMWFGPDYMKRPVVLVYQYRLGVGLSLKSENLNVPNGNLKDYVAL 194
Db 131 SSNYGASIAKN-----LCITKDVVVVITNRYLGVGFSTGDEVCOR--GNGLMDQPA 182
QY 195 LRMVKNIAIFGSDVNTVFGESAGASTHYMTTEQRLGFLFHGIMMSGMSKMSAST 254
Db 183 LEWVQENISFRODPDNTVIFGOSAGASVDLCLSPHSKGLFNRAIPMAGNCEDFAMR 242
QY 255 ECOSRA---LTMARVGYKEDNE--KDLEFLMKANPYDLIKEEPOVLTPEP---MONK 306
Db 243 TSGQQAQLSREFRKYLGWGSDNDSEDLQFDQGPLYKI-----EMGINPKRGFHSQAG 298
QY 307 VMEFPGPYEPIQTADCVVPRKPIREMYKSAWNSIPTLIGNTSYREL--LSNSVAKQYPE 364
Db 299 SLX-FVPNPD-----GDFPKPLNQNRKAPKQWIT--GTRKYDELFIACALSKNPE 350
QY 365 VYVE-----LESCVNYVPELADSESAPELTERALIVKKAHVDGELPILDNFMELCSY 419
Db 351 GIKKEMGRIFKEC-----DYGERA-----DVLQNVDF 379
QY 420 YF--LFP-----MAREFLQ--REFNTAGT-----PIYLRDPDSEELINXY 457
Db 380 YFKGVAPKDEKMMHDIYFIDGYSLNGGYRLANIMTDLQHDVYFYQGYHNSA---GF 436
QY 458 RIMRFGKGVKGVSHADELTYLFM-NLSKRLPKESREYKTIERNVGIWTEFATTKPYSN 516
Db 437 GVERFWLPLFEGSHTCEMRVVLQKGIISKFRPDN--DKRMILHMTYFTNFKAYGNPGE 495
QY 517 DIAGMENTLWDPKISGDDYKCLNIGDELKVMIDLPEMDKIKOGASIFDKKEL 569
Db 496 N---OETGEW---QKHDSAPRFRHFKITLDSEHVE--DYQERRAEIMDLRAL 541

RESULT 15

A33668

sterol esterase (EC 3.1.1.13) precursor - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C:Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 18-Jun-1999

C:Accession: A33668

R:Kyte, E.M.; Wiegand, R.C.; Lange, L.G.

Biochem. Biophys. Res. Commun. 164, 1302-1309, 1989

A:Title: Cloning of the bovine pancreatic cholesteryl ester/lysophospholipase.

A:Reference number: A33668; PMID:90073663; PMID:2590203

A:Accession: A33668

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-597 <KYG>

A:Cross-references: GB:M28402; NID:g598081; PIDN:AAA56788.1; PID:g598082

C:Superfamily: cholinesterase; cholinesterase homology

C:Keywords: carboxylic ester hydrolase

F:48-583/Domain: cholinesterase homology <CHE>

Query Match 17.2%; Score 523; DB 2; Length 597;

Best Local Similarity 30.1%; Pred. No. 4.9e-32;

Matches 167; Conservative 67; Mismatches 211; Indels 109; Gaps 22;

```
OY 37 TEYGOIKGV-KRMTYDSDSYSESIPYAKPPVGLRFKAPQRPVPEWEGVRCGCCPANRS 95
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 26 TEGFVEGVNKKLSLFGDSVDIFKGIFFAAPKA---LEKPERHPGMOGTLKAKSFKKRC 82
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
OY 96 VQTFDISGKPTGSEDLVNYTNDLNPDKRR-----PVMVFTHGDFIRGE----- 142
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 83 IQATLTQDSTYGNEDCLTLNTV---PQGRKEVSHDLPMIWIYGGAFMGASOGANFL 138
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
OY 143 ANRNKFGPDYEMKKPVVLVTVQYRLGLGLSLKSENINVPNGNLKQVVALRWKNSNI 202
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 139 SNVLTGGEIATRGVNIYVTFNYRGPLGLSTGDSNL--PGNYGLMDQHMAIAWVKNI 196
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
OY 203 AIFGGDVNTIVEGSGAGASTHYMTIEQTRGLFHRGIMSGNSMGCMASTECOSRALT 262
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 197 EAFGGDPNITLFGESAGASVSLQTLSPYNNKGLIKRAISOSGVLCPWA---IQDDPLF 253
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
OY 263 MAKR---VGYKGEEDNEKDILEFLMKANPYDLKEEPQVLTPEKQNKVMFPFGPT--- 314
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 254 WAKRIAELVGGCPVDTSK--MAGCLKIT-----DPRALF--LAKKL--PLGSTIEYRK 299
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
OY 315 -----VEPYQTADCVVPKPIREMWKSA-----WNSIPLILIGNTSYEGL 353
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 300 LHYLSFVYVIDGDFIPDDPVNLYANADVDYIAGTNDMDGHLFVGMDVPAL--NSNKQDV 357
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
OY 354 LSKSVAKQYF--EYVKELESC-----VNYVPWELADSRSAPEFLERAIYKKAHVDGET 406
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 358 TEEDFYKLVSGLTYKGLRGANATYEYTEPW---AODSSQETR-----KKTIVDLET 407
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
OY 407 PTLNFMELCSYFELFPMHREQLRFNHTAGTPILYLFREFDSEELINPYRIMRFGRGV 466
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 408 DIL-----FLIPTKIAVAOHKSHAKSANTYTYLFSQSRMPTIYKWM----- 449
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
OY 467 KGVSHADELYLENNILSKRLPKESREYKTIERNVGIETEPATGKPYSDNDIAGMENLTV 526
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 450 -GADHADLQYVFGKPFATPLGVRADRTVSKAMIAVYTNFAFTGDPNTGHSIVPAN--W 506
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
OY 527 DPIKSSDVPYKCLN 540
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 507 DPTLTEDDNYLEIN 520
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
```

Search completed: April 4, 2003, 09:17:18
Job time : 21.0734 secs

```

SQ      SEQUENCE      540 AA;  60806 MW;  F73B25B3A7157C95 CRC64;

```

```

SQ      SEQUENCE      540 AA;  60806 MW;  F73B25B3A7157C95 CRC64;

```

Query Match 31.3%; Score 954.5; DB 1; Length 540;
 Best Local Similarity 36.9%; Pred. No. 4.4e-66;
 Matches 203; Conservative 113; Mismatches 211; Indels 23; Gaps 10;

31 EQGIDTEGQKGVKRMVYDSDSYSESPYAKPVGELRFAKQRPVMEGVRD-- 88
 DB ESTVQTKYGPVGRKRVNLSLQGEVYSFOGIPYARAPGELRFAKQRPVMEGVRD 63
 4 ESTVQTKYGPVGRKRVNLSLQGEVYSFOGIPYARAPGELRFAKQRPVMEGVRD 63
 89 -CGPA---NRSVQTFISGKPTGSEDCLYLVNTDLPDRKRPVNVHGGDFIFGGAN 144
 DB 64 QCEPCYHDDRQ-----KIVGCEDSIKIVFAKEIPSPPLPMLTYGGEGTGTG 117
 145 RNMFGPDYPMKPPVLTVOYRVLGVLFSKSENANVGNAGIKDQYMAWRVKSNIAT 204
 DB 118 TELGPDPLVOKDVLVFNFRIGALGFLCCQSEDDGVPGNAGIKDQYMAWRVKSNIAT 177
 205 FGGVDNITVFESGASGASTHYMITEDTGLFRGIMSGNSMCNASTECOSRALTMA 264
 DB 178 FGGDKRTVTLGHSAGASVQYHILSDASKDFQRRIYMSGSTYSWSLFRORWVEKLA 237
 265 KRVGKGEDEKDLLEFLMKANPYDLKEBPQVLTPEKQKVMFPPGPTVEPYQTADCV 324
 DB 238 KAIGMDGCGGEGALRFLRAKPEDIVAHQEKLLTDQMODDITTPRGTYVEPYLTQCI 297
 325 VPKPIREWVKSAMGNSIPTLIGNTSYGLSKSVAKQYPEVKELESCVNVPELADSE 384
 DB 298 IPRAPFEKARTAWGDKIDIMIGTSEGLLLLOKIKLHPHLLSHPLFLGNVPELADSE 354
 385 RSAPETLEKRAIVKAVDGETPLDN--FMELCSFYFELFPHARLOLRNFHTAGTPI 441
 DB 355 ISMEKRIEPAKAKQRYPPSPISMENNLGYVHMSDRVWGHGHTILRAARSRAR-T 413
 442 YLVFDDSEELNIPYIMRGVGVSHADELTFLFNNILSKRLPKESREKTYTERMV 501
 DB 414 FVYRICDS--EFYHYRIMIDPLRGTAAHDELSTYLFSEFTQVPEKFEYRGIDTLY 472
 502 GIMTEFATGKPYSDNLAGMENLTPDKIKSDVYKCLNT-GEELKAVMDLPEMDKIKOGA 560
 DB 473 DVSAFYIINDP--NCGMTAKGVVFEFNQTKPFKCLNLIANDGVAFVDPDADRLMD 531
 561 SIFDKKKELF 570
 DB 532 AMV-VNDEL 540

RESULT 2
 ESTD_HELVI
 ID ESTD_HELVI STANDARD; PRT; 564 AA.
 AC P12992;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Juvenile hormone esterase precursor (EC 3.1.1.59) (JH esterase).
 OS Heliothis virescens (Noctuid moth) (Owllet moth).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;
 OC Diptera; Noctuoidea; Noctuidae; Heliothinae; Heliothis.
 NCBI_TaxID=7102;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 20-54.
 RX MEDLINE=89308671; PubMed=2745451;
 RA Hanzik T.N., Yehia A.I.A.-A., Harshman L.G., Hammock B.D.;
 RT "Isolation and sequencing of cDNA clones encoding for juvenile hormone
 RT esterase from *Heliothis virescens*. Evidence for a catalytic mechanism
 RT for the serine carboxylesterases different from that of the serine
 RT proteases.";
 RT J. Biol. Chem. 264:12419-12425 (1989).
 RN [2]
 RP REVISIONS.
 RA Hanzik T.N.;
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: JH ESTERASE PLAYS A CRUCIAL ROLE IN THE DECREASE OF

CC JH ACTIVITY IN LEPIDOPTERAN INSECTS, BY HYDROLYZING THE METHYL
 CC ESTER OF JH. IT IS ALSO INVOLVED IN THE TRANSPORT OF JH.
 CC -1- CATALYTIC ACTIVITY: Methyl (2E,6E)-(10R,11S)-10,11-epoxy-3,7,11-
 CC trimethyltrideca-2,6-dienoate + H(2)O = (2E,6E)-(10R,11S)-10,11-
 CC epoxy-3,7,11-trimethyltrideca-2,6-dienoate + methanol
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 CC -----
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb.ch/announce/>
 CC or send an email to license@isb.ch).
 CC -----
 DR EMBL: J04955; AAB8629.1;
 DR PIR: A34325; A34325.
 DR HSP: P37967; 10E3.
 DR InterPro: IPR002018; Carboxylesterase.
 DR InterPro: IPR000379; Ser-estrs-site.
 DR Pfam: PF00135; Coesterase; 1.
 DR PROSITE: PS00122; CARBOXYLESTERASE-B_1; 1.
 DR PROSITE: PS00941; CARBOXYLESTERASE-B_2; FALSE NEG.
 KW Hydrolyase; Serine esterase; Glycoprotein; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 564 JUVENILE HORMONE ESTERASE.
 FT ACT_SITE 220 220 BY SIMILARITY.
 FT ACT_SITE 351 351 BY SIMILARITY.
 FT ACT_SITE 465 465 BY SIMILARITY.
 FT DISULFID 89 109 BY SIMILARITY.
 FT CARBOHYD 81 81 N-LINKED (GLCNAc. . .) (POTENTIAL).
 FT CARBOHYD 180 180 N-LINKED (GLCNAc. . .) (POTENTIAL).
 FT CARBOHYD 402 402 N-LINKED (GLCNAc. . .) (POTENTIAL).
 FT CARBOHYD 515 515 N-LINKED (GLCNAc. . .) (POTENTIAL).
 FT VARIANT 29 29 V->L.
 FT VARIANT 52 52 F->P.
 SQ SEQUENCE 564 AA; 62614 MW; D1405DD91914E8D CRC64;

Query Match 19.7%; Score 600.5; DB 1; Length 564;
 Best Local Similarity 32.0%; Pred. No. 1e-38;
 Matches 166; Conservative 97; Mismatches 210; Indels 45; Gaps 19;

29 TNEQOIT-DTEGQIKGVKRMVYDSDSYSESPYAKPVGELRFAKQRPVMEGVRD 87
 DB 23 TNSRSVVAHLDSGLIRGVR-SADGIRKASPLGVPAKQRPVMEGVRD 81
 88 CCGPANKRSVQTFISGKPTG-----SEDCLYLVNT-----TNDLPDKRRPVWF 132
 DB 82 ATNBSGPTCFDVLXGRMAASENSEACTIVANIHVPMOSLPRVGRTPPL-----RPLTVE 136
 133 IHGGDFIFGEANRMWFGPDYPMKPPVLTVOYRVLGVLFSKSENANVGNAGIKDOV 192
 DB 137 IHGGFATGSGHEDLHGEVLTATKNVITFTNYNLNFGELSNMT--TKIPGNAGLRDOV 194
 193 MALRWVKSNIATIFGGVDNITVFESGASGASTHYMITEDTGLFRGIMSGNSMCNAST 252
 DB 195 TLLRWVGRNMAKNFGGSDSDITINQSGASAAHLLTSKATEGIFKRAILMSGHGYFF 254
 253 STEQCSRAITWAKRVKYGK--EDNEKDLLEFLMKANPYDLKEBPQVLTPEKQKVMF 310
 DB 255 TTSLFLFAAISKOLQTLGINTEDPEITHQDLIDL-PAELNANNAVL-----TEQIGLTV 309
 311 FGPVPE-PYQTADCVVPKPIREWVKSAMGNSIPTLIGNTSYGLSKSVAKQYPEVKELE 369
 DB 310 FLPIVESPLPGVTTIIDDEPEILAEGRKNVPLDGLGTSSECEFRNNRLNLDVKKIQ 369
 370 ESCVNVYPMELADSEKAPETL-ERAAIVKAVDGETPLDNFMELCSFYFLPMHFR 428
 DB 370 DNPITIIIPKLL--FMPPELMELEAKTIERKYYNG-TISIDNFVKSCDGFEYPAKRL 426
 429 LQLEFNHTAGTPIYLVFDDSEELNIPYIMRGVGVSHADELTFLFNNILSKRL 487
 DB 427 AKRR-AETGAPLILYRFAIEGONSITK-KVM--GLNHEGVGHIEDLYVFNVSSEAL 482

QY 488 ---PRESREKTYEMVGIWTEPATGKPYNSDIAGME 522
 DB 483 HASPSEN-DYMKMLMTCYFLNFKICSPCEDNNSLE 519

RESULT 3

PNBA_BACSU STANDARD; PRT: 489 AA.

AC P37967; 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Para-nitrobenzyl esterase (EC 3.1.1.-) (PNB carboxy-esterase) (PNCE).
 GN PNBA.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-22 AND 211-223.
 RC STRAIN-NRRL B8079;
 RX MEDLINE=95129891; PubMed=7828905;
 RA Zock J., Cantwell C., Swartling J., Hodges R., Pohl T., Sutton K.,
 RA Rostock P., Jr., McGillivray D., Queener S.;
 RT "The Bacillus subtilis pnbA gene encoding p-nitrobenzyl esterase;
 RT cloning, sequence and high-level expression in *Escherichia coli*.";
 RL Gene 151:37-43(1994).
 RN [2]
 RP SEQUENCE OF 1-22 AND 211-223, AND CHARACTERIZATION.
 RA Chen Y.-R., Usui S., Yu C.-A.;
 RT "Purification and properties of p-nitrobenzyl esterase from *Bacillus*
 RT subtilis.";
 RL FASEB J. 6:A332-A332(1991).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
 RX MEDLINE=20006229; PubMed=1035917;
 RA Spiller B., Gershenson A., Arnold F.H., Stevens R.C.;
 RT "A structural view of evolutionary divergence.";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:12305-12310(1999).
 CC -1- FUNCTION: CATALYZES HYDROLYSIS OF SEVERAL BETA-LACTAM ANTIBIOTIC
 CC -1- PNB ESTERS TO THE CORRESPONDING FREE ACID AND PNB ALCOHOL.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL-ESTERASE/LIPASE FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC -----
 CC EMBL: 006089; AAA61915.1; -;
 DR PDB: 1C7J; 29-MAR-00.
 DR PDB: 1C7J; 29-MAR-00.
 DR PDB: 1OE3; 21-JUL-99.
 DR InterPro: IPR002018; Carboxylesterase.
 DR InterPro: IPR000379; Ser-estrs-site.
 DR Pfam: PF00135; Coesterase_1.
 DR PROSITE: PS00122; CARBOXYL-ESTERASE_B_1; 1.
 DR PROSITE: PS00941; CARBOXYL-ESTERASE_B_2; 1.
 KM Hydrolyase; Serine esterase; 3D-structure.
 FT ACT SITE 189
 FT ACT SITE 17
 FT CONFLICT 17
 SEQUENCE 489 AA; 53998 MW; 6966BEFEDA47269 CRC64;

Query Match 18.8%; Score 572; DB 1; Length 489;
 Best Local Similarity 30.6%; Pred. No. 1.3e-36;
 Matches 171; Conservative 89; Mismatches 203; Indels 96; Gaps 24;

QY 33 QIITEYQIKGVKRMVYDSDYSFSPISIPAKPPVGLRPAQORPVPMEGVDP----- 87
 DB 4 QIVTVOYGVKGGT-----ENGVIHKWGIPIYAKPPVGOMRKAPPEPPEWEDVIDATATG 58

QY 88 ---CCGPAANSVQTDFTS-----GKPTGSEDCIYLNVTYNDLNDPKRRPVWFIHGGDFIG 141
 DB 59 PICPQP-----SDLLSTYELTLPQSEDCIYVNVAPD-TTSQNLPAWVHIGCAFYIG 111
 QY 142 EANRNMW-GPDYPMKKRVYLVQYRGLVYGLFLSKSENINPAGNALDQVAALEWVKS 200
 DB 112 AGSEPLDYDGSKLAAGGVIVYTLNRYLGPFGFLHSSPDEAVSDNLQDQAAALAKWRE 171
 QY 201 NIAIFGGVDNITVFEGSAGASTHYMMITTEQTRGLFHRIKIMSGSKMSMASTECQSR 260
 DB 172 NISAFGSDPNVTVFEGSAGMSIALIAMPARKGLFQKAIMESGASR-TMKQQA57A 230
 QY 261 LTMARKVGYGENENKILFEIKKANPYDILKEPQVLPFERQNVMPFGPTVEPYQT 320
 DB 231 AAFLOVLGI-----NESO-LDRLTHVAEDLLKADQRLIAEK-ENIFQLFGFALDPK- 282
 QY 321 ADCVVPKPIREMYSKANGNSIPTLIGNTSYEGLSKSVAKQYDEYVKELESCVNYVPMEL 360
 DB 283 ---TLPEPEKSIAGSAGSIPLLIGTRDEGYLF-----FTP--- 317
 QY 381 ADSERSAPETTERA-----ATYKKAHVDGEPTLDNEMELCSYFLPMPHRTQLRF 433
 DB 318 -DSVHSGQETLDALELYLGLKPLAEKA-ADLYPRSLQSJHMTDLLFMRPAVYASAS 375
 QY 434 NHTAGTPYLYRPFDESEELINPYRIMRFGVGVSHADELYLFWNT--LSKRLPK- 490
 DB 376 HY-----APVWMYRFPDWHPEK--PPY-----NKAFHALELPVFGNLDGERMAKEI 421
 QY 491 SREKTYTERMV-GIWTETATGKPYNSDIAGMENULTDPIKSDYVKCINDIGELKVM 549
 DB 422 TDEVKQLSHTIQSAMIYFAKGNP-----STEAVNMPAY--HEETREYILDSLETIEN 473
 QY 550 LPENDKIKOGASIFDKKE 568
 DB 474 DPESKRK-----LPFSKGE 489

RESULT 4

ESTF_MYZPE STANDARD; PRT: 564 AA.

AC P35502; 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE Esterase FE4 precursor (EC 3.1.1.1) (Carboxylic-ester hydrolase).
 OS Myzus persicae (Peach-potato aphid).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha;
 OC Aphidiformes; Aphidoidea; Aphididae; Macrosiphini; Myzus.
 OX NCBI_TaxID=13164;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 24-63.
 RC STRAIN=ISOLATE 800F;
 RX MEDLINE=93384534; PubMed=8373371;
 RA Field L.M., Williamson M.S., Moores G.D., Devonshire A.L.;
 RT "Cloning and analysis of the esterase genes conferring insecticide
 RT resistance in the peach-potato aphid, *Myzus persicae* (Sulzer).";
 RL Biochem. J. 294:569-574(1993).
 CC -1- FUNCTION: OVERPRODUCTION OF NONSPECIFIC ESTERASES IS A COMMON
 CC MECHANISM OF RESISTANCE TO ORGANOPHOSPHATE INSECTICIDES.
 CC -1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
 CC carboxylic anion.
 CC -1- MISCELLANEOUS: THIS ESTERASE CONFERS INSECTICIDE RESISTANCE.
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL-ESTERASE/LIPASE FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

ID	ESTD_MYZPE	STANDARD;	PRT;	552 AA.
AC	P35501;			

```

QY 182 VPGNGLKDQVMAALRWKSNIAIFGSDVDNITFEGSAGASTHMMITEQTLRGLEHRI 241
  || ||||| ||::: || ||| :::: || || : || : || : ||::|::|

```

Db 180 --GNNGKQVAAALKWIOQIVAFGDPNSVITGMSAGASSVHNHLSIPSKGLFNRAI 237
 QY 242 MMSGNSMCASTECOSRALIMAKRYGKGE-----DNEKDILEFLMKANPYDLIKEEP 295
 Db 238 IQSSSACCHWSTAE-----NVAOKTKYIANLMGCPINNSEIYECL-RSPAPAKIKSY 290
 QY 296 QVLTPEKQKVMPEPGTYE--DYGTADCVVPRPIREMYKSAMGNSIPTLIGNTSEGL 353
 Db 291 LNFMPWR--NEPTPEFGTVEAGYE-----KFLPDIPKELVPHDIPVLISIAQDEGL 341
 QY 354 LSKSVANQYPPVVELSCVN--VYPWELADSEBAPETL--ERAIYKKAHVDETP--- 407
 Db 342 IF-STFGLGENFELNNMNEHPLHLDNYTTISNENLRKTKODIKEFYF-GDKDISK 399
 QY 408 -TLDNFELCSYFYLFPFMRHFLQLRFNHAG--TPYLYRFPDSESEIINPYRIMRF- 462
 Db 400 ETKNLSMISIDRSFGYGTSKAAQ-----HIAAKTAPVYEFEGYSGN-----YSYAF 450
 QY 463 -----GRGVKGVSHADELYL-----FWNLISKRLPKESREYKTIERWVGITWTEFATGK 512
 Db 451 DPKSYSG-SSEPTHGDETSYVLKMDGFY-----VYDNEEDRKMKIKTMVIMATFIKSGV 503
 QY 513 PYSNDIAGMELTWDPRIKS 532
 Db 504 P---DTENSE--TWLPVSKN 518

RESULT 6
 ESTL_MESAU
 ID ESTL_MESAU STANDARD; PRT; 561 AA.
 AC 06419;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Liver carboxylesterase precursor (EC 3.1.1.1).
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Syrian golden; TISSUE-Liver;
 RX MEDLINE=94318665; PubMed=8043605;
 RA Sone T., Isebe M., Takabatake E., Wang C.Y.;
 RT Cloning and sequence analysis of a hamster liver cDNA encoding a
 RT novel putative carboxylesterase.";
 RL Biochim. Biophys. Acta 1207:138-142(1994).
 CC -1- FUNCTION: INVOLVED IN THE DETOXIFICATION OF XENOBIOTICS AND IN
 CC THE ACTIVATION OF ESTER AND AMIDE PRODRUGS.
 CC -1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
 CC carboxylic anion.
 CC -1- SUBCELLULAR LOCATION: Microsomal membrane, lumen of endoplasmic
 CC reticulum.
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 CC
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC at the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: D28566; BAA05913.1; -
 DR HSSP: P37967; 10E3.
 DR InterPro: IPR002018; CarbesteraseB.
 DR InterPro: IPR000379; Ser_estr_site.
 DR Pfam: PF00135; Coesterase_1.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
 DR Glycoprotein; Hydrolase; Serine esterase; Endoplasmic reticulum;
 KW Signal; Multigene family.

FT SIGNAL 1 27
 FT CHAIN 28 561
 FT ACT_SITE 227 227
 FT ACT_SITE 459 459
 FT DISULFID 95 122
 FT DISULFID 280 291
 FT SITE 558 561
 FT CARBOHYD 276 276
 FT CARBOHYD 362 362
 SO SEQUENCE 561 AA; 62330 MW; 48BA11E422475321 CRC64;

Query Match 17.8%; Score 542; DB 1; Length 561;
 Best Local Similarity 30.4%; Pred. No. 3, 2e-34;
 Matches 173; Conservative 87; Mismatches 204; Indels 106; Gaps 25;

QY 34 IIDTEYGOIKGVKRMVYD--DSYSEFSEIPAKPVGGLRKAQRPVPMGVDCCGP 91
 Db 33 IRNTHRGQVKG-KLVYKKEGTVGVAFGLIPAKPVGGLRPAPEPPEPMGVDGTSE 91
 QY 92 ANRSVOTDFISCK-----PT--GSEDCYLANYT-NDINPDKRPVAVFIHGDPFI 139
 Db 92 PAMCLOTDFMRPQISKERKILPTISMSBCLXNTYTAHAHESGNLPVWVHIGGALV 151
 QY 140 FGEANRMFGPDYEMKKPVVLYTVQYRLGVGLSLKSENLVNPGAGLKDQVALLRWYK 199
 Db 152 MGNASMN-DGSLLAATEDIVIVSIQYRLGILGFSTGDEHAR--GNMGYLDQVAAALHWQ 208
 QY 200 SNAIFGSDVDNTVFGESAGASTHYMMITDQRLGFRHGMGNSMCASTECOSR 259
 Db 209 QNTASFQNGOYTTIFGVSAGGTSSVSLVSPSKGLFAGLMOGVALPDLIDTPBA 268
 QY 260 ALT--MAKRVYKGEEDNEKDIIEFLKANKPYDLIKEEPVLTPEKQKVMPEPGTYEP 317
 Db 269 VYTPVAVNAGSCGCAKSKSEK-LVHCLRE-----KTEAFILA--INQVFI--MTP 311
 QY 318 YGTADCVVPRPIREMYKSAMGNSIPTLIGNTSE-----GL--LSKSYAKO-YPEV 365
 Db 312 GVVDGIFELFRHPELQSLASVDLPHVPISIIIGVDSQCGVGLPMGLDHYIKNITRETLPAF 371
 QY 366 VKLESCVNVVPELAD-----SRSAPETLERALYKKAHVGEPTLDNEFELCSY 418
 Db 372 LKSRAEHM-MLRPECSDLLMOEYMGVEDPOTQA-----QFRELKMD 413
 QY 419 FYELFPMHREFLQLRFNHAGTPYLYRFPDSESEIIN--PYRIMRFGYKGVSHADE 474
 Db 414 FMYVITA--LKAYQRSHAPVYEFYFQHOSSFLKNKARSHYR-----ADHGDH 462
 QY 475 LTYL-----FWNLISKRLPKESREYKTIERWVGITWTEFATGKPYNDIAGMELTWDPRIK 530
 Db 463 VAFVFGSDPWGL--KIDLTBEKLLNKRMMKYWAFRAGNPN-----EGLPYWPEL 513
 QY 531 KSDDYKCLNT-----GDELKVDLPEMDKI 556
 Db 514 VHDQYLLKLDIOPAVGRLKSKRLHFWTKI 543

RESULT 7
 BAL_BOVIN
 ID BAL_BOVIN STANDARD; PRT; 597 AA.
 AC P30122;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Bile-salt-activated lipase precursor (EC 3.1.1.3) (EC 3.1.1.13) (BAL
 DE (bile-salt-stimulated lipase) (BSSL) (Carboxyl ester lipase) (Sterol
 DE esterase) (Cholesterol esterase) (Pancreatic lysophospholipase)
 DE (Fragmen).
 DE CEL.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 NCBI_TaxID=9913;

RN [1] SEQUENCE FROM N.A.
 RX MEDLINE-90073663; PubMed-2590203;
 RA Kyger E.M., Wiegand R.C., Lange L.G.;
 RT "Cloning of the bovine pancreatic cholesterol
 RT esterase/lysophospholipase.";
 RL Biochem. Biophys. Res. Commun. 164:1302-1309(1989).
 RN [2]
 RP SEQUENCE OF 19-40.
 RC TISSUE-Pancreas;
 RX MEDLINE-99238708; PubMed-10220579;
 RA Tanaka H., Mierau I., Ito F.;
 RT "Purification and characterization of bovine pancreatic bile salt-
 RT activated lipase.";
 RL J. Biochem. 125:883-890(1999).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 19-565, AND REVISION TO 45.
 RX MEDLINE-97473004; PubMed-9331420;
 RA Wang X., Wang C.S., Tang J., Dyda F., Zhang X.C.;
 RT "The crystal structure of bovine bile salt activated lipase: insights
 RT into the bile salt activation mechanism.";
 RL structure 5:1209-1218(1997).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS) OF 19-597.
 RX MEDLINE-98215635; PubMed-9548741;
 RA Chen J.C.-H., Miercke L.J.W., Krucinski J., Starr J.R., Saenz G.,
 RA Wang X., Spilburg C.A., Lange L.G., Ellsworth J.L., Stroud R.M.;
 RT "Structure of bovine pancreatic cholesterol esterase at 1.6 A: novel
 RT structural features involved in lipase activation.";
 RL Biochemistry 37:5107-5117(1998).
 CC -1- FUNCTION: CATALYZES FAT AND VITAMIN ABSORPTION. ACTS IN CONCERT
 CC WITH PANCREATIC LIPASE AND COLIPASE FOR THE COMPLETE DIGESTION
 CC OF DIETARY TRIGLYCERIDES.
 CC -1- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a
 CC fatty acid anion.
 CC -1- CATALYTIC ACTIVITY: A sterol ester + H(2)O = a sterol + a fatty
 CC acid.
 CC -1- ENZYME REGULATION: ACTIVATED BY BILE SALTS CONTAINING A 7-HYDROXYL
 CC GROUP IN THE INFANTS INTESTINE WHERE IT AIDS TO DIGEST MILK FATS.
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL, M28402; AAA56788.1; -;
 DR EMBL; A33668; A33668.
 DR PDB; 1AKN; 27-MAY-98.
 DR PDB; 1AOL; 05-AUG-98.
 DR PDB; 2BCE; 23-MAR-99.
 DR InterPro; IPR002018; Carboxylesterase.
 DR InterPro; IPR000379; Ser-esterase.
 DR Pfam; PF00135; Coesterase; 1.
 DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
 KW Hydrolyase; Serine esterase; Lipid degradation; Glycoprotein; Signal;
 KW 3D-structure.
 FT NON_TER 1
 FT SIGNAL <1 18
 FT CHAIN 19 597
 FT ACT_SITE 212 212
 FT ACT_SITE 338 338
 FT ACT_SITE 455 455
 FT DISULFID 82 98
 FT DISULFID 264 275
 FT CARBOHYD 205 205
 FT CARBOHYD 379 379
 FT CONFLICT 30 30
 FT CONFLICT 45 45
 FT I -> V (IN REF. 1).
 FT N-LINKED (GLCNAC. . .)
 FT N-LINKED (GLCNAC. . .)
 FT F -> P (IN REF. 2).
 FT I -> V (IN REF. 1).

SEQUENCE 597 AA: 65161 MW: B23E7AED90EBFD1 CRC64;
 Query Match 17.2%; Score 523; DB 1; Length 597;
 Best Local Similarity 30.1%; Pred. No. 1e-37;
 Matches 167; Conservative 67; Mismatches 211; Indels 109; Gaps 22;
 QY 37 TEYGOIKGV-KRMVTYVDDSYSEFESIPYAKPVGELRFAPQRPVWEGVRCOCGPANRS 95
 DB 26 TEGGFVEGVNKKLSLEGDSIDIFKGIPIFAAPKA--LEKPRHPOWGTLLAKSPKRC 82
 QY 96 VOTDFISGKPTSEDCLYNTVNDINPKR-----PVWPIFGDIFGE----- 142
 DB 83 LGATLTQDSTYGENDCLYLNW---PGKREVSHDLEVMITVYGATLMAKASOGANFL 138
 QY 143 ANRNEGPDYFMKRPVLTVOYRLGLGFLSLKSENLVNPGNAGLKDQVMAIWRKNSI 202
 DB 139 SNLYDGEIATRGVIVTFTNRVGPLOFLSTGDSNL--PGNYGLMDHMLAWKRI 196
 QY 203 AIFGGDVNITVFGESAGASTHYMMITBOTRLPHRIGMSGNSMCSNASTECORALT 262
 DB 197 EAFGGDPNITLFGESAGASVSLQTLSPYKGLIKRAISQGVGLCPWA---IQDDPLF 253
 QY 263 MAKR-----VGYGDENEKILFELMKANPYDLKEBPVLTFERMKNKMPFGPT---- 314
 DB 254 WAKRIAEKVCVDDTSK--MGCLKIT-----DPRALT--LAVKL--PLGSTERYK 299
 QY 315 -----VEPYOTADCVVPKPIREWKSA-----WGSNIPILIGNSYEGL 353
 DB 300 IYLSFVPIDDDFIPDDVNLNANADVDYIAGTNDMGHLFVGVDVAL--NSNKQDV 357
 QY 354 LSKSAKQYP--EVKLESC-----VNVPWELADSESAPELRAIVKKAHVDGET 406
 DB 358 TEDEFYKLVSGLVITGGLGANATVEVTEPW---AODSOETR-----KKTWDLDT 407
 QY 407 PRLDNMELCSYFELFPMHRLQLRFNHTAGPIYLYFEDESEELINPYRIMRGRGV 466
 DB 408 DIL-----FLIPKIAVOHSHAKSANITYILFSPDSRPPIPKM----- 449
 QY 467 KGVSHADELYLEWNLISRLKPRESEYKTERMGVWTEFATGKPYSDIAGMENLW 526
 DB 450 -GADHADLDQYVGKPFAPPLGVRADRTVSKAMIMVMTNFATGDPNTHGSTVPAN--W 506
 QY 527 DPKKSDVYKCLN 540
 DB 507 DPTLEDVYLEIN 520
 RESULT 8
 CHIE HORSE
 AC CHIE HORSE STANDARD; PRT: 574 AA.
 ID P81908;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cholinesterase (EC 3.1.1.8) (Acylcholine acylhydrolase) (Choline
 DE esterase II) (Butyrylcholine esterase) (Pseudocholinesterase) (EO-
 DE BChE).
 GN GN
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OC NCBI_TaxID=9796;
 RN (1)
 RP SEQUENCE.
 RC TISSUE=Plasma;
 RA Moorad D.R., Luo C., Garcia G.E., Doctor B.P.;
 RT "Amino acid sequence of horse serum butyrylcholinesterase.";
 RL (In) Doctor B.P., Taylor P., Quinn D.M., Kotundo R.L., Gentry M.K.
 RL (eds.);
 RL structure and function of cholinesterases and related proteins,
 RL pp.145-146, Plenum Press, New York and London (1998).
 CC -1- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a
 CC carboxylic acid anion.

CC -1- SUBUNIT: HOMOTETRAMER. THE TETRAMER IS COMPOSED OF TWO DIMERS. THE
CC TWO SUBUNITS IN A DIMER ARE LINKED BY A DISULFIDE BOND.
CC -1- TISSUE SPECIFICITY: PRESENT IN MOST CELLS EXCEPT ERYTHROCYTES.
CC -1- MISCELLANEOUS: CHOLINESTERASE IS HIGHLY REACTIVE WITH
CC ORGANOPHOSPHATE ESTERS.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
CC HSPSP, p21836; IMAA.
DR InterPro: IPR002018; Carboxylesterase.
DR InterPro: IPR000997; Cholinesterase.
DR InterPro: IPR000379; Ser_esterase.
DR Pfam: PF00135; Coesterase, 1.
DR PRINTS: PR00878; CHOLNESTRASE.
DR PROSITE: PS00122; CARBOXYLESTERASE_B.1; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B.2; 1.
DR Hydrolyase; Serine esterase; Glycoprotein.
KW ACT_SITE 198 198 BY SIMILARITY.
FT ACT_SITE 198 198 BY SIMILARITY.
FT ACT_SITE 325 325 BY SIMILARITY.
FT ACT_SITE 438 438 BY SIMILARITY.
FT DISULFID 65 92 BY SIMILARITY.
FT DISULFID 252 263 BY SIMILARITY.
FT DISULFID 400 519 BY SIMILARITY.
FT DISULFID 571 571 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .).
FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .).
FT CARBOHYD 256 256 N-LINKED (GLCNAC. . .).
FT CARBOHYD 341 341 N-LINKED (GLCNAC. . .).
FT CARBOHYD 455 455 N-LINKED (GLCNAC. . .).
FT CARBOHYD 481 481 N-LINKED (GLCNAC. . .).
FT CARBOHYD 486 486 N-LINKED (GLCNAC. . .).
SQ SEQUENCE 574 AA; 65641 MW; 07755E9FB9CB3E CMC64;

Query Match 17.1%; Score 520.5; DB 1; Length 574;
Best local similarity 29.9%; Pred. No. 1.5e-32;
Matches 165; Conservative 97; Mismatches 200; Indels 89; Gaps 24;

QY 31 ETGIDTEKQIKGVKRMVYDDSYTSFESITPAKPVGELFKAPORPRVMEGVDCGG 90
DB 2 EDIIITTKNGKVG-NLPLVGLGTVAFLGIPAPDLRLFKPKFOSITLTKSNINWTK 60
QY 91 PARSVO-TD-----FISGKPTG-----SEDCILYLVNTINDIPDKRREPVNFHIGDPI 139
DB 61 YANSCTYNTOSPPGFLGSPMNPNTLESDCLYLVNWIAPKRP-KNATVMTIIVGSGGFEQ 119
QY 140 FGEANRMWFGPDYEMK-KPVYLVTVORYGVLGFLSKSENLVNPNGNAGLKDOVALRMV 198
DB 120 TGTSSLPVYDGKFLARVERIVVSMNRYVAGLGFAL-SENPEAPENMGLPDQOLALQNV 178
QY 199 KSNIAFGSDVNTITVGSAGSASTHYMTETOTRGLFHRGIMSGNCSMAST--E 255
DB 179 QKNTAAGGNRSYTLGEGSAGASVSLHLSRSPQLFTRALLOGSSNAPWAVTSIYE 238
QY 256 COSPALTMARVGVKGEDEKDLIEFLMKANPYDLIKEEQVUTPERMONKVVFPFGPIV 315
DB 239 ARNRTLLAKMGC-SRDNETEMIKLRDKDPOEIIINEVAVPYDTL--LSVNFQPIV 294
QY 316 EPIYQACVYKPIREWKSAMGNSIPTLIGNTSYEGL-----LSKS-----VARQ 361
DB 295 D-----GDFLTPMP-DTLIQLOQFKRTQIIVGVNDEGTALVYGAPFSKDNNSITTRKE 349
QY 362 YPEVVKEL-----ESCV-NYVPELADSEKSAPELEKRAIVYKKAHVDDEFTLQV 411
DB 356 FQEGKLIFFPRVSEFGRSILFHYMDW-LDD-----QRAENVREALDD--VQGD 395
QY 412 FHELCSTYFLEFPMHREFLOLRFNHTAGPIYLYRFDFDESEIINPYIMFEGRGVGVSH 471
DB 396 YNITCPALFE--TRKSEL-----GNDAFYFIEHNSITLPPPEMW-----GVMH 438
QY 472 ADELTYLEFNNILSKRLPRESREKTIERRVGIWTEPATGSPYISNDIAGEN--LTMDPI 529
DB 439 GYEIEVEVFLPERRVNTABEILSRIMKRWANFAKYNP-----NGTQNNSTAMPVF 493
QY 530 KRSDDVYKCLN 540

DB 494 KSTQKYLITLN 504
RESULT 9
ID CHLE_HUMAN STANDARD; PRT; 602 AA.
AC P06276;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cholinesterase precursor (EC 3.1.1.8) (Acylcholine acylhydrolase)
DE (Choline esterase II) (Butyrylcholine esterase)
DE (Pseudocholinesterase).
GN BCHF OR CHEL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=90212557; PubMed=2322535;
RA Arpegaus M., Kott M., Vatsis K.P., Bartels C.F., Ia Du B.N.,
RT "Structure of the gene for human butyrylcholinesterase. Evidence for
RL a single copy.";
RN Biochemistry 29:124-131(1990).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=retal;
RA MEDLINE=87231856; PubMed=3035536;
RX Prody C.A., Zevin-Sonkin D., Gnatt A., Goldberg O., Soreg H.,
RT "Isolation and characterization of full-length cDNA clones coding for
RL cholinesterase from fetal human tissues.";
RN Proc. Natl. Acad. Sci. U.S.A. 84:3555-3559(1987).
[3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA MEDLINE=88016155; PubMed=3477799;
RX McTierman C., Adkins S., Chatonnet A., Vaughan T.A., Bartels C.F.,
RT Kott M., Rosenberry T.L., Ia Du B.N., Lockridge O.,
RL "Brain cDNA clone for human cholinesterase.";
RN Proc. Natl. Acad. Sci. U.S.A. 84:6682-6686(1987).
[4]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.
[5]
RP SEQUENCE OF 29-602.
RC TISSUE=Plasma;
RA MEDLINE=87109144; PubMed=3542989;
RX Lockridge O., Bartels C.F., Vaughan T.A., Wong C.K., Norton S.E.,
RT Johnson L.L.;
RL "Complete amino acid sequence of human serum cholinesterase.";
RN J. Biol. Chem. 262:549-557(1987).
[6]
RP DISULFIDE BONDS.
RA MEDLINE=88007487; PubMed=3115973;
RX Lockridge O., Adkins S., Ia Du B.N.;
RL "Location of disulfide bonds within the sequence of human serum
RN cholinesterase.";
RN J. Biol. Chem. 262:12945-12952(1987).
[7]
RP REVIEW.
RA MEDLINE=89149758; PubMed=3067729;
RX Lockridge O.;
RL "Structure of human serum cholinesterase.";
RN Bioessays 9:125-128(1988).
[8]
RP VARIANT ATYPICAL GLY-98.
RA MEDLINE=89128896; PubMed=2915989;
RX McGuire M.C., Nogueira C.P., Bartels C.F., Lightstone H., Hajra A.,
RA

[illegible]

DE Acetylcholinesterase precursor (EC 3.1.1.7) (ACHE).
 GN ACHE.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP MEDLINE=90380429; PubMed=2400605;
 RA Rechinsky T.L., Camp S., Li Y., Ekstrom T.J., Newton M., Taylor P.;
 RT "Molecular cloning of mouse acetylcholinesterase: tissue distribution
 of alternatively spliced mRNA species.";
 RT Neuron 5:317-327(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SV;
 RX MEDLINE=21138439; PubMed=11239002;
 RA Wilson M.D., Riemer C., Martindale D.W., Schnupf P., Boright A.P.,
 RA Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Tsui L.-C.,
 RA Miller W., Koop B.F.;
 RT "Comparative analysis of the gene-dense ACHE/TFR2 region on human
 RT chromosome 7q22 with the orthologous region on mouse chromosome 5.";
 RT Nucleic Acids Res. 29:1352-1365(2001).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS) OF COMPLEX WITH FASCICULIN.
 RX MEDLINE=96067648; PubMed=8521480;
 RA Bourne Y., Taylor P., Marchot P.;
 RT "Acetylcholinesterase inhibition by fasciculin: crystal structure of
 RT the complex.";
 RT Cell 83:503-512(1995).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE=99115643; PubMed=9915834;
 RA Bourne Y., Taylor P., Bougis P.E., Marchot P.;
 RT "Crystal structure of mouse acetylcholinesterase. A peripheral site-
 RT occluding loop in a tetrameric assembly.";
 RT J. Biol. Chem. 274:2963-2970(1999).
 RN [5]
 RP FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.
 CC -1 CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
 CC -1 SUBUNIT: ISOFORM H GENERATES GPI-ANCHORED DIMERS, DISULFIDE
 CC LINKED. ISOFORM T GENERATES MULTIPLE STRUCTURES, RANGING FROM
 CC MONOMERS AND DIMERS TO COLLAGEN-TAILED AND HYDROPHOBIC-TAILED
 CC FORMS, IN WHICH CATALYTIC TETRAMERS ARE ASSOCIATED WITH ANCHORING
 CC PROTEINS THAT ATTACH THEM TO THE BASAL LAMINA OR TO CELL
 CC MEMBRANES. IN THE COLLAGEN-TAILED FORMS, ISOFORM T SUBUNITS ARE
 CC ASSOCIATED WITH A SPECIFIC COLLAGEN COLO. WHICH TRIGGERS THE
 CC FORMATION OF ISOFORM T TETRAMERS, FROM MONOMERS AND DIMERS (BY
 CC SIMILARITY).
 CC -1 ALTERNATIVE PRODUCTS: 2 ISOFORMS; H AND T (SHOWN HERE); MAY BE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1 TISSUE SPECIFICITY: PREDOMINATES IN MOST EXPRESSING TISSUES
 CC EXCEPT ERYTHROCYTES WHERE A GLYCOPHOSPHOLIPID-ATTACHED FORM OF
 CC ACHE PREDOMINATES.
 CC -1 MISCELLANEOUS: SYNAPSES USUALLY CONTAIN ASYMMETRIC MOLECULES OF
 CC CHOLINESTERASE, WITH A COLLAGEN-LIKE PART DISULFIDE-BONDED TO THE
 CC CATALYTIC PART. A DIFFERENT, GLOBULAR TYPE OF CHOLINESTERASE
 CC OCCURS ON THE OUTER SURFACES OF CELL MEMBRANES, INCLUDING THOSE OF
 CC ERYTHROCYTES.
 CC -1 MISCELLANEOUS: THIS IS THE CATALYTIC SUBUNIT OF AN ASYMMETRIC OR
 CC SOLUBLE FORM OF ACHE.
 CC -1 SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC EMBL: X56518; CA39967.1; -
 CC EMBL: AF312033; AKK28816.1; -
 CC PIR: JH0314; JH0314.

PDB: 1MAH; 03-APR-96.
 DR PDB: 1MAA; 20-APR-99.
 DR MGD: MGI:87876; Ache.
 DR InterPro: IPR002018; Carboxylase.
 DR InterPro: IPR000997; Cholinesterase.
 DR InterPro: IPR000379; Ser-estrs-site.
 DR Pfam: PF00135; Coesterase; 1.
 DR PRINTS: PR00878; CHOLINESTERASE.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE: PS00941; CARBOXYLESTERASE_D_2; 1.
 DR Hydroxylase; Serine esterase; Synapse; Membrane; Nerve; Muscle; Signal;
 KW Neurotransmitter degradation; Glycoprotein; Alternative splicing;
 KW 3d-structure.
 FT SIGNAL 1 31
 FT CHAIN 32 614 ACETYLCHOLINESTERASE.
 FT ACT_SITE 234 234
 FT ACT_SITE 365 365
 FT ACT_SITE 478 478
 FT DISULFID 100 127
 FT DISULFID 288 303
 FT DISULFID 440 560
 FT DISULFID 611 611
 FT CARBOHYD 266 266 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 381 381 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 495 495 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 614 AA; 68168 MW; 66E2512463C21172 CRC64;
 Query Match 16.9%; Score 515.5; DB 1; Length 614;
 Best local Similarity 30.2%; Pred. No. 4,1e-32;
 Matches 159; Conservative 81; Mismatches 236; Indels 51; Gaps 17;
 QY 40 GQIKGVKRMVYDDSYSEFISPIYAKPPVGLFKAPQRPVMEGVGDCGGRANSVQ-- 97
 DB 46 GQIRGI-RLKAPGPGVSAFLGIPFAPVPSRRFMPPEPPKRGVLDATFQNCYGV 104
 QY 98 -----TDFISGKPTGSEDDLYLVYNDLPKRRPVMTFNGGPFCEANRMF 148
 DB 105 DTLVPGEGTEEMNPNRSESDCLYLVWTPYPRPASPPVLWTWIGGGYSCANSLDY 164
 QY 149 GPDVPMK-KPVVLTVOYRGLVGLFLSKSENLTNPGNAGLKDQVALRMVNSIAIFG 207
 DB 165 DGRFAOVGAVLVSMYRVGTGFLALPSR-EARGNGLDRLALQWQENIAFG 223
 QY 208 DVDNITVFGSAGASTHYMTTEQRTGLFRGIMNSGMSWAST--ECOSRALYMA 264
 DB 224 DPMVLTGFSAGASGMHILSLPSRSLFRVALOSGTGPGWATVVSAGEARRATLLA 283
 QY 265 KRVGK---GENDKDLLEFLMKANPYDLKEEPVLTPERMGNKMPGPPVEPYQTA 321
 DB 284 RLVCGRPGAGGNDTELIACTRRPADLDVHEHVLPOEST--FRFSVPVVD----G 336
 QY 322 DCVVPKPIREVMKSAVNSIPTLIGNTSYGLLSKSAVAKYPRVVELESCVNVPMELA 381
 DB 337 DFLSDTP-EALINTGPDQDQVLYGVYKDEG--SYFLVGVGVPFSKDNESLISRAQF-LA 392
 QY 382 DSESAPELTERAALYKAKH---VGEETP--LDNFMELCSFYFLFPHRRLQLRFN 435
 DB 393 GVRIGVQASDLAAEAVLVLTDMILAPEDPTHLRDANSAAVAGDHNVCPV---AQLAGRL 449
 QY 436 TA-GTPIYIVRPFDSSEIINPYRIMRFGVGVSHADELTVFNMLIKRLPKSREY 494
 DB 450 AAGCARVAYIFERASTLTWPLM-----GVPGYTEIEPIFGLPDPSLNTYTER 501
 QY 495 KTIEMVGIWTEPATTKPYSDIAGNEMLTWPIKSSDVYKCLNT 541
 DB 502 IFAGRLMKWYNFARTGDP--NDPRDSKSPQMPYTTAAQOYSLNL 546
 RESULT 11
 CHLE_RABIT STANDARD; PRT; 581 AA.
 ID CHLE_RABIT
 AC P21927;
 DT 01-MAY-1991 (Rel. 18, Created)

Query Match 16.8%; Score 512.5; DB 1; Length 581;
 Best Local Similarity: 29.0%; Pred. No. 6.5e-32;
 Matches 165; Conservative 92; Mismatches 196; Indels 113; Gaps 26;

FT CAROHD 488 488 N-LINKED (GLICNAC. . .) (POTENTIAL).
 FT CAROHD 492 492 N-LINKED (GLICNAC. . .) (POTENTIAL).
 FT CAROHD 493 493 N-LINKED (GLICNAC. . .) (POTENTIAL).
 SQ SEQUENCE 581 AA; 66156 MW; FEB8199E7B32EB0A CRC64;

QY 26 RLSTNETOIIDTEYGOIKVRKMTYYDSYSFESIPAKPVGELREFKAPRPWEGV 85
 D 4 RSSHEDVITTKNKRIRGI-NLPVFGGHVTAFLGIPYAQPLGLRIRKPKQSLTKMSDI 62
 QY 86 -----RDCCGPANRSV-----QDFISGKPTGSDCLLYNVTYDNLDPDKR 127
 D 63 WNAITYANSCCNIDQSPFGHSGEMMNNDTL-----SDCLYLNWIPTPKP-KNA 114
 QY 128 PYWVEIHGGDFLEFGANRWFGPDYFMK-KPVLYTVQYRLGLVLGSLKSENLVNPGNA 186
 D 115 TYMIWITGGFGQTGSHSLQYVDGRKLTVERIYIVSMNRYVALGOLFALPG-NPAPGGM 173
 QY 187 GLKDQVMAALRWYKSNIALFGGVDNITVFGSAGASTHYMMITQOTGLFHRGIMSGN 246
 D 174 GLFDQALLOWQKXIAAFGGMKPSVTLFGESAGAASVSLHLSRSHPLFTFRALLOSGS 233
 QY 247 SMCSSW---ASTFCSQSRALTMKRVYKCEDNKDILFEIMKANPVDLKEEPQVLTPERM 303
 D 234 SNAPEVWMSLHARRKRTILAKFYGCSTF-NETETIKLRKNDQELILEYFVYV---F 289
 QY 304 QNRVNEPFGPEYPTQADCVVPRP-----IREWYKSAAGNSIPTLLIGNTSYEG- 353
 D 290 DLSLTVNNGPPIVD-----GDFLTDMPDITLLQGLQTKT-----QLTVGNKDEGAFIVY 339
 QY 354 -----LSKS-----VAKQYEVYVKEL-----ESCQ-NVYPWELASESAPTLERA 394
 D 340 GAFGSKNTSILITRKKEQEGIKTFPGVSERKESILFHTDW--VDEQR--PENREA 395
 QY 395 AIVKAAVHGETPLDNLNEMELCSYFFLDPNHRFLQLRPNFTAGTPIVLYRFPDSEBII 454
 D 396 -----LD-----DVAGDYNFCPALDFPK-KFEMW-GNNAFYFEHRSSKLP 436
 QY 455 NPYRIMRGRCVKVSHADELTLYLFWNLISRLKPRESENYKTIERWAGIWFEPATGKPY 514
 D 437 WPEMW-----GVMGHEYLEFVFGDLERRVNTYAEELISIRKMANFAKYGMP- 487
 QY 515 SNDIAGEN--LTWDPILKSDVYKCLN 540
 D 488 ----NGTQNNSTRMPVFEKSTEQKTYLLN 511

RESULT 12
 ACES_ELEEL
 ID ACES_ELEEL STANDARD; PRT; 633 AA.
 AC 042275;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Aethylcholinesterase precursor (EC 3.1.1.7) (ACHE).
 OS Electrophorus electricus (Electric eel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 AC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Gymnotiformes;
 OX Electrophoridae; Electrophorus.
 OX NCBI_TaxID=8005;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98070504; Pubmed=9407087;
 RA Simon S., Massoulié J.;
 RT Cloning and expression of acetylcholinesterase from Electrophorus.
 RT Splicing pattern of the 3' exons in vivo and in transfected mammalian
 cells.";
 RL J. Biol. Chem. 272:33045-33055(1997).
 CC - FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.
 CC - CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.

QY	369	LESCVNYVPEWLADERSAPET	-----	LERAIYKKAHVDEPT	-----	TLDNM	-----	EL	415
Db	368	NESLITREDF	-LQGVKNSVPHANEIGLEAVILQYTDWMDEDNPKNREADDIVGHN	Y	426				
QY	416	C-SYEFELFPMHNFLO	-----	LRNMHAG	-----	TPILYRFPDSEIIN	455		
Db	427	CPLOHFAKMAKQVSILOGQTGTA	SOQNLGNMNSSASNSGNSQVSYLLMFEDRASLW	486					
QY	456	PYRIMRFGRCVGVSHADELYLF	FWNLISKLRLPRESREKYTTERMGQITWTEPATGTG	515					
Db	487	PEWM	-----	GVLHGIEIFVGLPLEKRLANTLEBKLSRMMKYMAMFATGNPI	538				
QY	516	NDIAGMEN	-LTMWDPKRSDDVYKCLTINDELT	547					
Db	539	NVDGSDISRRRPVFTSTQKHV	INT-DLSKV	570					
RESULT 13									
ID	ESTL_CAEBR	STANDARD;	PRT;	562	AA.				
AC	Q04456;								
DT	01-OCT-1993	(Rel. 27, Created)							
DT	01-OCT-1993	(Rel. 27, Last sequence update)							
DT	15-JUN-2002	(Rel. 41, Last annotation update)							
DE	Gut esterase 1 precursor	(EC 3.1.1.1) (Non-specific carboxylesterase).							
GN	GES-1,								
OS	Caenorhabditis briggsae,								
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;								
CC	Rhabditidae; Peloderinae; Caenorhabditis.								
OX	NCBI_Taxid=6238;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RX	MEDLINE=93188021; PubMed=8445654;								
RA	Kennedy B.P., Annott E.J., Allen F.L., Chung M.A., Heschl M.F.P.,								
RT	McGhee J.D.;								
RT	"The gut esterase gene (ges-1) from the nematodes Caenorhabditis								
RL	elegans and Caenorhabditis briggsae.";								
J.	Mol. Biol. 223:890-908(1993).								
CC	-1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a								
CC	carboxylic anion.								
CC	-1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.								
CC	-1- TISSUE SPECIFICITY: EXPRESSED ONLY IN THE INTESTINE.								
CC	-1- DEVELOPMENTAL STAGE: APPEARS IN MID-PROLIFERATION PHASE WHEN								
CC	THE DEVELOPING GUT HAS FOUR TO EIGHT CELLS								
CC	-1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.								
CC	-----								
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration								
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -								
CC	the European Bioinformatics Institute. There are no restrictions on its								
CC	use by non-profit institutions as long as its content is in no way								
CC	modified and this statement is not removed. Usage by and for commercial								
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/								
CC	or send an email to license@isb-sib.ch).								
CC	-----								
DR	EMBL: M96144; AAA28056.1; -								
DR	PIR: S27782; S27782.								
DR	HSSP: P37967; IGB3.								
DR	InterPro: IPR002018; Carboxylesteraseb.								
DR	InterPro: IPR000886; ER_target.								
DR	InterPro: IPR000379; Ser_estr_s-site.								
DR	Pfam: PF00135; Coesterase; 1.								
DR	PROSITE: PS00014; ER_TARGET; 1.								
DR	PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.								
DR	PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.								
KW	Hydroxylase; Serine esterase; Signal; Endoplasmic reticulum.								
FT	SIGNAL	1	16						
FT	CHAIN	17	562						
FT	ACT_SITE	199	199						
FT	ACT_SITE	451	451						
FT	DISULFID	75	259						
FT	DISULFID	251	259						

Query Match	16.8%;	Score 512;	DB 1;	Length 562;
Best Local Similarity	28.7%;	Pred. No. 6.7e-32;		
Matches 160;	Conservative 89;	Mismatches 187;	Indels 122;	Gaps 22

QY	34	IIDTEGGLIKGVKRMVYDDSYSS	----	FESTIPYAKPPYGLERAKQAPRPVEGV	----	85
Db	19	VVNTVNGKKEGFE	-----	YGAENVLALIPFAKPPVDNIRFEKPEAPPEPDEVYQAT	-----	69
QY	86	--RDCCGPANRSV-QNDTISGKPTSGEDDLTVNVTNDLNP--	----	DKRRVWVEFHGGDFI	-----	13
Db	70	QFNDCTPHRLVAQCSYSYG	-----	EDDLTLNV	-----	12
QY	140	EGANRNMV--FGDDYFMKKRPVVLVTVQYRLGVGLSLKSENLVNPNGAGLKQDYMALRW	19			
Db	121	ISGSGOHGEFFEDRYTSQGVIVTVIQLRIGFMGFEFS	----	EGTSAPAGNVGLFDQAAALRF	17	
QY	198	VKSNIALFEGGDVNIIVTFEGESAGASTHYMTLEDTQGLFHHGIMASGNSMCNASTECQ	25			
Db	179	VKNINIEFGDDPDITIMQYSAGAASVSOLITSPYTHDYSKALIMASASFVGWAT	----		23	
QY	258	SRALIMAKRVYKGEDNEKDILEFLMKANPYDLIEEPQVILPERMQKV	----		30	
Db	235	-----GPNVITDSKOLAEIK--GCPWPGAKECKKKTILHIEIPAVETQGWITGTI	28			
QY	308	-MPPGPTVE-----PYQADCVVPRPIRENMKSANGNISPLILGNTSTEGE	----	LSK	35	
Db	283	DILRMSPVIDGDTLKRNPENLINDPIK	-----	PLIGSNKESGYFATMNGR	33	
QY	357	SVA-----KQYPEVYKLESCVNVYPMELAD	----	SERSAPTELRRAIYK	39	
Db	332	VVADGSLSPPEELPKVDEDFIS	-----	EIIDRKLNNRYGENRQKQWQDILDYTKQG	38	
QY	399	KAHVGEPTPLDNPELICSYFELFPMHRFLQLRNHTAGPIPLYLRDPFSEETIMPYR	45			
Db	385	KEERDLNGFYDVRVALLSDITTFVNPILRETTAREK--TPVWTYRDHNEQIMKY	44			
QY	459	IMRFRGVKGVSHADELTLYLFMNLISKRLLPRESERYKIER-AMGIMTEFATTKPSND	51			
Db	442	---IPEQAGKSHANEHYHLENMYPMAQIDFKKEPESWLQNDLIDMVVSFAKICVPHIQD	49			
QY	518	IAGMENLMDPKKSDOV	535			
Db	499	V-----EMRPVSPDDV	510			
RESULT 14						
ACES_TORCA						
ID	ACES_TORCA	STANDARD:	PRT:	586	AA.	
AC	P04058:					
DT	01-NOV-1986 (Rel. 03, Created)					
DT	01-JUN-1994 (Rel. 29, Last sequence update)					
DT	16-OCT-2001 (Rel. 40, Last annotation update)					
DE	Acetylcholinesterase precursor (EC 3.1.1.7) (ACHE).					
OS	Torpedo californica (Pacific electric ray).					
OC	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Chondrichthyes;					
OC	Elasmobranchii: Squalae; Hypnosqualae; Pristigastera; Batoidae;					
OC	Torpediniformes; Torpedinidae; Torpedo.					
OX	NCBI_Taxid=7787;					
RN	[1]					
RP	SEQUENCE OF 10-586 FROM N.A.					
RX	MEDLINE=86118676; Pubmed=3753747;					
RA	Schumacher M., Camp S., Maullet Y., Newton M., McPhee-Quigley K.,					
RA	Taylor S.S., Friedmann T., Taylor P.,					
RT	"Primary structure of torpedo californica acetylcholinesterase					
RT	deduced from its cDNA sequence."					
RL	Nature 319:407-409(1986).					
RN	[2]					
RP	SEQUENCE OF 1-9 FROM N.A.					
RX	MEDLINE=89066695; Pubmed=3138606;					
RA	Schumacher M.,					
RT	"Multiple messenger RNA species give rise to the structural diversity					
RT	in acetylcholinesterase."					

RL J. Biol. Chem. 263:18979-18987(1988).
 RN [3]
 RP SEQUENCE OF 552-558.
 RA MEDLINE=88087239; PubMed=3335534;
 RA Gibney G., Macphée-Quigley K., Thompson B., Vedvick T., Low M.G.,
 RA Taylor S.S., Taylor P.;
 RT "Divergence in primary structure between the molecular forms of
 RL acetylcholinesterase.";
 RL J. Biol. Chem. 263:1140-1145(1988).
 RN [4]
 RP ALTERNATIVE SPLICING.
 RA MEDLINE=90166618; PubMed=2306366;
 RA Maulet Y., Camp S., Gibney G., Raachnasky T.L., Ekstrom T.J.,
 RA Taylor P.;
 RT "Single gene encodes glycopospholipid-anchored and asymmetric
 RT acetylcholinesterase forms: alternative coding exons contain inverted
 RT repeat sequences.";
 RL Neuron 4:289-301(1990).
 RN [5]
 RP DISULFIDE BONDS.
 RA MEDLINE=87008586; PubMed=3759980;
 RA McPhee-Quigley K., Vedvick T.S., Taylor P., Taylor S.S.;
 RT "Profile of the disulfide bonds in acetylcholinesterase.";
 RL J. Biol. Chem. 261:13565-13570(1986).
 RN [6]
 RP STRUCTURE OF THE GPI-ANCHOR.
 RA MEDLINE=94079692; PubMed=8257440;
 RA Mehert A., Varon L., Silman I., Homans S.W., Ferguson M.A.;
 RT "Structure of the glycosyl-phosphatidylinositol membrane anchor of
 RT acetylcholinesterase from the electric organ of the electric fish,
 RT Torpedo californica.";
 RL Biochem. J. 296:473-479(1993).
 RN [7]
 RP GPI-ANCHOR.
 RA MEDLINE=96176849; PubMed=8597567;
 RA Bucht G., Hjalmarsson K.;
 RT "Residues in Torpedo californica acetylcholinesterase necessary for
 RT processing to a glycosyl phosphatidylinositol-anchored form.";
 RL Biochim. Biophys. Acta 1292:223-232(1996).
 RN [8]
 RP MUTAGENESIS.
 RA MEDLINE=91017542; PubMed=2217185;
 RA Gibney G., Camp S., Dionne M., McPhee-Quigley K., Taylor P.;
 RT "Mutagenesis of essential functional residues in
 RT acetylcholinesterase.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:7546-7550(1990).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
 RA MEDLINE=91343928; PubMed=1678899;
 RA Sussman J.L., Harel M., Frolow F., Oefner C., Goldman A., Tokor L.,
 RA Silman I.;
 RT "Atomic structure of acetylcholinesterase from Torpedo californica: a
 RT prototypic acetylcholine-binding protein.";
 RL Science 253:872-879(1991).
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF COMPLEX WITH FASCICULIN.
 RA MEDLINE=96363673; PubMed=8747462;
 RA Harel M., Kleywegt G.J., Ravelli R.B., Silman I., Sussman J.L.;
 RT "Crystal structure of an acetylcholinesterase-fasciculin complex:
 RT intersection of a three-fingered toxin from snake venom with its
 RT target.";
 RL Structure 3:1355-1366(1995).
 RN [11]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RA MEDLINE=97143314; PubMed=8989325;
 RA Raes M.L., Harel M., Pang Y.P., Silman I., Kozlikowski A.P.,
 RA Sussman J.L.;
 RT "Structure of acetylcholinesterase complexed with the nootropic
 RT alkaloid, (-)-lupercine A.";
 RL Nat. Struct. Biol. 4:57-63(1997).
 RN [12]
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
 RA MEDLINE=99249780; PubMed=102331521;
 RN

Query Match	Best Local Similarity	Score	DB 1	Length	566
Matches	152	Conservative	89	Mismatches	218
				Indels	76
				Gaps	18
11	16.8%;	511;	DB 1;	Length	566;
13	28.4%;	32;	Pred. No. 8.5e-		
64	89;	218;	Mismatches		
117					
176					
180					
236					
239					
293					
298					
353					
349					
398					
407					
458					
513					
503					

GenCore version 5.1.4.P5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2003, 09:09:58 ; Search time 56.8533 Seconds
(without alignments)
2065.788 Million cell updates/sec

Title: us-09-776-910-13

Perfect score: 3045
Sequence: 1 MFELKQFIRLKLCKVCWVN.....PEMDKIKQKASIFDKKELF 570

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: SPREMBL_21:*
2: sp-archaea:*
3: sp-bacteria:*
4: sp-fungi:*
5: sp-human:*
6: sp-invertebrate:*
7: sp-mammal:*
8: sp-mmc:*
9: sp-organelle:*
10: sp-phage:*
11: sp-plant:*
12: sp-rodent:*
13: sp-virus:*
14: sp-vertebrate:*
15: sp-unclassified:*
16: sp-rvirs:*
17: sp-bacteriap:*
17: sp-archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2945	96.7	570	09XZ70	09XZ70 musca domes
2	2348	77.1	570	025252	025252 lucilia cup
3	2311	75.9	572	09VIB5	09VIB5 haematobia
4	1844.5	60.6	572	09VIB5	09VIB5 drosophila
5	1835.5	60.3	556	024201	024201 drosophila
6	1330	43.7	554	09VIB0	09VIB0 drosophila
7	1312.5	43.1	555	09VIB0	09VIB0 drosophila
8	1311	42.7	572	09VIB1	09VIB1 drosophila
9	1299	42.7	572	024203	024203 drosophila
10	1298.5	42.6	567	09VIB3	09VIB3 drosophila
11	1297.5	42.6	558	024202	024202 drosophila
12	1281.5	42.1	566	0961N0	0961N0 drosophila
13	1277.5	42.0	554	09VIC2	09VIC2 drosophila
14	1267.5	41.6	556	09W243	09W243 drosophila
15	1264.5	41.5	554	024195	024195 drosophila
16	1236.5	40.6	563	09VIC3	09VIC3 drosophila

17	1235	40.5	549	024204	024204 drosophila
18	1233.5	40.5	564	09N161	09N161 drosophila
19	1223.5	40.2	553	024194	024194 drosophila
20	1217	40.0	530	0917L5	0917L5 drosophila
21	1204	39.5	542	09VIB9	09VIB9 drosophila
22	1202	39.5	542	095U30	095U30 drosophila
23	1196	39.3	542	024198	024198 drosophila
24	1186	36.7	345	09N153	09N153 drosophila
25	1164	34.3	540	08W089	08W089 culix pipie
26	1036	34.0	540	P92025	P92025 culix quing
27	1034	34.0	540	08W088	08W088 culix pipie
28	1029	33.9	540	023733	023733 culix quing
29	1021	33.8	446	09N155	09N155 drosophila
30	994	32.6	551	09VIC1	09VIC1 drosophila
31	987.5	32.4	541	09N158	09N158 drosophila
32	987.5	32.4	541	0852W5	0852W5 drosophila
33	987.5	32.4	548	024196	024196 drosophila
34	977	32.1	540	09G095	09G095 culix trita
35	959.5	31.5	540	023734	023734 culix quing
36	950.5	31.2	540	P91920	P91920 culix tarsa
37	948.5	31.1	541	024197	024197 drosophila
38	948.5	31.1	541	09VIC0	09VIC0 drosophila
39	943.5	31.1	568	023735	023735 culix quing
40	899	29.5	544	09VIB6	09VIB6 drosophila
41	893	29.3	544	09N157	09N157 drosophila
42	886.5	29.1	467	P91597	P91597 culix pipie
43	884.5	29.0	467	P91598	P91598 culix pipie
44	881.5	28.9	467	P91596	P91596 culix pipie
45	878	28.8	401	09N160	09N160 drosophila

ALIGNMENTS

RESULT 1

ID 09XZ70 PRELIMINARY: PRT: 570 AA.

AC 09XZ70;

DT 01-NOV-1999 (TREMBLrel. 12, Created)

DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)

DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

DE Carboxylesterase Mdae7 (EC 3.1.1.1).

GN MDAE7, Musca domestica (House fly).

OS Musca domestica (House fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Muscoidea; Muscidae; Musca.

OX NCBI_TaxID=7370;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=RUTGERS DIAZINON-R;

RX MEDLINE=99361228; PubMed=10451921;

RA Claudianos C., Russell R.J., Oakshott J.G.;

RT "The same amino acid substitution in orthologous esterases confers

RT organophosphate resistance on the house fly and a blowfly."

PL Insect Biochem. Mol. Biol. 29:675-686(1999).

CC -!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.

CC ENBL: AF133341; AAD29685.1; -

DR HSBP; P37967; I0E3

DR InterPro: IPR002018; Carboxylesterase.

DR InterPro: IPR000379; Ser_estrs-site.

DR Pfam: PF00135; Coesterase; 1.

DR PROSITE: PS00122; CARBOXYLESTERASE_B.1; 1.

KW Hydroxylase.

SO SEQUENCE 570 AA; 65421 MW; 08AFEBFE284003BB CRC64;

Query Match 96.7%; Score 2945; DB 5; Length 570;
Best Local Similarity 97.0%; Pred. No. 2.8e-226;
Matches 553; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY 1 MFELKQFIRLKLCKVCWVNRYRLSTNETQITIDREYQIKVKRMVYDSDSYFS 60
DB 1 MFELKQFIRLKLCKVCWVNRYRLSTNETQITIDREYQIKVKRMVYDSDSYFS 60

QY 61 IPYAKPVGELRFAKQPRVPEWEGVBDCCGPANRSVOTDFISGKSGSEDCILYNTND 120
 Db 61 IPYAKPVGELRFAKQPRVPEWEGVBDCCGPANRSVOTDFISGKSGSEDCILYNTND 120
 QY 121 LNPDKRRPVAFYFHGGDFEIGEANRNWFGPDYFMKKPVVLYVOYRLGVGLFSLKSEN 180
 Db 121 LNPDKRRPVAFYFHGGDFEIGEANRNWFGPDYFMKKPVVLYVOYRLGVGLFSLKSEN 180
 QY 181 NVPGNAGLKQVMAALRWKSNIAIFGGDVNITVEGSGAGASTHYMMTEOTRGLEFHG 240
 Db 181 NVPGNAGLKQVMAALRWKSNIAIFGGDVNITVEGSGAGASTHYMMTEOTRGLEFHG 240
 QY 241 IMMSGNSMCWASTECOSRALYMAKRVYKGEDEKDIIEFLMKANPYDLIKEEPOVLT 300
 Db 241 IMMSGNSMCWASTECOSRALYMAKRVYKGEDEKDIIEFLMKANPYDLIKEEPOVLT 300
 QY 301 ERMQNKVMEFGPTVEPYOTADCVPRPIREMYKSAMGNSIPTLIGNTSYEGLSKSVAK 360
 Db 301 ERMQNKVMEFGPTVEPYOTADCVPRPIREMYKSAMGNSIPTLIGNTSYEGLSKSVAK 360
 QY 361 QYPRVVELSCVNYVPEWELADSESAPELTERAIVKKAHYDGETPLDNMELCSYFY 420
 Db 361 QYPRVVELSCVNYVPEWELADSESAPELTERAIVKKAHYDGETPLDNMELCSYFY 420
 QY 421 FLEPMHRLQLRNHTAGPIYLYRFPDSEELINPRIMRGVKGVSADDELTYLFW 480
 Db 421 FLEPMHRLQLRNHTAGPIYLYRFPDSEELINPRIMRGVKGVSADDELTYLFW 480
 QY 481 NILSKRLPKESREYKTIERNVGIWTEFATGKPYSDIAGMENLTPWPIKSDVYKCLN 540
 Db 481 NILSKRLPKESREYKTIERNVGIWTEFATGKPYSDIAGMENLTPWPIKSDVYKCLN 540
 QY 541 IGDELKVMIDLPEMDKIKQASIFDKKKELF 570
 Db 541 IGDELKVMIDLPEMDKIKQASIFDKKKELF 570

RESULT 2
 025252 PRELIMINARY: PRT: 570 AA.
 AC 025252: 025247: PRT: 570 AA.
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update).
 DE Alpha esterase (UCAE7) (Carboxylesterase).
 GN LCAE7.
 OS Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Oestriidae; Calliphoridae; Lucilia.
 OX NCBI_TaxID=7375;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LS2;
 RA Newcomb R.D., East P.D., Russell R.J., Oakeshott J.G.;
 RL Insect Mol. Biol. 5:0-0(0).
 RT [2]
 RP SEQUENCE OF 70-181 FROM N.A.
 RC STRAIN=LS2;
 RA Newcomb R.D., East P.D., Russell R.J., Oakeshott J.G.;
 RL Insect Mol. Biol. 0:0-0(0).
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 DR EMBL: U56636; AAB67728.1; -;
 DR EMBL: U49421; AAA92012.1; -;
 DR HSSP: P37967; IOE3.
 DR InterPro: IPR002018; Carbesterase.
 DR InterPro: IPR000379; Ser.estr._site.
 DR Pfam: PF00135; Coesterase; 1.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
 KW Hydrolase.
 SQ SEQUENCE 570 AA: 65416 MW: 399D72B3A0F38FD CRC64:

Query Match 77.1%; Score 2348; DB 5; Length 570;
 Best Local Similarity 74.2%; Pred. No. 1.1e-178;
 Matches 423; Conservative 73; Mismatches 74; Indels 0; Gaps 0;

QY 1 MFLKQFIFRLKLCVCKMKNYTNVRLSTNETOIIDTEGQIKGVKRMVYDSDYSFES 60
 Db 1 MFLKQFIFRLKLCVCKMKNYTNVRLSTNETOIIDTEGQIKGVKRMVYDSDYSFES 60
 QY 61 IPYAKPVGELRFAKQPRVPEWEGVBDCCGPANRSVOTDFISGKSGSEDCILYNTND 120
 Db 61 IPYAKPVGELRFAKQPRVPEWEGVBDCCGPANRSVOTDFISGKSGSEDCILYNTND 120
 QY 121 LNPDKRRPVAFYFHGGDFEIGEANRNWFGPDYFMKKPVVLYVOYRLGVGLFSLKSEN 180
 Db 121 LNPDKRRPVAFYFHGGDFEIGEANRNWFGPDYFMKKPVVLYVOYRLGVGLFSLKSEN 180
 QY 181 NVPGNAGLKQVMAALRWKSNIAIFGGDVNITVEGSGAGASTHYMMTEOTRGLEFHG 240
 Db 181 NVPGNAGLKQVMAALRWKSNIAIFGGDVNITVEGSGAGASTHYMMTEOTRGLEFHG 240
 QY 241 IMMSGNSMCWASTECOSRALYMAKRVYKGEDEKDIIEFLMKANPYDLIKEEPOVLT 300
 Db 241 IMMSGNSMCWASTECOSRALYMAKRVYKGEDEKDIIEFLMKANPYDLIKEEPOVLT 300
 QY 301 ERMQNKVMEFGPTVEPYOTADCVPRPIREMYKSAMGNSIPTLIGNTSYEGLSKSVAK 360
 Db 301 ERMQNKVMEFGPTVEPYOTADCVPRPIREMYKSAMGNSIPTLIGNTSYEGLSKSVAK 360
 QY 361 QYPRVVELSCVNYVPEWELADSESAPELTERAIVKKAHYDGETPLDNMELCSYFY 420
 Db 361 QYPRVVELSCVNYVPEWELADSESAPELTERAIVKKAHYDGETPLDNMELCSYFY 420
 QY 421 FLEPMHRLQLRNHTAGPIYLYRFPDSEELINPRIMRGVKGVSADDELTYLFW 480
 Db 421 FLEPMHRLQLRNHTAGPIYLYRFPDSEELINPRIMRGVKGVSADDELTYLFW 480
 QY 481 NILSKRLPKESREYKTIERNVGIWTEFATGKPYSDIAGMENLTPWPIKSDVYKCLN 540
 Db 481 NILSKRLPKESREYKTIERNVGIWTEFATGKPYSDIAGMENLTPWPIKSDVYKCLN 540
 QY 541 IGDELKVMIDLPEMDKIKQASIFDKKKELF 570
 Db 541 IGDELKVMIDLPEMDKIKQASIFDKKKELF 570

RESULT 3
 09U409 PRELIMINARY: PRT: 570 AA.
 AC 09U409: 09U409: PRT: 570 AA.
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Alpha E7 esterase.
 GN AEF7.
 OS Haematobia irritans irritans.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Muscidae; Muscidae; Haematobia.
 OX NCBI_TaxID=75445;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CAMP COOLEY 4/97;
 RA MEDLINE=20445807; PubMed=10989298;
 RT Guerrero F.D.;
 RT Cloning of a horn fly cDNA, H1alpha7, encoding an esterase whose
 RT transcript concentration is elevated in diazinon-resistant flies.;
 RT Insect Biochem. Mol. Biol. 30:1107-1115(2000).
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 DR EMBL: A1139082; AAF1517.1; -;
 DR HSSP: P37967; IOE3.
 DR InterPro: IPR002018; Carbesterase.
 DR InterPro: IPR000379; Ser.estr._site.
 DR Pfam: PF00135; Coesterase; 1.

RA Adams M.G., Centurion S.E., Holt K.A., Evans C.A., Gocayne J.D.,
RA Amanalides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazaj R.G., Chame M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
RA Abdl J.F., Aggagani A., An H.-J., Andrews-Plamkoch C., Baldwin J.,
RA Ballew R.M., Besu A., Vaxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Bezos P.V., Bereman B.P., Bhendari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Days A.D., Dew I., Dietz S.C.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.S., Dunn P.,
RA Durnin K.J., Evangelista C.G., Ferraz S., Ferliera S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Gloder A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Moberly C., Morris J., Moshfati A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nollard D.R., Patel J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

00 341 MEMIALPEAYALAIWDIFIDR 361

09Y1B1
ID 09Y1B1 PRELIMINARY: PRT: 572 AA.
AC 09Y1B1:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Alpha-EST9 protein.
CN ALPHA-EST9 OR CG1128.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers J.H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernier B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brockstein P., Brotter P.,
RA Burks K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jatali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasok P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paollet J.M.,
RA Palazzolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reibert C., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svrtkars R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RT Science 287:2185-2195(2000).
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
CC EMBL: AE003671; AAF54015.1; -;
DR HSSP: P37967; 1OE3.
DR FLYBASE: FBgn0015577; alpha-Est9.
DR InterPro: IPR002018; Carboxylesterase.
DR InterPro: IPR000997; Cholinesterase.
DR InterPro: IPR000379; Ser_estrs.site.
DR Pfam: PF00135; Coesterase; 1.
DR PRINTS: PR00878; CHOLINESTERASE.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 2.
KW Hydrolase.
SQ SEQUENCE 572 AA; 65767 MW; 9138FB95713DF350 CRC64;

Query Match 43.1%; Score 1311; DB 5; Length 572;
Best Local Similarity 46.1%; Pred. No. 5.7e-96;
Matches 264; Conservative 95; Mismatches 184; Indels 30; Gaps 8;

21 KTYNRLSTNEFOIIDTEYGOIKGVKRMVYDDSYISFESIPAKPPVGLAFKAPORPV 80

DB 5 KVOORRTSEKTVAGSTTGPICKGVKRSISYGSYSFERRIFPAKPPVGLAFKAPORPE 64
QY 81 PMEGVRDCCGPNARSVQTPDISKPTGSDCLYNTYNDLNDKRRPWNVTHGGDFTF 140
DB 65 VMEVRSCTISQGRPKLQKHVEFMKDSDECLNLYTNKLYPTKPMVMWITGGGFOF 124
QY 141 GEANRMWFGDYPMKRPVVLVTVQVRLGVY-----GFLSKSENLNV 182
DB 125 GEASRECYSDYLLRELVVVISINRYLGLPTNDTDFMKKKHFNISLPGFLCLDDPELDV 184
QY 183 PGNAGLKDYVALRWKANSNIAHGGVDNITYGESAGASTHYMMITQTLGRFRGTM 242
DB 185 PGNAGLKDYVALRWKANSNIAHGGVDNITYGESAGASTHYMMITQTLGRFRGTM 244
QY 243 MSGNSMCSASTGCGSRALFMKRVGKGEDEKDLLEFLMKANPYDLIKEEPOVLTPEP 302
DB 245 MSGNTLSFMAVTVQRMKPRFLAVQAGTAGENNRDYMELKNAKSGEITKANCLDICE 304
QY 303 MONKMPFPGPTVEPYOTADCVPKPIREWKSAMGNSIPTLLIGNTSYEGLLSKSVAKOY 362
DB 305 KKERIGSFPGVIEPYTSHCVPKPIEMKPRAMSNIPILLIGVSNGLLYSETKTN 364
QY 363 PEVVKELSCVNVYPMELADSEKSAPELTERAIVKAAHVDGETPLD---NFMELCSYF 419
DB 365 PKCLNELDRCFVFWPIEL--WMDRESALCREYGDQQLQCYGGDTPSLDLTHELVQVSH 423
QY 420 YELFPMHRLQLRNHNAGPIYLYRPDPDEEITNPIRMRGVKGVSNADELTYLF 479
DB 424 YFMPPIYRVLRSQVARSAPVLYRFDPSKA-FNHLRLSCGKVRGCHDDLSYLF 482
QY 480 WNLISKRLLPESREYKTIEMVGIWTEFATYTGKPYSDNIAGMENLTW---DPIKSDVY 536
DB 483 YNLSARLKLHNTREYKIERLGVLTWTFHACGNP--NFDEQBDL-WQVPDAVAEKHOL 539
QY 537 KCLNIGDELKVMDEPKDKIKGASIFDKKEL 569
DB 540 KCLNISELKLVIDVPELKLKLWSEFP-RDEL 571
RESULT 9
024203
ID 024203 PRELIMINARY: PRT: 572 AA.
AC 024203:
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Alpha esterase.
CN ALPHA-EST9 OR AE9 OR CG1128.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC Robin C., Medveczky K.M., Russell R.J., Oakeshott J.G.;
RA J. Mol. Evol. 0:0-0(0).
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
CC EMBL: U51053; BAB01152.1; -;
DR HSSP: P37967; 1OE3.
DR FLYBASE: FBgn0015577; alpha-Est9.
DR InterPro: IPR002018; Carboxylesterase.
DR InterPro: IPR000379; Ser_estrs.site.
DR Pfam: PF00135; Coesterase; 1.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
KW Hydrolase.
SQ SEQUENCE 572 AA; 65680 MW; 37F1440F8FAD2BD8 CRC64;

Query Match 42.7%; Score 1299; DB 5; Length 572;
Best Local Similarity 45.7%; Pred. No. 5.2e-95;
Matches 262; Conservative 96; Mismatches 185; Indels 30; Gaps 8;

21 KYTNRLSTNETQIITDEYGOIKGVKRMFYDSDYSFESIPYAKPPVGLRFRKAPQRY 80
 5 KYQGRRTSTSEKVTSTYTPKIKGKRSITGSGYFSEPRFPKPPVGVGRKAKRPPRE 64
 81 PHEGVRDCCGPNRNVOTDFISGKPTGSEDLVNTVNTDNDPKRRPVWFIHGDSEIF 140
 65 VITEVRSCTSGCPKPLQTFPEWEMDSEDLVNTVNTDNDPKRRPVWFIHGDSEIF 124
 141 GEANRWEGPDYEMKPVVLTVOYRGLVY-----GELSLKSENLY 182
 125 GEASRRCYSPDYLRDEYVVISINRLOPLGTNDTMMKKHIFNISLDPGLCLDPELDV 184
 183 PGAGAGKDOVMAIRWYKSNIAIFGGDVNITVYFGEAGASTHYMMITQTRGLFHRCIM 242
 185 PGAGAGKDOVMAIRWYKSNIAIFGGDVNITVYFGEAGASTHYMMITQTRGLFHRCIM 244
 243 MSGNSMCWASTEGOSRALTMAKRVGYKGEDEKIDLEFLMKANPYDLKEEPOVLPER 302
 245 MSGNTLSMAVTEFORNWPYRLAVOAGYAGENTRDMVWELNAKSGEILKANGELCIDEE 304
 303 MOKWMPFPGPPYEPYOTADCVYPRKPRIRWYKSNIAIFGGDVNITVYFGEAGASTHYMMITQTRGLFHRCIM 362
 305 KKEKIGFSGPVLEPYVTSICVYPRKPRIRWYKSNIAIFGGDVNITVYFGEAGASTHYMMITQTRGLFHRCIM 364
 363 PEVWKELESQVNVPELADSESADETERAIYKKAHVDEPPLD---NFMELCSYF 419
 365 PKCLNELDRCFVYPIEL--NMDRESALCREYGDOLKOCYGDGTSLDLHEYLDMVSH 423
 420 YELFPMHREFQLEFNHACPIYLYRPDPSEIINPYRIMRGRGVKSHADELITLYF 479
 424 YFMPPIRYTLRLOYSAPYLYLRDEDSK-FHMLRLSGKAVRGTGDDLSYLS 482
 480 WNLKRLPKESREKYTEIRWAGIWEFATGTPKPSYNDIAGMENLTV---DPIKSDVY 536
 483 YNSLARLKNTREYKCTIERLVGMTHFAAGNP--NFDEQEDL-WOPVDATYVEKHOL 539
 537 KCLNIGDELKAMDLEPMCKIKQASITDKKEL 569
 540 KCLNIDELKVIDVDLKLKLMWESF-RKDEL 571
 RESULT 10
 09VIB3 PRELIMINARY: PRT: 567 AA.
 AC 09VIB3: 01-MAY-2000 (Tremblrel, 13, Created)
 DT 01-MAY-2000 (Tremblrel, 13, Last sequence update)
 DT 01-JUN-2002 (Tremblrel, 21, Last annotation update)
 DE Alpha-EST8 OR CG1121.
 GN Alpha-EST8 protein.
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Burks K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes K., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Gladis A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Houston D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,
 RA Jatali M., Kalush F., Karpen G.H., Ke Z., Kemison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusken D.R., Pacio J.M.,
 RA Palczold M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington C., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RA "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 DR EMBL: AE003671; AAF54012.1; -.
 DR HSSP: P37967; I0E3.
 DR Flybase: FBgn0015576; alpha-Est8.
 DR InterPro: IPR002018; Carboxylesterase.
 DR InterPro: IPR000379; Ser-estrs_site.
 DR Pfam: PF00135; Coesterase_1.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
 KW Hydrolase.
 SO SEQUENCE 567 AA; 64831 MW; 07D6ACC72786F14A CRC64;
 Query Match 42.6%; Score 1298.5; DB 5; Length 567;
 Best Local Similarity 46.8%; Pred. No. 56-95;
 Matches 261; Conservative 91; Mismatches 187; Indels 19; Gaps 7;
 21 KYTNRLSTNETQIITDEYGOIKGVKRMFYDSDYSFESIPYAKPPVGLRFRKAPQRY 80
 14 KTNQRLRSNDKVALDYGVKVKWQSIYGNVYFEGIPKPPVGLRFRKAPQRY 73
 81 PHEGVRDCCGPNRNVOTDFISGKPTGSEDLVNTVNTDNDPKRRPVWFIHGDSEIF 140
 74 HMSDVRCRTHVARPCQVNIKQVQSEDLVNTVNTDNDPKRRPVWFIHGDSEIF 133
 141 GEANRWEGPDYEMKPVVLTVOYRGLVYFGEAGASTHYMMITQTRGLFHRCIM 242
 134 GEASRRCYSPDYLRDEYVVISINRLOPLGTNDTMMKKHIFNISLDPGLCLDPELDV 200
 201 NTAIFGVDNITVYFGEAGASTHYMMITQTRGLFHRCIM 259
 194 NQCFGCPDNTVYFGEAGASTHYMMITQTRGLFHRCIM 253
 260 ALTMKRVGYKGEDEKIDLEFLMKANPYDLKEEPOVL-PEKONKVPFPGPYEY 318
 254 PYRLQAGTGTGDANDRDPFAHKKRCKASMLKVAEDITWEERHQRITMSEFGPTIEY 313
 319 QTAADVCPKPIEMKPVVLTVOYRGLVYFGEAGASTHYMMITQTRGLFHRCIM 378
 314 LPHCVIPIRSPLEMMRDCGNSIPVIGNSFEGILMPPEVKNKPELLOGLDGENLAPO 373
 379 ELADSESADETERAIYKKAHVDEPPLD---NFMELCSYFLEPMHREFQLE 432
 374 DAVHDEQ-----ORAFKCRKRELYFGDRTPGKRTILEYDLSYKFWMGHRTLSR 427
 433 FNNHACTPIYLRFPDSEIINPYRIMRGRGVKSHADELITLYLENNILSKLPRESR 492
 428 AHNAPLAPPELVIRFEDDSKH-FNIMKRIITGCRKVGCTCHADLSYFNAAKRLKRRTA 486
 493 EYKTIERWAGIWEFATGTPKPSYNDIAGMENLTVDPKPSDYVYKCLNIGDELKVM 548

Db 487 EFKTKRLVSMVYHFAISGDPNIPMWCODEKQPGAMLPISKDKKVCGLNISHDVHVI 546
 QY 549 DLEPMKIKOGASIFDKK 566
 Db 547 DLPEAKRLMLDCIYDRE 564

RESULT 11

Q24202 PRELIMINARY; PRT; 558 AA.

AC Q24202
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Alpha esterase (Fragment).
 GN ALPHA-EST8 OR CG1121.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;

SEQUENCE FROM N.A.
 RA Robin C., Medveczky K.M., Russell R.J., Oakeshott J.G.;
 RL J. Mol. Evol. 0:0-0(0).
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 DR EMBL: U51052; AAB01151.1;
 DR HSSP: P37967; 10E3
 DR FlyBase: FBgn0015576; alpha-Est8.
 DR InterPro: IPR002018; Carboxylesterase.
 DR InterPro: IPR000379; Ser_estrs_site.
 DR Pfam: PF00135; Coesterase; 1.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
 KM Hydrolase.
 FT NON_TER
 SQ SEQUENCE 558 AA; 63916 MW; BF6F62C8FF212720 CRC64;

Query Match 42.6%; Score 1297.5; DB 5; Length 556;
 Best Local Similarity 46.6%; Pred. No. 6 6e-95;

Matches 260; Conservative 92; Mismatches 187; Indels 19; Gaps 7;

QY 21 KYNYRLSTNEQIITTEYGQIKGVRMTYDDSYSPESIPAKPPVGLERKAPORPV 80
 Db 5 KYNQQLRSNDKVIADTYGKVGKVMOSIYGNYSFEGIFAPKPPVGLERKAPVEBE 64
 QY 81 PWEGVBDCCGPANRSYQTFISGKPTGSEDCILYNTDLPDKRRPYMTIHGGDTF 140
 Db 65 HNSDVYKRCRHVNAKPCQVNIIVLKQVGSBDCILYNTRELPHRPLVWLYGGGFGQ 124
 QY 141 GEANRMFGPDYFMKKPVVLYVQYRLGVLGLSKSENLANPGNAGLKQVMALRWYKS 200
 Db 125 GEARSDLYSPDYIMEHVLYVYIRLGLGLSLADELDVPGNAGLKQVMALRWYKR 184
 QY 201 NTAIFGVDNITTFGESAGSTHYMMITTEOTRGLPHRIGIMSGNSMCWMASTECO-SR 259
 Db 185 NQGFPGSDNITTFGESAGSTHYMMITTEOTRGLPHRIGIMSGNSMCWMASTECO-SR 259
 QY 260 ALTKARVYKGEDEKIDLEFLMKANPYDLIKEPQVLT-PERQNVNPPFGTVPY 318
 Db 245 PYRLQAQVGYGDANDRIDIFALHKCKKASMLKVAEDITTEERQRLTMTSEGTTEPY 304
 QY 319 QTADCVNPKPREMVKWSAMGNSIPTLIGNTSYEGILSKSVAKQYPEVVKELSCVNYVPW 378
 Db 305 LTPHCYIKSPLEEMKRDGWSNIPVIGNSFEGILMPEVANKMPELLCQGDENLAPQ 364
 QY 379 ELADSESAPELTERAAIVKKA---HYDGEPP---TLDNEMELCSYFYLEFPMARFLOLR 432
 Db 365 DAHVEDQ-----QRKAFGKVRRELYFGDRTPGKRTTLESYDLFSYKRYFMHGIRTLISR 418
 QY 433 FNNHAGPPIYIYRPDESEELINPYRIMRFGVKGVSADDELTYLPMNLISKRLLPESR 492

Db 419 AHNAPLAFTELYRPDEFSKH-FNIMRIITGCRKVRGTCHADLSYLEYNAAKKLRRRA 477
 QY 493 EYKTIEMVGIWTEFAATGKP---YSNDIAGENLTMWDIKKSDVYKCLNIGDELKYM 548
 Db 478 EFKTKRLVSMVYHFAISGDPNIPMWCODEKQPGAMLPISKDKKVCGLNISHDVHVI 537
 QY 549 DLEPMKIKOGASIFDKK 566
 Db 538 DLPEAKRLMLDCIYDRE 555

RESULT 12

Q961N0 PRELIMINARY; PRT; 566 AA.

AC Q961N0
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE GH15053p.
 GN ALPHA-EST2 OR CG2505.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;

SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RA Stapleton M., Brocksstein P., Hong L., Abdayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise R., George R.,
 RA Gonzalez M., Guarini H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nuno J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celnikier S.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 DR EMBL: AY051497; AAK92921.1;
 DR FlyBase: FBgn0015570; alpha-Est2.
 DR InterPro: IPR002018; Carboxylesterase.
 DR InterPro: IPR000379; Ser_estrs_site.
 DR Pfam: PF00135; Coesterase; 1.
 KM Hydrolase.
 SQ SEQUENCE 566 AA; 64664 MW; 84C4FFAE3CC0CF312 CRC64;

Query Match 42.1%; Score 1281.5; DB 5; Length 566;
 Best Local Similarity 45.6%; Pred. No. 1.3e-93;

Matches 251; Conservative 110; Mismatches 174; Indels 15; Gaps 9;

QY 11 LKLCVCKVKNKYNYRLSTNEQIITTEYGQIKGVRMTYD-DSYSPESIPAKPPVG 69
 Db 11 IKMAQVLVGHVQOYRLSTGHTVLDTKYGVKGLQKRTYDKEPYFAFGIYAKPPVG 70
 QY 70 ELRFKAPQRPVMEGVBDCCGPANRSYQTFISGKPTGSEDCILYNTDLPDKRRPY 129
 Db 71 DLRFAPQRPPEPMQVNLCTNRSKPMQRMILGIVGSEDCILHNVYKALKSEKPLEY 130
 QY 130 MVEFHGDFITGEANRMFGPDYFMKKPVVLYVQYRLGVLGLSKSENLANPGNAGLK 189
 Db 131 IWTLYGGGFGGARSRLTSPDYFMKKPVVFAINRLAIGLISLKDPLKPLVPGNAGLK 190
 QY 190 DQVMALRWYKSNTAIFGVDNITTFGESAGSTHYMMITTEOTRGLPHRIGIMSGNSMC 249
 Db 191 DQVMALRWISQNTAIFHNGDPNITTFGESAGSTHYMMITTEOTRGLPHRIGIMSGNSMC 250
 QY 250 SMASTECQSAALTKARVYKGEDEKIDLEFLMKANPYDLIKEPQVLTPEPMONKVMF 309
 Db 251 EWESEPDNMWAFRLAONLGYKGEKEDADVLSKVCARQAIADQVAINDEVASFLLF 310
 QY 310 PFGTVEPYQTAQCVKPKPREMVKWSAMGNSIPTLIGNTSYEGILSKSVAKQYPEVVKEL 369
 Db 311 ARGPVATEPEYETHCHVYKHKHDLSEAWGNDIPVIVGGSEFGLSYDLVVRDKPALKNF 370
 QY 370 ESCVNVVPELAD-SERSAPELTERAAIVKKAHVGE-TPTLDNF--MELCSYFTEFLPM 425

DB 371 H---NILPREVETSSLEGODLVR--LKOLYFNNEQESMEFALNIFSHQIWHDT 425
 QY 426 HRFLOLNFNTACTPIYLYRFPDSEELINPRIMRGRGVKGVSHADELTLYFWNLISK 485
 DB 426 HRFILNAGSVAPKPTPTLYLRFPDSPH-FNQFRILVCGDRIKVAHDELSTLYFNILAS 484
 QY 486 RLPEKSERYTIERMVGITWEPATTKGPKYSNDIAGMENITWDPK-KSDVYKCLNIGDE 544
 DB 485 KLKSSMEYKTIERMVGMWMTSPASSGNPCPELGSAK---WEAVOLKENAVEKCFNISHD 541
 QY 545 LKXWDLPEDM 554
 DB 542 LEMDLPESD 551
 RESULT 13
 QYVTC2 PRELIMINARY; PRT; 554 AA.
 AC 09VTC2;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Alpha-EST2 protein.
 GN ALPHA-EST2 OR CG2505.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxId=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Aghayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,
 RA Ballaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin R.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegram C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhou M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 CC -I- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL ESTERASE/LIPASE FAMILY.
 DB EMBL; AE003671; AAF54003.1; -

DR HSSP; P37967; 10E3.
 DR Flyase; FBgn0015570; alpha-est2.
 DR Interpro; IPR002018; Carboxylase.
 DR Interpro; IPR000997; Cholinesterase.
 DR Interpro; IPR000379; Ser_estrs_site.
 DR Pfam; PF00135; Coesterase; 1.
 DR PRINTS; PR00878; CHOLINESTERASE.
 KW Hydrolyase.
 SQ SEQUENCE 554 AA; 63254 MW; 6E4AC221A45B02D CRC64;
 Query Match 42.0%; Score 1277.5; DB 5; Length 554;
 Best Local Similarity 46.2%; Pred. No. 2,6e-93;
 Matches 250; Conservative 106; Mismatches 170; Indels 15; Gaps 9;
 QY 20 NKTYNRLSTNQTQIDPEYGOIKGVKRTVYD--SYSFSEIPYAKPPVGLRPAKFOR 78
 DB 8 HKVQORLSTGHTVILDTKYGVGRLOKRTYDKPRYAFEGITPAKPPVGLRPAKFOR 67
 QY 79 PVWEGVRDCCGPANKSVOTDFISGKPTGSEDCILNYYTNDLNDKRRPVWFLHGDF 138
 DB 68 PEPWGVNCTNNRSKPMQRMNLLGIVESDCILNYYVAKSEKPLPIVWLYGGGF 127
 QY 139 TGEANRNMFGPDYFKKPVLYVQYRLGVGLSLKSENLNPGNAGLKDQVWALRW 198
 DB 128 QKGASRDYSPDYFMKKPVVVAIVRYLALGLFLSLKDPKLDVPGNAGLKDQVWALRW 187
 QY 199 KSNIAIFGGDVNTIFGSGAGASTHYMTITQTRGLFHHGIMMGSMSKMASTEQS 258
 DB 188 SONIAHFNGDPNNITLMDGSASASVHVMTEQTRGLFHHKIMSGCALSEWESPDNN 247
 QY 259 RALTMKRVYKGEDENEKIDLEFLKAMPYDLIKEEPVLTPERQNVMPFPGTVEPY 318
 DB 248 WAFRLAQNGYGDGKADVLSFLSKVCAQRLAIDQVINDVRSPLLFAFGVIEPY 307
 QY 319 QTADEVKPEIKEMKSAWNSIPPLIGNTSTEGILSSVAKQPEVYKELSCVNYPW 378
 DB 308 ETDHCVPKRRHDLSEAMGNDIPVIVGNSFEGFLSYQLVRKPPWALKNPH--NILPR 364
 QY 379 ELAD--SERAPETLRAAIVKKAHYDGE--TPRLDNF--MELCSYVFLFPMHRLQLRPN 434
 DB 365 EYRETSLEGGDLVR--LKOLYFNNEQESMEFALNIFSHQIWHDTFRILAROS 422
 QY 435 HPACTPIYLRFPDSEELINPRIMRGRGVKGVSHADELTLYFWNLISRLPRESREY 494
 DB 423 YAPKPTPTLYLRFPDSPH-FNQFRILVCGDRIKVAHDELSTLYFNILASIKLKSMEY 481
 QY 495 KTIERNVGIWEPATTKGPKYSNDIAGMENITWDPK-KSDVYKCLNIGDELKXWDLPEDM 553
 DB 482 KTIERNVGMWMTSPASSGNPCPELGSAK---WEAVOLKENAVEKCFNISHDLEMDLPES 538
 QY 554 D 554
 DB 539 D 539
 RESULT 14
 QYVTC2 PRELIMINARY; PRT; 566 AA.
 AC 09W243;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE CG6018 protein.
 GN CG6018
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxId=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;

GenCore version 5.1.4-p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2003, 09:10:57 ; Search time 15.7722 Seconds
(Without alignments)
1063.331 Million cell updates/sec

Title: US-09-776-910-13

Perfect score: 3045

Sequence: 1 MFLLKQFIFRLKLCVCMVN.....PEMDKIKGASIFDKKELF 570

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*\n2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*\n3: /cgn2_6/prodata/1/1aa/5C_COMB.pep:*\n4: /cgn2_6/prodata/1/1aa/5D_COMB.pep:*\n5: /cgn2_6/prodata/1/1aa/5E_COMB.pep:*\n6: /cgn2_6/prodata/1/1aa/5F_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	3045	100.0	570	4	US-09-068-960-13 Sequence 13, Appl
2	2348	77.1	570	4	US-09-068-960-8 Sequence 8, Appl
3	2342	76.9	570	2	US-08-669-524-3 Sequence 3, Appl
4	2335	76.7	570	4	US-09-068-960-2 Sequence 2, Appl
5	2335	76.7	570	4	US-09-068-960-4 Sequence 4, Appl
6	2335	76.7	570	4	US-09-068-960-6 Sequence 6, Appl
7	2335	76.7	570	4	US-09-068-960-10 Sequence 10, Appl
8	2330	76.5	570	2	US-08-669-524-4 Sequence 4, Appl
9	1847.5	60.7	572	2	US-08-669-524-8 Sequence 8, Appl
10	1062	34.9	207	4	US-09-068-960-15 Sequence 15, Appl
11	819	26.9	528	3	US-08-747-221B-37 Sequence 37, Appl
12	795	26.1	528	3	US-09-005-051-37 Sequence 37, Appl
13	795	26.1	528	3	US-08-747-221B-19 Sequence 19, Appl
14	735.5	24.2	550	3	US-08-747-221B-58 Sequence 58, Appl
15	735.5	24.2	550	3	US-09-005-051-58 Sequence 58, Appl
16	735.5	24.2	550	4	US-09-005-051-19 Sequence 19, Appl
17	735.5	24.2	550	4	US-09-005-051-55 Sequence 55, Appl
18	733.5	24.1	530	4	US-08-747-221B-53 Sequence 53, Appl
19	733.5	24.1	530	4	US-09-005-051-53 Sequence 53, Appl
20	723.5	23.8	505	3	US-08-747-221B-14 Sequence 14, Appl
21	723.5	23.8	505	4	US-09-005-051-14 Sequence 14, Appl
22	624	20.5	570	3	US-08-747-221B-55 Sequence 55, Appl
23	624	20.5	570	4	US-09-005-051-55 Sequence 55, Appl
24	624	20.5	595	3	US-08-747-221B-31 Sequence 31, Appl
25	624	20.5	595	4	US-09-005-051-31 Sequence 31, Appl
26	609	20.0	570	3	US-08-747-221B-54 Sequence 54, Appl
27	609	20.0	570	4	US-09-005-051-54 Sequence 54, Appl

28	609	20.0	596	3	US-08-747-221B-25 Sequence 25, Appl
29	609	20.0	596	4	US-09-005-051-25 Sequence 25, Appl
30	574	18.9	489	1	US-08-589-893-14 Sequence 14, Appl
31	574	18.9	489	2	US-09-020-991-14 Sequence 14, Appl
32	574	18.9	489	2	US-09-062-890-14 Sequence 14, Appl
33	573	18.8	489	1	US-08-589-893-6 Sequence 6, Appl
34	573	18.8	489	1	US-08-589-893-6 Sequence 6, Appl
35	573	18.8	489	2	US-09-020-991-6 Sequence 6, Appl
36	573	18.8	489	2	US-09-062-890-6 Sequence 6, Appl
37	573	18.8	489	2	US-09-062-890-6 Sequence 6, Appl
38	573	18.8	489	2	US-09-062-890-6 Sequence 6, Appl
39	573	18.8	489	2	US-09-062-890-32 Sequence 32, Appl
40	572	18.8	489	1	US-08-124-674-2 Sequence 2, Appl
41	572	18.8	489	1	US-08-589-893-16 Sequence 16, Appl
42	572	18.8	489	2	US-09-020-991-16 Sequence 16, Appl
43	572	18.8	489	2	US-09-062-890-16 Sequence 16, Appl
44	572	18.8	489	2	US-09-062-890-30 Sequence 30, Appl
45	571	18.8	489	1	US-08-589-893-8 Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-09-068-960-13
; Sequence 13, Application US/09068960A
; Patent No. 6235515
; GENERAL INFORMATION:
; APPLICANT: Commonwealth Scientific and Industrial Rerch. Org.
; TITLE OF INVENTION: MALATION CARBOXYL ESTERASE
; FILE REFERENCE: Attorney Docket No. 6235515 50179-051
; CURRENT APPLICATION NUMBER: US/09/068,960A
; CURRENT FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: PCT/AU96/00746
; EARLIER FILING DATE: 1996-11-22
; EARLIER APPLICATION NUMBER: AU 6751
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Musca domestica
US-09-068-960-13

Query Match	100.0%	Score 3045	DB 4	Length 570
Best Local Similarity	100.0%	Pred. No. 3.6e-296		
Matches 570: Conservative	0	Mismatches 0	Indels 0	Gaps 0
1 MFLLKQFIFRLKLCVCMVNKYTNRLSTNFTQIIDTEYGOIKGVRMTYVDDSYSPES 60				
1 MFLLKQFIFRLKLCVCMVNKYTNRLSTNFTQIIDTEYGOIKGVRMTYVDDSYSPES 60				
1 MFLLKQFIFRLKLCVCMVNKYTNRLSTNFTQIIDTEYGOIKGVRMTYVDDSYSPES 60				
61 IPYAPKPVGELPFKAPQRPVPEWEGVDCGPPANRSVQDFISGKPTGSEDCLYLVNTND 120				
61 IPYAPKPVGELPFKAPQRPVPEWEGVDCGPPANRSVQDFISGKPTGSEDCLYLVNTND 120				
61 IPYAPKPVGELPFKAPQRPVPEWEGVDCGPPANRSVQDFISGKPTGSEDCLYLVNTND 120				
121 LMPDKRRPVPVITHGDFLFGANRNRRGPDYFMKKPVYLYVYRLGVLGFLSKSNL 180				
121 LMPDKRRPVPVITHGDFLFGANRNRRGPDYFMKKPVYLYVYRLGVLGFLSKSNL 180				
121 LMPDKRRPVPVITHGDFLFGANRNRRGPDYFMKKPVYLYVYRLGVLGFLSKSNL 180				
181 NVPGNAGLKDQVMALRWKXSNIAIFGQVDNITVGEISAGASTHYMMITQTRGLFPRG 240				
181 NVPGNAGLKDQVMALRWKXSNIAIFGQVDNITVGEISAGASTHYMMITQTRGLFPRG 240				
181 NVPGNAGLKDQVMALRWKXSNIAIFGQVDNITVGEISAGASTHYMMITQTRGLFPRG 240				
241 IMMSGNSMCMASTECOSRALTMAKRVGKGDNEKDIIEFLMKANPYDLIKEPOVLTLP 300				
241 IMMSGNSMCMASTECOSRALTMAKRVGKGDNEKDIIEFLMKANPYDLIKEPOVLTLP 300				
301 EEMQKKVMPFPPVPEPOTACVVPKPIREKVKASNGSIPTLIGNTSGGLLSKSVAK 360				
301 EEMQKKVMPFPPVPEPOTACVVPKPIREKVKASNGSIPTLIGNTSGGLLSKSVAK 360				

QY 361 QYEVVKELESQVNVVPEWELADSESAPELLERAIYKKAHVDEGPTLIDNFMELCSFY 420
 DB 361 QYEVVKELESQVNVVPEWELADSESAPELLERAIYKKAHVDEGPTLIDNFMELCSFY 420
 QY 421 FLFPMHRLQJLRFNHTAGTPIYLYRFDPSDEIINPYRIMFGRGVKSVADELTLYFW 480
 DB 421 FLFPMHRLQJLRFNHTAGTPIYLYRFDPSDEIINPYRIMFGRGVKSVADELTLYFW 480
 QY 481 NILSKRLPKRESREKTYTERMWGIGTTEFATGTGKPSNDIAGMENLTPDIKSSDYYKCLN 540
 DB 481 NILSKRLPKRESREKTYTERMWGIGTTEFATGTGKPSNDIAGMENLTPDIKSSDYYKCLN 540
 QY 541 IGDELKVMIDPEMDKIKOGASIFDKKKELEF 570
 DB 541 IGDELKVMIDPEMDKIKOGASIFDKKKELEF 570

RESULT 2

US-09-068-960-8
 ; Sequence 8, Application US/09068960A
 ; Patent No. 6235515
 ; GENERAL INFORMATION:
 ; APPLICANT: Commonwealth Scientific and Industrial Resrch. Org.
 ; TITLE OF INVENTION: MALATHION CARBOXYL ESTERASE
 ; FILE REFERENCE: Attorney Docket No. 6235515 50179-051
 ; CURRENT APPLICATION NUMBER: US/09/068, 960A
 ; EARLIER FILING DATE: 1998-05-20
 ; EARLIER APPLICATION NUMBER: PCT/AU96/00746
 ; EARLIER FILING DATE: 1996-11-22
 ; EARLIER APPLICATION NUMBER: AU 6751
 ; EARLIER FILING DATE: 1995-11-23
 ; NUMBER OF SEQ ID NOS: 43
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO: 8
 ; LENGTH: 570
 ; TYPE: PRT
 ; ORGANISM: Lucilia cuprina
 US-09-068-960-8

Query Match 77.1%; Score 2348; DB 4; Length 570;
 Best Local Similarity 74.2%; Pred. No. 2.4e-226;

Matches 423; Conservative 73; Mismatches 74; Indels 0; Gaps 0;

QY 1 MTFLEKQIFRLKLCVCKVNVKNTYRLSTNETQIIDTEYQIGVKKMTYDDSYSES 60
 DB 1 MTFLEKQIFRLKLCVCKVNVKNTYRLSTNETQIIDTEYQIGVKKMTYDDSYSES 60
 QY 61 IYVAPPVGELRFAKAPQRPVMEGVRDCCGPARNSVQDTFISGKRTGSEDCLYLVNTND 120
 DB 61 IYVAPPVGELRFAKAPQRPVMEGVRDCCGPARNSVQDTFISGKRTGSEDCLYLVNTND 120
 QY 121 LNPDKRPVAVFIFHGDFEFGANRMFGPDYFMKKPVLVTVQYRLGVGLSLKSENL 180
 DB 121 LNPDKRPVAVFIFHGDFEFGANRMFGPDYFMKKPVLVTVQYRLGVGLSLKSENL 180
 QY 181 NVPGNAGLKDQVVALRWKNSNIAIFGSDVNDITVFESAGASTHYMMITBQTRGLFHRG 240
 DB 181 NVPGNAGLKDQVVALRWKNSNIAIFGSDVNDITVFESAGASTHYMMITBQTRGLFHRG 240
 QY 241 IMMSGMSQVMASTEGOSALMAKRVGKGDENKDIPEFLMKRNPDLIKKEEOVLTP 300
 DB 241 IMMSGMSQVMASTEGOSALMAKRVGKGDENKDIPEFLMKRNPDLIKKEEOVLTP 300
 QY 301 ERMQNVMPFPGPTVEPYOTADCVVKKPIRENVKSWAGNSIPTLIGNSYEGILSKSVAK 360
 DB 301 ERMQNVMPFPGPTVEPYOTADCVVKKPIRENVKSWAGNSIPTLIGNSYEGILSKSVAK 360
 QY 361 QYEVVKELESQVNVVPEWELADSESAPELLERAIYKKAHVDEGPTLIDNFMELCSFY 420
 DB 361 QYEVVKELESQVNVVPEWELADSESAPELLERAIYKKAHVDEGPTLIDNFMELCSFY 420
 QY 421 FLFPMHRLQJLRFNHTAGTPIYLYRFDPSDEIINPYRIMFGRGVKSVADELTLYFW 480
 DB 421 FLFPMHRLQJLRFNHTAGTPIYLYRFDPSDEIINPYRIMFGRGVKSVADELTLYFW 480

DB 421 FNEPMHRLQJLRFNHTAGTPIYLYRFDPSDEIINPYRIMFGRGVKSVADELTLYFW 480
 QY 481 NILSKRLPKRESREKTYTERMWGIGTTEFATGTGKPSNDIAGMENLTPDIKSSDYYKCLN 540
 DB 481 NILSKRLPKRESREKTYTERMWGIGTTEFATGTGKPSNDIAGMENLTPDIKSSDYYKCLN 540
 QY 541 IGDELKVMIDPEMDKIKOGASIFDKKKELEF 570
 DB 541 IGDELKVMIDPEMDKIKOGASIFDKKKELEF 570

RESULT 3

US-08-669-524-3
 ; Sequence 3, Application US/08669524
 ; Patent No. 5843758
 ; GENERAL INFORMATION:
 ; APPLICANT: RUSSELL, Robyn J.
 ; APPLICANT: NEWCOMB, Richard D.
 ; APPLICANT: ROBIN, Geoffrey C.
 ; APPLICANT: BOYCE, Thomas M.
 ; APPLICANT: CAMPBELL, Peter M.
 ; APPLICANT: PARKER, Anthony G.
 ; APPLICANT: OAKSHOTT, John G.
 ; APPLICANT: SMITH, Kertie A.
 ; TITLE OF INVENTION: ENZYME BASED BIOMEDIATION
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lowe Price Leblanc & Becker
 ; STREET: 99 Canal Center Plaza, Suite 300
 ; CITY: Alexandria
 ; STATE: Virginia
 ; COUNTRY: USA
 ; ZIP: 22314
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/669,524
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Price, Robert L.
 ; REGISTRATION NUMBER: 22,685
 ; REFERENCE/DOCKET NUMBER: 1451-021
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 703-684-1111
 ; TELEFAX: 703-684-1124
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 570 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-669-524-3

Query Match 76.9%; Score 2342; DB 2; Length 570;
 Best Local Similarity 73.9%; Pred. No. 9.7e-226;

Matches 421; Conservative 75; Mismatches 74; Indels 0; Gaps 0;

QY 1 MTFLEKQIFRLKLCVCKVNVKNTYRLSTNETQIIDTEYQIGVKKMTYDDSYSES 60
 DB 1 MTFLEKQIFRLKLCVCKVNVKNTYRLSTNETQIIDTEYQIGVKKMTYDDSYSES 60
 QY 61 IYVAPPVGELRFAKAPQRPVMEGVRDCCGPARNSVQDTFISGKRTGSEDCLYLVNTND 120
 DB 61 IYVAPPVGELRFAKAPQRPVMEGVRDCCGPARNSVQDTFISGKRTGSEDCLYLVNTND 120
 QY 121 LNPDKRPVAVFIFHGDFEFGANRMFGPDYFMKKPVLVTVQYRLGVGLSLKSENL 180
 DB 121 LNPDKRPVAVFIFHGDFEFGANRMFGPDYFMKKPVLVTVQYRLGVGLSLKSENL 180

[illegible]

100

```

1 QTDFIGSKPTGSEDCLYLVNTNDLNPKRPVMTIHGGFTFGANRBNWYCPDYEMK 60
1 QTDFIGSKPTGSEDCLYLVNTNDLNPKRPVMTIHGGFTFGANRBNWYCPDYEMK 60

```

CHENEY, 1025 Sharp Point Drive
CITY: Fort Collins

CITY: Fort Collins
STATE: Colorado

COUNTRY: USA
 ZIP: 80525
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: Wordperfect for Windows, Version 7.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/747, 2218
 FILING DATE: No. 6063610ember 12, 1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Verser, Carol Talkington
 REGISTRATION NUMBER: 37,459
 REFERENCE/DOCKET NUMBER: FC-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 970/493-7272
 TELEFAX: 970/484-9505
 INFORMATION FOR SEQ ID NO. 37:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 528 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-747-221B-37

Query Match 26.1%; Score 795; DB 3; Length 528;
 Best Local Similarity 35.6%; Pred. No. 8.3e-71;
 Matches 190; Conservative 105; Mismatches 202; Indels 36; Gaps 15;

QY 40 GOIKGVKMTVYDDSYSEFSPYAKPPVGLRFAAPRPVPEWEGVDCGPNRNSVQTD 99
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 DB 11 GLTKKEQISEKGNVHSHSYGIPYAKPPVGLRFAAPRPVPEWEGVDCGPNRNSVQTD 70
 QY 100 FISGKPTGSEDCILYLVNTYNDLNPDKRRPVWVFHIGGDFIFGEANRNWFGPDYEMKRPV 159
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 DB 71 FIKIRKVGAECDLYLVNTYVPTSEKSLPVMWVHIGGDFIFGEANRNWFGPDYEMKRPV 130
 QY 160 LVTVOYRGLVGLFLSKSENLVPGNAGLKDOVMALRWKSNIAIFGGDVNITVFGESA 219
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 DB 131 LVTENYRGLVGLFLNGIE--EAPGNVGLMDQVEALKWKNNINASFSGDPNNVTIFGESA 188
 QY 220 GGAATHYMMITEOTRGLFHRGIMSGNSMCNASTECOSR--ALTMARKVGYKGEDNEKD 277
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 DB 189 GCASVHYIMLSDLSKGLFKHAISSGSAFNPWALQHDNNKENAFRLCKLGHV--VDNETE 247
 QY 278 ILEFLMKANPYDLIKEPQVLTPEKQNVKVPFGPTVPE--YQTADCVVPKPIREKWSA 336
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 DB 248 ALKILKQAPIDDLI--DNRIKPKDKGOLIIDYPLPTIEKRYQNPFFLDQSPLSKMOG 305
 QY 337 WGNSTPLTIGNTSYEGLISKVAKQYPEVVKEL--CVNYVPMELADSEKSAPETLERAA 395
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 DB 306 NPTKVPFICGYNASAGILGLMDPKDDPNIFKFEADFEFVVDLNLTLRS--KESKILAE 364
 QY 396 IVKKAHVDEPTLDN---FMELCSYFYLFPFMRHFLQLRNHTAGTPYLYRFPD--- 449
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 DB 365 EMKRFYQDEPVSSDNKEKFEVSIQDTPWFLRGINKTARYIIHSS--EPLLYLVYSFDDFG 423
 QY 450 --SEIINPYRIMRGKGVSHADELYTLF--WNILSKRLPKESREKYTEIRMGVIG 504
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 DB 424 FLKLVLVLDP-----NIEGAHGDGLYLFKMSFTEFPDLS---AVYNNRRLQLQW 472
 QY 505 TEFTFTCKPYSNDIAGMENTLWPIKSDVYKCLNIGDELKAVMDPEMDKIK 557
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 DB 473 TNFAKTGMP--TPEINDVITTKWD--KATEEKSDHMDIDNLTLMIPDDAKRLR 522

RESULT 13
 US-09-005-051-37
 ; Sequence 37, Application US/09005051
 ; Patent No. 6291222
 ; GENERAL INFORMATION:
 ; APPLICANT: Silver, Gary W.

APPLICANT: Wisniewski, Nancy
 TITLE OF INVENTION: No. 6291222e1 Carboxylesterase Nucleic Acid
 TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
 NUMBER OF SEQUENCES: 66
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Carol Talkington Verser, Ph.D.
 ADDRESSEE: Haska Corporation
 STREET: 1825 Sharp Point Drive
 CITY: Fort Collins
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80525
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: Wordperfect for Windows, Version 7.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/005, 051
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/747, 221
 FILING DATE: No. 6291222ember 12, 1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Verser, Carol Talkington
 REGISTRATION NUMBER: 37,459
 REFERENCE/DOCKET NUMBER: FC-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 970/493-7272
 TELEFAX: 970/484-9505
 INFORMATION FOR SEQ ID NO. 37:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 528 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-005-051-37

Query Match 26.1%; Score 795; DB 4; Length 528;
 Best Local Similarity 35.6%; Pred. No. 8.3e-71;
 Matches 190; Conservative 105; Mismatches 202; Indels 36; Gaps 15;

QY 40 GOIKGVKMTVYDDSYSEFSPYAKPPVGLRFAAPRPVPEWEGVDCGPNRNSVQTD 99
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 DB 11 GLTKKEQISEKGNVHSHSYGIPYAKPPVGLRFAAPRPVPEWEGVDCGPNRNSVQTD 70
 QY 100 FISGKPTGSEDCILYLVNTYNDLNPDKRRPVWVFHIGGDFIFGEANRNWFGPDYEMKRPV 159
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 DB 71 FIKIRKVGAECDLYLVNTYVPTSEKSLPVMWVHIGGDFIFGEANRNWFGPDYEMKRPV 130
 QY 160 LVTVOYRGLVGLFLSKSENLVPGNAGLKDOVMALRWKSNIAIFGGDVNITVFGESA 219
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 DB 131 LVTENYRGLVGLFLNGIE--EAPGNVGLMDQVEALKWKNNINASFSGDPNNVTIFGESA 188
 QY 220 GGAATHYMMITEOTRGLFHRGIMSGNSMCNASTECOSR--ALTMARKVGYKGEDNEKD 277
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 DB 189 GCASVHYIMLSDLSKGLFKHAISSGSAFNPWALQHDNNKENAFRLCKLGHV--VDNETE 247
 QY 278 ILEFLMKANPYDLIKEPQVLTPEKQNVKVPFGPTVPE--YQTADCVVPKPIREKWSA 336
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 DB 248 ALKILKQAPIDDLI--DNRIKPKDKGOLIIDYPLPTIEKRYQNPFFLDQSPLSKMOG 305
 QY 337 WGNSTPLTIGNTSYEGLISKVAKQYPEVVKEL--CVNYVPMELADSEKSAPETLERAA 395
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 DB 306 NPTKVPFICGYNASAGILGLMDPKDDPNIFKFEADFEFVVDLNLTLRS--KESKILAE 364
 QY 396 IVKKAHVDEPTLDN---FMELCSYFYLFPFMRHFLQLRNHTAGTPYLYRFPD--- 449
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 DB 365 EMKRFYQDEPVSSDNKEKFEVSIQDTPWFLRGINKTARYIIHSS--EPLLYLVYSFDDFG 423
 QY 450 --SEIINPYRIMRGKGVSHADELYTLF--WNILSKRLPKESREKYTEIRMGVIG 504
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 DB 424 FLKLVLVLDP-----NIEGAHGDGLYLFKMSFTEFPDLS---AVYNNRRLQLQW 472

Db 424 ELKVLVDP-----NIEGAHDELGLVLFKMSFTEPKDLPSS---AVNRERLQTM 472
 QY 505 TEFATGKPYSDIAGMENLTWPIKSDVYKCLINIGDLKMDLPEMKIK 557
 Db 473 TNEAKTGNP-TPEINDVITTKWD--KATEBKSDHMDIDNLRMIPODRAKLR 522

RESULT 14 US-08-747-221B-19

; Sequence 19, Application US/08747221B
 ; Patent No. 6063610

GENERAL INFORMATION:

APPLICANT: Silver, Gary W.
 APPLICANT: Wisniewski, Nancy
 TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid
 TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
 NUMBER OF SEQUENCES: 66
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Carol Talkington Verser, Ph.D.
 ADDRESSEE: Hesk Corporation
 STREET: 1825 Sharp Point Drive
 CITY: Fort Collins
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80525

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: WordPerfect for Windows, Version 7.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/747,221B
 FILING DATE: No. 6063610ember 12, 1996
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Verser, Carol Talkington
 REGISTRATION NUMBER: 37,459
 REFERENCE/DOCKET NUMBER: FC-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 970/493-7272
 TELEFAX: 970/484-9505

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:
 LENGTH: 550 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-747-221B-19

Query Match

Best Local Similarity 32.8%; Score 735.5; DB 3; Length 550;
 Matches 188; Conservative 89; Mismatches 233; Indels 63; Gaps 16;

QY 3 FLKQIFRLKLCVCKMKNKTYNRLSTNETOIIDTEYGOIKGVKRMVYDDSYSESIP 62
 Db 11 FLESEFN-----IKC-----DPTVTLPGDELVGKALITNENKEVEYSYGV 52
 QY 63 YAKPVGELRFKAPQRPVMEGVRCDCGPANRSVQDTFISGKPTGSEDCILYLVNTDNL 122
 Db 53 YAKPVGELRFKAPQRPVMEGVRCDCGPANRSVQDTFISGKPTGSEDCILYLVNTDNL 112
 QY 123 PDKRRVYVFIHGDFIFGEANRNMGPDYEMKRPVLYVQYRLGVIGFLSLSENINLV 182
 Db 113 SOKKLPIVFEVHVGGFVGTSGNLEFQSPDYLVNVDIVETENYRLGPIGLNLELE--GA 170
 QY 183 PENAGLKQVYALRWKYSIAIFGGDVNITVFGESAGASHYVMITEQTFGDFHRTM 242
 Db 171 PENAGLIDVVALKWKTEIEKFGDPENITIGVSAGASVHLLSHHTTGLTKRAIA 230
 QY 243 MGNNSMCWA--STECOSRALTMKRVGYKGEDNEKIDLEFLKANPYDLIKEEPOVLPE 301
 Db 231 QSGSALNPMAPQRPVMEGVRCDCGPANRSVQDTFISGKPTGSEDCILYLVNTDNL 289

QY 302 RMQNVMEP---FGPTVEPYQADCVVPKPIREKVSAMQNSIPTLIGNTSYGLSKS 357
 Db 290 IIEFEVPSIEKVPSPHQPF-----LEESPLAR-KSGSFNKVPLLVGFNSAGGLLYF 343
 QY 358 VAKQPEVYKELSCVNVYPMELADESAP-----ETTERAIVKKAHVDGETP 407
 Db 344 FMKEKPEMLNOAE-----ADFERLVPAEFLANGSESKKLAKIKKTFD-DKP 392
 QY 408 TLDN---FMELCSYFYLFPMPHRLQRLFNHTAGTPIYLYRFPDSEELINPYRMRGR 464
 Db 393 VEENKQKFLDLDGDMFTGTGIDKHVLSV-EKQDEPYYVEYSFSES--HPAKGTFGDH 448
 QY 465 GVGVSADDELTYLFWMNLKRLPKESREYKTIEMVGIGWIEFATGKPYSDIAGMENL 524
 Db 449 NLTGACHGEELVNLFEVEMKLEKDKRPVYLTKDRVLAAMTFIKGNP-TPEYELLV 507
 QY 525 TWDPIKSDVYKCLINIGDLKMDLPEMDKIK 557
 Db 508 KWEPAVR--DKLNLNIDATLTGLTNPEETRYK 538

RESULT 15

US-08-747-221B-58
 ; Sequence 38, Application US/08747221B
 ; Patent No. 6063610

GENERAL INFORMATION:

APPLICANT: Silver, Gary W.
 APPLICANT: Wisniewski, Nancy
 TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid
 TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
 NUMBER OF SEQUENCES: 66
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Carol Talkington Verser, Ph.D.
 ADDRESSEE: Hesk Corporation
 STREET: 1825 Sharp Point Drive
 CITY: Fort Collins
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80525

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: WordPerfect for Windows, Version 7.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/747,221B
 FILING DATE: No. 6063610ember 12, 1996
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Verser, Carol Talkington
 REGISTRATION NUMBER: 37,459
 REFERENCE/DOCKET NUMBER: FC-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 970/493-7272
 TELEFAX: 970/484-9505

INFORMATION FOR SEQ ID NO: 58:

SEQUENCE CHARACTERISTICS:
 LENGTH: 550 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-747-221B-58

Query Match

Best Local Similarity 24.2%; Score 735.5; DB 3; Length 550;
 Matches 188; Conservative 91; Mismatches 231; Indels 63; Gaps 16;

QY 3 FLKQIFRLKLCVCKMKNKTYNRLSTNETOIIDTEYGOIKGVKRMVYDDSYSESIP 62
 Db 11 FLESEFN-----IKC-----DPTVTLPGDELVGKALITNENKEVEYSYGV 52
 QY 63 YAKPVGELRFKAPQRPVMEGVRCDCGPANRSVQDTFISGKPTGSEDCILYLVNTDNL 122

```

Db 53 YAKPVGELFKPPQKAEPMQGVNATLYGNVCKSLNFIKLTGDEDECLVNVVAPKTT 112
QY 123 PDKRRPVMEFIHGGDEITGEANRNMWEGPDYFMKKPVVLTVOYRGLGVGLSLKSENLV 182
Db 113 SDKKLPEFVFWHGGFVYTGSGNLEFOSPDYLVBEVDVLEFVFNRYRLGFLNLELE--GA 170
QY 183 PGNAGLDOVMALRWVKSNAIFGGVDNITVGESAGSTHYMMTEQTRGLFHRGIM 242
Db 171 PGNYGLDDOYVAALKWTEENLEKFGDPENITIGVSAGASVHLLSHTTGILKRAIA 230
QY 243 MSGNSMCSMA-STECOSRALTMKRVGKGEDEKDIIEFLMKANPYDLIKEEPVLTPE 301
Db 231 QSSSAFNPMAFQRRPVKRSIQIAEILGH--TNNTQDALFEFLQKAPVDSILKKMPAEPEGE 289
QY 302 RMQNKVMP---FGPTVEPYOTADCVVPPKPIRBMVKSANGNSIPTILIGNTSYEGLSKS 357
Db 290 IIEEFVFPSTIEKVPSHOPF---LEESPLARM-KSGSFNKVPPLLVGFNSAEGLLFKF 343
QY 358 VAKQYPEVVKELSCVNVVPMELADSESRAP-----ETLERAIYKKAHVDSGTP 407
Db 344 FMKEKPEMLNQAEE-----ADFERLYPAEPELVHGSSESKKLAETKREYFD-DKP 392
QY 408 TLDN---FMELCSYFYFLFPMHRLQLEFNHTAGTPITYLYREDFDSEELINPYRIMRGR 464
Db 393 VPENQKFIIDLIGDIWFTRGVDKHKLSV--EKODEPYYYEYSESES---HPAKGTFGDH 448
QY 465 GYKGVSHADELTYLFMNLKRLPKRESREYKTIERMVGIWTEFATGKPYSDIAGMENL 524
Db 449 NLTGACHGEELVNLFKVEMKLEKDPVLLTKDRVLAMMTNFIKNGNP--TPEVTELLPV 507
QY 525 TWDPFKSDVYKCLINIGDELKVMDLPEMDKIK 557
Db 508 KMEPATK--DKLNYLNIDATITLGTNPEANRYK 538

```

Search completed: April 4, 2003, 09:18:08
 Job time : 17.7722 secs

GenCore version 5.1.4.p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2003, 09:16:33 ; Search time 24.5753 Seconds

(without alignments)
1417.991 Million cell updates/sec

Title: US-09-776-910-13

Perfect score: 3045

Sequence: 1 MTFKQIFRKLKVCNMV.....PEMDKIKGASIFDKKELF 570

Scoring table:

BLOSUM62
Gap 10.0, Gapext 0.5

Searched: 248812 seqs, 61136040 residues

Total number of hits satisfying chosen parameters: 248812

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Published Applications AA: *
2: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep: *
3: /cgn2_6/ptodata/2/pubpaa/FCY_NEW_PUB.pep: *
4: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep: *
5: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep: *
6: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep: *
7: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep: *
8: /cgn2_6/ptodata/2/pubpaa/PCYS_PUBCOMB.pep: *
9: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep: *
10: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep: *
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep: *
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep: *
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep: *
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	642	21.1	612	9 US-09-875-353-4	Sequence 4, Appl1
2	640.5	21.0	574	9 US-10-023-515-4	Sequence 4, Appl1
3	630	20.7	585	10 US-09-934-323-4	Sequence 4, Appl1
4	520.5	17.1	574	10 US-09-748-739A-21	Sequence 21, Appl1
5	518	17.0	602	10 US-09-748-739A-2	Sequence 2, Appl1
6	514	16.9	574	10 US-09-748-739A-6	Sequence 6, Appl1
7	514	16.9	574	10 US-09-748-739A-17	Sequence 17, Appl1
8	514	16.9	574	10 US-09-748-739A-20	Sequence 20, Appl1
9	513	16.8	574	10 US-09-748-739A-4	Sequence 4, Appl1
10	513	16.8	574	10 US-09-748-739A-18	Sequence 18, Appl1
11	511	16.8	574	10 US-09-748-739A-8	Sequence 8, Appl1
12	509	16.7	574	10 US-09-748-739A-19	Sequence 19, Appl1
13	508.5	16.7	574	10 US-09-748-739A-23	Sequence 23, Appl1
14	501.5	16.5	549	9 US-10-102-806-689	Sequence 689, App
15	500	16.4	549	9 US-09-895-860-5	Sequence 5, Appl1
16	498.5	16.4	554	10 US-09-895-860-4	Sequence 4, Appl1
17	488	15.9	816	9 US-09-978-295A-375	Sequence 375, App
18	485	15.9	816	9 US-09-978-295A-375	Sequence 375, App
19	485	15.9	816	9 US-09-978-295A-375	Sequence 375, App

20	485	15.9	816	9 US-09-978-192A-375	Sequence 375, App
21	485	15.9	816	9 US-09-999-832A-375	Sequence 375, App
22	485	15.9	816	9 US-09-978-189-375	Sequence 375, App
23	485	15.9	816	9 US-09-978-608A-375	Sequence 375, App
24	485	15.9	816	9 US-09-978-191A-375	Sequence 375, App
25	485	15.9	816	9 US-09-978-403A-375	Sequence 375, App
26	485	15.9	816	9 US-09-978-564A-375	Sequence 375, App
27	485	15.9	816	9 US-09-978-585A-375	Sequence 375, App
28	485	15.9	816	9 US-10-017-081A-375	Sequence 375, App
29	485	15.9	816	9 US-09-978-824-375	Sequence 375, App
30	485	15.9	816	9 US-09-981-915A-375	Sequence 375, App
31	485	15.9	816	9 US-09-999-833A-375	Sequence 375, App
32	485	15.9	816	9 US-10-167-749-375	Sequence 375, App
33	485	15.9	816	9 US-09-918-585A-375	Sequence 375, App
34	484.5	15.9	816	9 US-09-875-353-2	Sequence 2, Appl1
35	484.5	15.9	816	9 US-09-934-323-5	Sequence 5, Appl1
36	481.5	15.8	835	10 US-09-925-301-1177	Sequence 2, Appl1
37	479.5	15.7	583	10 US-09-925-301-1177	Sequence 1177, App
38	476.5	15.6	547	10 US-09-895-860-2	Sequence 23, Appl1
39	476.5	15.6	571	9 US-10-036-041-23	Sequence 542, App
40	476.5	15.6	571	9 US-10-028-072-542	Sequence 23, Appl1
41	476.5	15.6	571	9 US-10-035-855-23	Sequence 542, App
42	476.5	15.6	571	9 US-10-121-049-542	Sequence 542, App
43	476.5	15.6	571	9 US-10-123-904-542	Sequence 542, App
44	476.5	15.6	571	9 US-10-140-470-542	Sequence 542, App
45	476.5	15.6	571	9 US-09-931-836-23	Sequence 23, Appl1

ALIGNMENTS

RESULT 1

US-09-875-353-4
Sequence 4, Application US/09875353
Patent No. US20020168713A1

GENERAL INFORMATION:

APPLICANT: Curtiss, Roy A. J.

TITLE OF INVENTION: 46960, A NOVEL HUMAN NEUROLOGIN FAMILY

FILE REFERENCE: 10448-058001

CURRENT APPLICATION NUMBER: US/09/875,353

PRIOR APPLICATION NUMBER: 2001-06-06

PRIOR FILING DATE: 2000-06-06

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 4

LENGTH: 612

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: consensus sequence

US-09-875-353-4

Query Match 21.1%, Score 642; DB 9; Length 612;
Best Local Similarity 30.3%; Pred. No. 4.7e-51;

Matches 187; Conservative 95; Mismatches 252; Indels 84; Gaps 22;

QY	1	MTFKQIFRKLKVCNMV.....PEMDKIKGASIFDKKELF	570
DB	1	MTFKQIFRKLKVCNMV.....PEMDKIKGASIFDKKELF	570
QY	57	SPESIPYKPPVGGELRFAPO-RPYPMGVGRDCGPNRSVQDFIS-----	102
DB	57	SPESIPYKPPVGGELRFAPO-RPYPMGVGRDCGPNRSVQDFIS-----	102
QY	57	SLGIPYKPPVGGELRFAPO-RPYPMGVGRDCGPNRSVQDFIS-----	102
DB	57	SLGIPYKPPVGGELRFAPO-RPYPMGVGRDCGPNRSVQDFIS-----	102
QY	103	-----GKPPG-----SDCLYLVNT-NDLNPDKRRPVVFINGDFIFGEAN-----	150
DB	103	-----GKPPG-----SDCLYLVNT-NDLNPDKRRPVVFINGDFIFGEAN-----	150
QY	117	SLGKMKVLGLTSEDCYLYNYTPKNTKPLPVWVHIGGFMFGSGSLPLSLYDDE	176
DB	117	SLGKMKVLGLTSEDCYLYNYTPKNTKPLPVWVHIGGFMFGSGSLPLSLYDDE	176
QY	151	DYFKKPPVLTVOYRGVIGFSLKSENLVNPGMAGLKKQVVALKMKVSNIAIFGDDV	210
DB	151	DYFKKPPVLTVOYRGVIGFSLKSENLVNPGMAGLKKQVVALKMKVSNIAIFGDDV	210
QY	177	SLARGNVIVYSIKRGLPGLFSTGDDKLPFGSGNGLDQRLALMKWVDNIAAFGDPN	236
DB	177	SLARGNVIVYSIKRGLPGLFSTGDDKLPFGSGNGLDQRLALMKWVDNIAAFGDPN	236


```

QY 211 NITVFGSAGASTHYMITE-----QTRGLFRGIMSGNSMCMA---STECOSRAL 261
Db 237 SVTTFGESAGASVSLLLNSGNDPSSKGLFHRALISQSGALSALPATOSESNAKRAK 296
QY 262 TMAKRVGKGDNDNEDELEFLMKANPYDLKEEPQVLTPEKQKVMF-PFGTPEBYQT 320
Db 297 ELARLIGC-NETSSSELDCRSKSAEELLEATSSELLFEYVPLPLFLAFGVPVDDGDA 355
QY 321 ADCVVPKPIREKVSAMGNSIPTLIGNTSYG-----LLSSVAKQYREYVKELESCVNY 375
Db 356 PEAFIPEDEPEELIKGKFAVDYLVLTGDKGFGYFAALLNASSGDEDELEKTEINPDV-- 413
QY 376 VFW-----ELADERSAPELLER-AAIVKKAHVDEPTLLDNEMELCSYF 419
Db 414 --WLELLKLYLFYASALINIKMDLADKLYLEKPGDVDSVESRKP---NLQDMLTDL 468
QY 420 YELFPMHRELQIRFNHTAGTPIYLYRFPDSEETINPRIMFGVGKVSADDELTYLF 479
Db 469 LFKCPTRYAADLHAKH-GGSPYAVVFDHPASFGIGQFLAKVDPDFGGAHVGDIEFYF 527
QY 480 VN-ILSKRLPK--ESREKTIERMGVITFEATGKPYSDIAGNENLTWPIKKSDDVY 536
Db 528 GNPLKEQLYKATEEERKSSKTMNMYANFAKTGNPNNGTSNGL--VWPKYTSEOKY 585
QY 537 KCLNI-----GDELKMYD 549
Db 586 SLILITTTTAAKLRKARD 603

```

```

RESULT 2
US-10-023-515-4
; Sequence 4, Application US/10023515
; Publication No. US20020182656A1
; GENERAL INFORMATION:
; APPLICANT: Curtiss, Rory A. J.
; TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYL ESTERASE
; FILE REFERENCE: 10448-122001
; CURRENT APPLICATION NUMBER: US/10/023, 515
; PRIOR FILING DATE: 2001-12-18
; PRIOR FILING DATE: 2000-12-18
; PRIOR FILING DATE: 2000-12-18
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 4
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence
US-10-023-515-4

```

```

Query Match 21.0%; Score 640.5; DB 9; Length 574;
Best Local Similarity 31.2%; Pred. No. 5.8e-51;
Matches 180; Conservative 88; Mismatches 231; Indels 77; Gaps 20;

```

```

QY 40 GOIKGVKRMITYV-DDSYSPESIPYAKPPVGLERKAPQ-RPVMEGVYRDCGPNRVSQ 97
Db 1 GKVRSVNEKTDNGEVSYSFLGIPYAPBPVGNLREKAPQYKEPMSDVLDAKTPPSCLO 60
QY 98 TDFIS-----GKPTG---SEDCLYLNYT--NDLNPDKRRPVWVFTHGG 136
Db 61 DDDFGSLDLKVALKMLSLGNKLVGLKLSDECLYLVNTPKPKRPSKLPVWVWTHGG 120
QY 137 DFIPEAN-----RNWFGPDYFMKKRPVLYTVQYRLGVIGLSKSENLVNPGNAGLKQY 192
Db 121 GFMFGSHSLPLSLYDGESELAGENYIVYSINYLGLPLGLSTGDKLPJSGNYGLDOR 180
QY 193 MALRWKSNIAIFGQVDNITVFGESAGASTHYMITE-----QTRGLFRGIMSGN 246

```

```

Db 181 LAKWQDNIAPFGDPNVTTFGESAGASVSLLLNSGNDPSSKGLFHRALISQSGS 240
QY 247 SMCMA---STECOSRALTMARVGTGKDNKDLLEFLMKANPYDLKEEPQVLTPEPM 303
Db 241 ALSFMAIOSESNAKRAKELARLIGC-NETSSSELDCRSKSAEELLEATSSELLFEYV 299
QY 304 QNKVMF-PFGTPEBYQTADCVVPKPIREKVSAMGNSIPTLIGNTSYG-----LLSS 357
Db 300 PLPLFLAFGEVVDGDAPEAFIPEDEPEELIKGKFAVDYLVLTGDKGFGYFAALLN 359
QY 358 VAKQYREYVKELESCVNYVFW-----ELADERSAPELLER-AAIVKKAH 401
Db 360 SSGDELEKTEINPDV---WLELLKLYLFYASALINIKMDLADKLYLEKPGDVDS 415
QY 402 VDEETPLDMFMELCSYFYLFPFMHRELQIRFNHTAGTPIYLYRFPDSEETINPRIM 461
Db 416 VESRKP---NLQDMLTDLFLKCTRYAADLHAKH-GGSPYAVVFDHPASFGIGQFLAK 471
QY 462 FGRGVKGVSHADELTLYLFWN-ILSKRLPK--ESREKTIERMGVITFEATGKPYSDI 518
Db 472 VDPEFGAVHGDIEFYFVGNPLKEQLYKATEEERKSSKTMNMYANFAKTGNPNNGTS 531
QY 519 AGENLTWDPPIKKSDDVYKCLNI-----GDELKMYD 549
Db 532 NGL--VWPKYTSEOKYSLILITTTTAAKLRKARD 565

```

```

RESULT 3
US-09-934-323-4
; Sequence 4, Application US/09934323
; Patent No. US20020150910A1
; GENERAL INFORMATION:
; APPLICANT: Curtiss, Rory A. J.
; TITLE OF INVENTION: 33410, A NOVEL HUMAN CARBOXYL ESTERASE
; FILE REFERENCE: 10448-081001
; CURRENT APPLICATION NUMBER: US/09/934, 323
; PRIOR FILING DATE: 2001-08-21
; PRIOR FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 4
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence
US-09-934-323-4

```

```

Query Match 20.7%; Score 630; DB 10; Length 585;
Best Local Similarity 31.2%; Pred. No. 5.7e-50;
Matches 180; Conservative 88; Mismatches 231; Indels 78; Gaps 21;

```

```

QY 40 GOIKGVKRMITYV-DDSYSPESIPYAKPPVGLERKAPQ-RPVMEGVYRDCGPNRVSQ 97
Db 11 GKVRSVNEKTDNGEVSYSFLGIPYAPBPVGNLREKAPQYKEPMSDVLDAKTPPSCLO 70
QY 98 TDFIS-----GKPTG---SEDCLYLNYT--NDLNPDKRRPVWVFTHGG 136
Db 71 DDDFGSLDLKVALKMLSLGNKLVGLKLSDECLYLVNTPKPKRPSKLPVWVWTHGG 130
QY 137 DFIPEAN-----RNWFGPDYFMKKRPVLYTVQYRLGVIGLSKSENLVNPGNAG-LKQD 191
Db 131 GFMFGSHSLPLSLYDGESELAGENYIVYSINYLGLPLGLSTGDKLPJSGNYGLDOR 190
QY 192 VMLRWKSNIAIFGQVDNITVFGESAGASTHYMITE-----QTRGLFRGIMSG 245
Db 191 FLAKWQDNIAPFGDPNVTTFGESAGASVSLLLNSGNDPSSKGLFHRALISQSG 250
QY 246 NSMCMA---STECOSRALTMARVGTGKDNKDLLEFLMKANPYDLKEEPQVLTPEP 302

```

Db 251 SALSPAIOSESNAERAEALALLC--NETSSSELDICRSKASABELLEATRSFLFLEY 309
 QY 303 MONKVMF--PEGPVEPYQADCVVPPKPIREMYKSANGNSIPLLIGNTSYEG-----LSK 356
 Db 310 VPEPLFLAFAGPYVDDDAPEAFIPEDPELLEKGFADVPYILGTCKDEGGFAMLLN 369
 QY 357 SVAKOPEVVKELSECVNYVPW-----ELADERSAPETLER-AAIVKKA 400
 Db 370 ASSKGEDELKKTNPV-----WLELTKYLLFYASEALNKKMDLADLKYLEKPGVDJDF 425
 QY 401 HVGEPPTLDNFMELCSYFLEPMHPTQLRNHTAGPIYILXRDPESEELINRYIM 460
 Db 426 SVESKRP---NLQMDLTDLFCPTVAADLNAKH--GSSPYAYAYVDHPASFCIGQFLAK 481
 QY 461 REGRGVKVSADDELTYLFMN--ILSKRLPK--ESREKTIERWVGITWTEFATGKYSND 517
 Db 482 RVDPERGAVHGEIIFVFGNPLKQOLKATEEKEKSSKIMMNYANFATGNPNNGT 541
 QY 518 IAGMELTDPYIKSDVYKCLNI-----GDELKYM 549
 Db 542 SNGL--VWPKYTSEROKYSLILLTTIYAKLIKARD 576

RESULT 4
 US-09-748-739A-21
 ; Sequence 21, Application US/09748739A
 ; Patent No. US20020119489A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lockridge, Oksana
 ; APPLICANT: Watkins, Jeffrey D.
 ; TITLE OF INVENTION: Butyrylcholinesterase Variants and
 ; TITLE OF INVENTION: Methods of Use
 ; FILE REFERENCE: P-IX 4143
 ; CURRENT APPLICATION NUMBER: US/09/748,739A
 ; CURRENT FILING DATE: 2000-12-06
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 21
 ; LENGTH: 574
 ; TYPE: PRT
 ; ORGANISM: Equus caballus
 US-09-748-739A-21

Query Match 17.1%; Score 520.5; DB 10; Length 574;
 Best Local Similarity 29.9%; Pred. No. 8.5e-40;
 Matches 165; Conservative 97; Mismatches 200; Indels 89; Gaps 24;

QY 31 ETOIIDTEGQIKVKRMVYDDSYSESIYAKPVGELRFAKQRPVMEGRDCCG 90
 Db 2 EDIIITTKNGKVRGM--NLPLVGGITVATFLGIPYAOPLGRLEKFKPOSLLTKWSNIMWTK 60
 QY 91 PANRSVQ--TD-----FISGKPTG-----SEDLVLYNTDLPDKRRPVWVFIHGDFI 139
 Db 61 YANSQYQNTDQSFPGFLSEMMNPTELSEDLVLYNWIPAPK--KNATVIMWIYGGGFO 119
 QY 140 FEARNNFPGPDYEMK--KPVILVYQYVLGVLGFLSKSENLNPGNAGLKQDYWALRW 198
 Db 120 TGTSSLPYDGFELARVRYIVVSNRYVAGLGFAL--SENPEARNGNGLPDQOLALOW 178
 QY 199 KSNIAIFGADVNTIVFESAGASTHYMMITEOTRGLEFHGIMMGSNCSMAST---E 255
 Db 179 OKNIAPFGNPRSVTLFESGASVSJLHLSRQPLFTAILIQQSGSNAPMVAVTSIYE 238
 QY 256 COSRALYMAKRYGKEDNEKIDLEFLKANDYLIKEEPOVLTPERMONKVMPEFGPTV 315
 Db 239 ANNRFLTLAKRMGC--SRNETEMIKCLRDKDPQETILNEVEVVPYDTL---LSVNFPTV 294
 QY 316 EYQTAQCVVPPKIREMYKSANGNSIPLLIGNTSYEG-----LSKS-----YAKQ 361
 Db 295 D-----GDLITMP--DTLQLOQOFKQTQLLVKNDEGTAFLVYGAPGFSKDNNSITIRKE 349
 QY 362 YPEVVKEL-----ESCV--NYVPELADERSAPETLERAAIVKKAHVDEGPTLDN 411

Db 350 FOEGKIFFPVSSEFRESILFHYMDW-LDD-----QRAENREALD-----VYGD 395
 QY 412 EHELCSYFFLEPMHPTQLRNHTAGPIYILXRDPESEELINRYIMRGKGVKYS 471
 Db 366 YNIDPALEF---TRKSEL-----GNDAFFYFEHSTLTPPEWMA-----CYMH 438
 QY 472 ADELTYLFMNILSKRLPESREKTIERWVGITWTEFATGKPYNDIAGMEN--LTWDP 529
 Db 439 GYEIIFVGLPLERAVNTTRAEBILSRSMKRNFAKYNP-----NGTIONSTRWPF 493
 QY 530 KKSDDVYKCLN 540
 Db 494 KSTEQKYLTLN 504

RESULT 5
 US-09-748-739A-2
 ; Sequence 2, Application US/09748739A
 ; Patent No. US20020119489A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lockridge, Oksana
 ; APPLICANT: Watkins, Jeffrey D.
 ; TITLE OF INVENTION: Butyrylcholinesterase Variants and
 ; TITLE OF INVENTION: Methods of Use
 ; FILE REFERENCE: P-IX 4143
 ; CURRENT APPLICATION NUMBER: US/09/748,739A
 ; CURRENT FILING DATE: 2000-12-06
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 602
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Human Butyrylcholinesterase variant
 US-09-748-739A-2

Query Match 17.0%; Score 518; DB 10; Length 602;
 Best Local Similarity 28.0%; Pred. No. 1.6e-39;
 Matches 175; Conservative 103; Mismatches 212; Indels 134; Gaps 31;

QY 6 QFIR-RLKLCYKCVNKNYTRYLSTNETQIIDTEYQIKVKRMVYDDSYSESIY 64
 Db 11 RFLFWFLTLCC--LIGK-----SHTEDDIIATKNGVRGM--NLTVGCVTAFLGIPYA 62
 QY 65 KPPVGEIREFKAPQRPVMEGY-----RQCCGANSV-----QTFPISGKPT 106
 Db 63 QPPLGRLEFRKPOSLLTKWSDIMNATKYANSCCONIDQSFPGHSEMMNPNTDL----- 116
 QY 107 GSEDLVLYNTDLPDKRRPVWVFIHGDFIFGEANRWMPGPDYEMK--KPVILVYQY 165
 Db 117 -SEDCVLYLWIPAPK--KNATVIMWIYGGGFGTQTSLSLHVQKFLARERKIYVSMNY 174
 QY 166 RLGVGLSLKSENLNPGNAGLKQDYWALRWKSNIAIFGADVNTIVFESAGASG 225
 Db 175 RVGALGFIALPG--NPEAPGNGWGLFDQOLALOWOKNIAPFGNPKSVTLFESAGAS 233
 QY 226 YMMITEOTRGLEFHGIMMGSNCSMAST---ECQSALTMARVYKGGDNKDLLEFL 282
 Db 234 LHLISPSGSHLFTAILIQQSGSNAPMVAVTSLYEARNRTNLALATQCSRP--NETELIKCL 292
 QY 283 MKANPYDLIKEEPOVLT---TPERMONKVMPEFGPTVEYQTAQCVVPPKIREMYKSANGN 339
 Db 293 RNKQPOETILNEAFVYVYGP-----LSVNFQPTVDGDLTD--MPDILLELGGF---K 341
 QY 340 SIPTLIGNTSYEG-----LSKS-----YAKQPEVVKEL-----ESCV--NY 375
 Db 342 KTOILVGNDEGFWELVYGAPGFSKDNNSITIRKEFOELKIFPGVSEFGKESITLPHY 401
 QY 376 VPELADERSAPETLERAAIVKKAHVDEGPTLDNFM-----LCSYFLEPMHPTQL 431
 Db 402 TDM-----VDQGRP--ENYREALDGVGDYINFICPALEFTR-- 435

```

QY 432 RENTACTPIYLAFEDDSEELINPIMPFGRGVCKSHADELTLYFNNILSKRPKES 491
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 436 KESFM-GNNAFYFHEHRSKLPPEMM-----GVMHGLEYEYF-----GLPLR 480
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 492 RE-EKTER-----MVGIMTEFATGKRPYSGNDLAGMENTLWDPDKSDVYKCLNTGDEL 545
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 481 RDNTYKAEILISRIYKRWANFAFYGNPNETQ---NNSTSPVPEKSTEQKYLTLNT-EST 536
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 546 KVMDLPEMDKIKOGASIFDKKEL 569
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 537 RIMTKLRAGQGRFWMTSFEPPKLELM 560
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

RESULT 6
US-09-748-739A-6
; Sequence 6, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Butyrylcholinesterase Variants and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: P-IX 4143
; CURRENT APPLICATION NUMBER: US/09/748,739A
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ. ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human Butyrylcholinesterase variant
US-09-748-739A-6

```

Query Match	16.9%	Score 514;	DB 10;	Length 574;
Best Local Similarity	28.5%	Pred. No. 3,4e-39;		
Matches 169;	Conservative 96;	Mismatches 207;	Indels 120;	Gaps 28;

```

0Y      34 IIDEVGYIKGKRMVTVDDSDYSFESEIPYAKPPVGEIKRKPAPVPMWGV-----R 86
0Y      5 IIAIKNGKVRGM-NLTVGGTVTFALGIPYMQPLGRLEFKPKPOSTLRMSDIDINATKYAN 63
0Y      87 DCCGANSV-----QTDPIISKPTGSGDCILYINVTNDLMPDRRPMPVEIHG 135
0Y      64 SCCONIDISPEGEHSEKMANENTID-----SEDCILILINWIPAPKP-KNATYILITIG 115
0Y      136 GDPFIEGANNRMWFGEDYFPMK-KPVVLTVVOYRLUGLGFSLIKSENLVWPNAGIKDOVA 194
0Y      116 GGFQGTGSSLHYDOKFLARVERVIVSAMNRYVALGFALPG-NPEAPGNMGFTDOLA 174
0Y      195 LPMWSNIAIEGVDNDITTVGESAGASGATHYMMITQTRGLPHRIGIMSGNSMCWAST 254
0Y      175 LQWVKRNTIAEFGNKSVTLTEGSEGAASVSLHLISSHSLFTRALIOSSSFAPAPAVT 234
0Y      255 ---ECOSRALTKARVYKGEDNEKIDLEFLMKANPYDLKEEPOVLTPEBKQVMEFP 311
0Y      235 SLYERARNRITLAKLTGCSRE-NETETIILKCLRNDPOEILINAEFV-PYGTOLSV--NF 290
0Y      312 GPTVEPYGTQADVCKPIREMYKSMGSIPTLIGNSYEGL-----LSKS-----357
0Y      291 GPTVGGDTLTD-MEDILLETQF---KKTQILVGNKDEBTALVYGAGGFSKDNNSII 345
0Y      358 VAKQYPEVVKEL-----ESCV-NYVPWELADSEBSAETLELARIYKKAHVGETP 407
0Y      346 TKREFOEGKILFPFVSEFGKSIIEFHTDW-----VDDQRP 382
0Y      408 TLDNME-----LCSYFYLFPWHRLQLRFNHTAGTPILYLRFPDSEELINPYRIRFG 463
0Y      383 ---ENTREALGVGDVGNFCALPETLK-KTESW-GNNAFFYFFEHRSKALPWPBWM-----433
0Y      464 RGVKYGSHADELTJYLFWMILSKRLPKESRE-YKTIER-----WVGWITERATICKPYSD 517

```

```

Db      435  ---GVMGIGELEEF-----GLPLERDRONTKAEILLRSIRYKRWANFAAYGNPNETQ 484
Oy      518  IAGMENTLWDPKKSDDYKCLNICDEKLWMDLPMDKIKGCASTFDKKEL 569
          :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      485  ---NNSTSWPVFKSTQKRYLTLNT-ESTRIMTKLRAQOCREWTSFFPVLEM 532

RESULT 7
US-09-748-739A-17
; Sequence 17, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
; APPLICANT: Lockridge, Oksana
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants and
; TITLE OF INVENTION: Methods of use
; FILE REFERENCE: P-IX 4143
; CURRENT APPLICATION NUMBER: US/09/748,739A
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 574
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-748-739A-17

```

Query Match	16.9%	Score 514	DB 10	Length 574
Best Local Similarity	28.2%	Pred No. 3,4e-39		
Matches 166	Conservative 97	Mismatches 204	Indels 126	Gaps 28

[illegible]

```

US-09-748-739A-20
; Sequence 20, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
; APPLICANT: Lockridge, Oksana
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants and
; FILE REFERENCE: P-IX 4143
; CURRENT APPLICATION NUMBER: US/09/748,739A
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 574
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-748-739A-20

```

```

Query Match      16.9%; Score 514; DB 10; Length 574;
Best Local Similarity 28.2%; Pred. No. 3,4e-39;
Matches 168; Conservative 97; Mismatches 204; Indels 126; Gaps 28;

```

```

QY 34 IIDPEYQIKGVKMTYDDSYSPESIPYAKPVGELRFKAPQRPVMEGV-----R 86
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 5 IIAIKNGKVRGM-NLTVFGGTVAFLGIPYAQPLRLRKKPQSLTKMSDINNAKRYAN 63
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 87 DCCGPANRSV-----QTFISGKPTGSEDCLYLNVYTNIDLPDKRRPVVFIHG 135
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 64 SCCQNIQSPFGHSEMMNPNTDL-----SEDCILYNWIPAKP-KNATVLTWIMG 115
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 136 GDFIFGEANRMWGPDPYFMK-KPVVLTVOYRLGVGLSLKSENINVPNGNGLKDOYMA 194
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 116 GGFOTGSSLSHYVQDKFLARVERIYVSMNRVAGLGLALPG-NPEAGNMGLEPQOLA 174
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 195 LRWKSNTAIFGGVDNITVFGESAGASTHYMMITEQTRGLFHRIGMGSNMGSCMAST 254
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 175 LQWQKNTAIAAGNPKSVTLFGESAGASVSLHLSPGSHLFTRAILQSGSFNAPMAVT 234
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 255 ---ECOSRALTMAKRVGKGEDEKDLIEFLMKANPYDLIKEPQVL--TPERMQKVM 308
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 235 SLYEARKNTLNLAKLTGCSRE-NETELIKLRNKDQELLNFAVVPYGLVAVT 287
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 309 FPGPTVEPYQTADCVVPKPIREMKVKSAMGNSIPTLIGNTSYEGL-----LSKS- 357
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 288 VNFEPYVDGDELTD--MPDILLELQGF--KKTQILGVNKKDEGTAFVYGAPGFSKDN 342
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 358 ---VAKOYPEVVKEL-----ESCV-NYVPWELADSESAPETLERAIYKKAHVDG 404
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 343 SIITRKEFOGLKIFPGVSEFGKESILFHYTDW-----VDD 379
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 405 EPTPLDNFME---LCSYFELFPMHRLQLRNHTAGTPILYLRPDPSEELINPYRIM 460
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 380 QRP--ENYREALGDVGDVNFICPALEFTK-KFSEW-GNNAFFYYFEHRSKLPWPEWM- 434
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 461 RFGGVGVSHADELTLYLFWNLSKRLPKESRE-YKTIER-----MVGITFEATGKPY 514
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 435 -----GVWNGYEIEFV-----GLPLERNQNTYKAEILLRSYKRWANFAKYGNNP 481
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 515 SNDIAGMENTLWDPIKKSDDVYKCLINIGDELKVMDLPEMDKIKOGASIFDKKEL 569
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 482 ETQ---NNSTSMWPFKSTEQKYLTLNT-ESTRIMTKLRAQOGRWTSFFPKVLEM 532
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```

```

RESULT 9
US-09-748-739A-4
; Sequence 4, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
; APPLICANT: Lockridge, Oksana
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants and
; FILE REFERENCE: P-IX 4143
; CURRENT APPLICATION NUMBER: US/09/748,739A
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18

```

```

; FILE REFERENCE: P-IX 4143
; CURRENT APPLICATION NUMBER: US/09/748,739A
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 574
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human Butyrylcholinesterase variant
US-09-748-739A-4

```

```

Query Match      16.8%; Score 513; DB 10; Length 574;
Best Local Similarity 28.2%; Pred. No. 4.2e-39;
Matches 168; Conservative 97; Mismatches 204; Indels 126; Gaps 28;

```

```

QY 34 IIDPEYQIKGVKMTYDDSYSPESIPYAKPVGELRFKAPQRPVMEGV-----R 86
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 5 IIAIKNGKVRGM-NLTVFGGTVAFLGIPYAQPLRLRKKPQSLTKMSDINNAKRYAN 63
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 87 DCCGPANRSV-----QTFISGKPTGSEDCLYLNVYTNIDLPDKRRPVVFIHG 135
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 64 SCCQNIQSPFGHSEMMNPNTDL-----SEDCILYNWIPAKP-KNATVLTWIMG 115
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 136 GDFIFGEANRMWGPDPYFMK-KPVVLTVOYRLGVGLSLKSENINVPNGNGLKDOYMA 194
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 116 GGFOTGSSLSHYVQDKFLARVERIYVSMNRVAGLGLALPG-NPEAGNMGLEPQOLA 174
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 195 LRWKSNTAIFGGVDNITVFGESAGASTHYMMITEQTRGLFHRIGMGSNMGSCMAST 254
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 175 LQWQKNTAIAAGNPKSVTLFGESAGASVSLHLSPGSHLFTRAILQSGSFNAPMAVT 234
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 255 ---ECOSRALTMAKRVGKGEDEKDLIEFLMKANPYDLIKEPQVL--TPERMQKVM 308
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 235 SLYEARKNTLNLAKLTGCSRE-NETELIKLRNKDQELLNFAVVPYGLVAVT 287
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 309 FPGPTVEPYQTADCVVPKPIREMKVKSAMGNSIPTLIGNTSYEGL-----LSKS- 357
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 290 --FGPTVDGDELTD--MPDILLELQGF--KKTQILGVNKKDEGTAFVYGAPGFSKDN 342
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 358 ---VAKOYPEVVKEL-----ESCV-NYVPWELADSESAPETLERAIYKKAHVDG 404
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 343 SIITRKEFOGLKIFPGVSEFGKESILFHYTDW-----VDD 379
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 405 EPTPLDNFME---LCSYFELFPMHRLQLRNHTAGTPILYLRPDPSEELINPYRIM 460
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 380 QRP--ENYREALGDVGDVNFICPALEFTK-KFSEW-GNNAFFYYFEHRSKLPWPEWM- 434
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 461 RFGGVGVSHADELTLYLFWNLSKRLPKESRE-YKTIER-----MVGITFEATGKPY 514
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 435 -----GVWNGYEIEFV-----GLPLERNQNTYKAEILLRSYKRWANFAKYGNNP 481
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 515 SNDIAGMENTLWDPIKKSDDVYKCLINIGDELKVMDLPEMDKIKOGASIFDKKEL 569
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 482 ETQ---NNSTSMWPFKSTEQKYLTLNT-ESTRIMTKLRAQOGRWTSFFPKVLEM 532
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```

```

RESULT 10
US-09-748-739A-18
; Sequence 18, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
; APPLICANT: Lockridge, Oksana
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants and
; FILE REFERENCE: P-IX 4143
; CURRENT APPLICATION NUMBER: US/09/748,739A
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18

```

```

; LENGTH: 574
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-748-739A-18

```

Query Match	16.8%;	Score 513;	DB 10;	Length 574;
Best Local Similarity	28.2%;	Pred. No. 4.2e-39;		
Matches 168;	Conservative 96;	Mismatches 205;	Indels 126;	Gaps 28;

```

OY 34 IIDEYGOIKGVKMMVYADDSYFEEISIPAKPVGLKARKAQORVPMGV-----R 86
Db 5 IIAIKNGKVRMA-NLIVFGGIVTAFLGIPAPQPLIGLRKRRKQOSLTKMSDIIINAIKYAN 63
OY 87 DCCGPRANSV-----QIDFISKPTGSEDCLYLVNVTINDLPDKRREPVYFIHG 135
Db 64 SCCQNIQGSFPGFHGSEMKNNTDL-----SEDCILVNWVPIAPKP-KNATVLIWIG 115
OY 136 GDFIFGEGNNRWVEGDEYFMK-KPVVLVTVQYRLGVGLFSLSKSENLNVPGNGLKQOWA 194
Db 116 GGFOGTGSSLHVYDGKFLARIVERYIVSMYRGVALGFLFLPG-NEDAPRNMGLFPQOLA 174
OY 195 LRWXSNAITAGGVDNTVYSGAGASAHYMMITQGTGRLFHRIIGMSGMSGMSAZ 254
Db 175 LQWQKNNTAAAGGNGPKSYTLTEGSEGAASVSLHLGSGSHSLTRAILLOSGSNAPWAVT 234
OY 255 ---ECOSRALFMARVKGEGEDNKDILFELMKANPYDLKEEPOVL---TPERMONKYA 308
Db 235 SLYEKRNNTLMAKTGCSRE-NETELIKLCIRKNDPOEILINAEFVYPTP-----LS 287
OY 309 FPFGEYVEPYOTADCVPKPIREYVWKSAMGNSIPTLIGNTSYGCL-----LSKS-- 357
Db 288 VNFGEYVGDGLFTD-MPDILLELGEF---KTQDILGVYKRDGETAVLYUGAGFGSKDNN 342
OY 358 ---VAKOYREYVKEL-----ESCV-NVYVPELADSRSAPELTERAIYKKAHVNG 404
Db 343 SLITRKEPOESLITFPBGVSEFGESILFHTDN-----VDD 379
OY 405 ETPTLDNFMEM---LCSYFYLFPFMHFLDREHNTAGTELYLURPDFDEEELIINYRIM 460
Db 380 QNR--ENVRREALGDVVGYNICALEBTK-KFSEW-GNNAFFUYEHRSSKLPWEPM-- 434
OY 461 RFRGVKGVSHADELTYLFWNLSKRLPKESRE-YKTIER-----MVGITERTATTKPR 514
Db 435 -----GVMHGYLEIEFYF-----GPLERRDNYTAEELLSKYSIKYRMANAKYGNPM 481
OY 515 SMDIGMENLIMDPRIKSDSDVYKCLINIGDELKVDLREMDKIKOGASIFPKKEL 569
Db 482 ETQ---NNSTSPVPEKSTEQKYLTLNT-ESTRITTKLRAOQCRWISFFFKVLDM 532

```

Best Local Similarity 28.0%; Pred. No. 6.5e-39;
Matches 166; Conservative 97; Mismatches 209; Indels 120; Gaps 27;

OY	34	IIIDREYQIIGVGRMYDDSYFSFESIPAKPVPGLERKAPORBPVEGV-----R	86
Db	5	IIAKNKQVKGCM-NLIYFGSTVTAFLGIPAPQRPDLRLRKRKQOSITKMSDLMNATKAN	63
OY	87	DCCGPANRSY-----QTFDSGKFTSEDCLLYLVNTDNLDPKRRPVMYFING	135
Db	64	SCCQNIQSPFGFHGSEMMAMPNDL-----SEDCILVLWVMPAPK-P-KMAYLLIWI	115
OY	136	GDFIFEGANRNMWEPDVEFM-KPVLVLTVOYRLRGVIGFLSKSENLNVGNGALQDVMA	194
Db	116	GGFQGTSSLHAYDGKTLAVERIYVSMYRGALGFLALPG-NEPAFGNMGCLFPQOLA	174
OY	195	LRAWKSNLAFGGVDNITVYFGESAGASTHYMMITEQTKGLFHRGIMNSGMSMAST	254
Db	175	LQWQKNLNAFGGNPKSVTLFESGAGAAVSLHLLSPGSHSLFTRALQSGSFNAPAVT	234
OY	255	--ECQSRATMAKRVYKGEDNEKDILFELMKANPYDLIKEEPQVLTPEPRMOKMYFP	311
Db	235	SLYEARNTLNLATLGCSSRE-NETELIKCLRKDDQELILNLEAFVVP--YQTSLSVNE	290
OY	312	GPVYEPYQATDCVYPRKIREMKSAMONSITLIGNTSYGL-----LSKS-----	357
Db	291	GPVYDGGFLND-MPDLILLEGG--KTKQILLVGNKDGTAFLVYAGABGFSKDNNSII	345
OY	358	VAKOYPEVVKEL-----ESCV-NYVWELADSERAPETLERALYKKAHVDGETP	407
Db	346	TKRFQEGELKTFPGVSEFPKESLFLPYTDM-----YDDQRP	382
OY	408	TLDNFM-----LCSYFYLEPMEHFLQLRNNHAGPIPIYLRDPDSEELINPYRIMRG	463
Db	383	--ENYRELAGVDVQDYNFICPALEFTK-KFSEW-GNNAFYYEHRSSKLPEWM-----	434
OY	464	RGVGVSHADLTYLFPNNILSKRLPKESRE-YKTIER-----NVGIATEPATGKRPYND	517
Db	435	---GVMGYTIEVF-----GLPELRDNYTKAEILSRISYKRRANAKKGNNEHQ	484
OY	518	IAGNENLTWDPKIRSDDYKCLNIGDELKAYMDLPENDKIKOGASIEDKKEL	569
Db	485	---NNSTSWPVFKSTEQKYTLINT-ESTRIIMTKLRAOCCRFMTSFPFKYLEM	532
RESULT 12			
US-09-748-739A-19			
Sequence 19, Application US/09748739A			
Patent No. US20020119489A1			
GENERAL INFORMATION:			
APPLICANT: Lockridge, Oksana			
APPLICANT: Watkins, Jeffrey D.			
TITLE OF INVENTION: Butyrylcholinesterase Variants and			
TITLE OF INVENTION: Methods of use			
FILE REFERENCE: P-1X 4143			
CURRENT APPLICATION NUMBER: US/09/748,739A			
CURRENT FILING DATE: 2000-12-06			
NUMBER OF SEQ ID NOS: 31			
SOFTWARE: FastSeq for Windows Version 4.0			
SEQ ID NO 19			
LENGTH: 574			
TYPE: PRT			
ORGANISM: Homo sapiens			
US-09-748-739A-19			

```

; SEQ_ID NO 8
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human Butyrylcholinesterase variantt
US-09-748-739A-8
Query Match      16.8%; Score 511; DB 10; Leng

```

[illegible]


```

Db 295 D-----GDFLDMF-DTLQLGQFKKTQILVGVNKGEGTAFVYGAAGFGKNDNSITRKE 349
QY 369 LESCVN-YYPW-----ELADSEKSAPELTERAIVKKAHVDEGETPILDNFM 413
Db 350 FQEGKIKTFPGVSEFGREAILFYVDLDDORA-----EKYREALDDVLDGDN 397
QY 414 ELCSYFELFPMHREFLQLRNFHTAGTPILYLRFPDSEELINPYRIMRGKGVSHAD 473
Db 398 IICPALF---TTKSEL-----GNAFFYFEHRSSQLPPEWM-----GYMHGY 440
QY 474 ELTYLPMNLSKRLPKESREYKTIERMGWTEFATGKPYSDIAGMEN--LTWDPK 531
Db 441 ELIEFVFGJLERRVNYTRAEEILSRIMNYMANFAKYNP-----NGTQNNSTRMPAFRS 495
QY 532 SDDVYKCLN 540
Db 496 TDQKTLTLN 504

```

RESULT 15

```

US-10-102-806-689
: Sequence 689, Application US/10102806
: Publication No. US20030054421A1
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
: FILE REFERENCE: PA103P1C1
: CURRENT APPLICATION NUMBER: US/10/102,806
: CURRENT FILING DATE: 2002-03-22
: PRIOR APPLICATION NUMBER: 09/925,298
: PRIOR FILING DATE: 2001-08-10
: PRIOR APPLICATION NUMBER: PCT/US00/05881
: PRIOR FILING DATE: 2000-03-08
: PRIOR APPLICATION NUMBER: 60/124,270
: PRIOR FILING DATE: 1999-03-12
: NUMBER OF SEQ.ID NOS: 846
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 689
: LENGTH: 549
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: SITE
: LOCATION: (1)
: OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
: NAME/KEY: SITE
: LOCATION: (7)
: OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
US-10-102-806-689

```

```

Query Match 16.4%; Score 500; DB 9; Length 549;
Best Local Similarly 29.1%; Pred. No. 6.4e-38;
Matches 161; Conservative 88; Mismatches 203; Indels 102; Gaps 22;

```

```

QY 37 TEYGOIKG-YKRMIVYDSDSYSPESIPAKPPVGELEKAPORPVMEGVRD-----CC 89
Db 26 THTQVLCISLVHVGANAGVOTFLGIPPAKPLGLRPAPEPESWSGVDRGDTTHPAMC 85
QY 90 GPANRSVQTFDIS-----GKPTGSEDLVLYNT-NDLNPDKRRPVAFTHGDFIGE 142
Db 86 LQDLTAVESSEFLSQFNTFPDSMSSEDLVLYITPAHSHGSLNPVAVWTHHGALVRGM 145
QY 143 ANRMWFGPDYFMKKPVVLYVQYRLGYGLSLKSENLPNGANGLKQVNALRWKSN 202
Db 146 ASL-YDGSMLAALENVVVIQYRLGYLGFPS--TGDKHATGNMGYLDQVAALRWQONI 202
QY 203 AIFGADVNTIVFGEAGAGSTHYMTTEOTRGLFHRGIMSGMSMSW-----251
Db 203 AHFGGNDRVTIGESAGGTSVSLVSPISQGLFHGALMESGVALLDGLIASSADVI 262
QY 252 -----ASTECQSRALTMARVG-YKGEDNKEKDLFEFLMKANPYDLIKEPQVLTPE 304

```

```

Db 263 VVANLSACQVDSSEAL-----VQCLGRKSKK-----EILAINPKFKMI-----300
QY 305 NKVMEPEGFTVEPYQADCVPRKPIRENVKSAWGNISPTLLIG-NTSYELLKSKVAKOYP 363
Db 301 -----PGYVDGVFLFRHPOELLASADFCQVPVSVIGVNNNEFGMLIPKVMRIV- 347
QY 364 EYVKELESCVNYVPMELADSEKSAPELTERAIVKKAHV--DGETPTLD-NMELCSYFY 420
Db 348 DQKEMDREASQALQKMLTLMLPPTF--GDILREYTGDNQDPQTLOAQFOEMWADSM 405
QY 421 FLPMHREFLQLRNFHTAGTPILYLRFPDSEELIN--PYRIMRGKGVSHADELY 477
Db 406 FVIPA--LQVAHFQCSRAPVYFEEQHPSLMKINIRPH-----MKADHGDELPE 453
QY 478 LFMNLSKRLPKESREYKTIER-MVGWTEFATGKPYSDIAGMENLTWDPKSDVY 536
Db 454 VRSFEGGYIKFTEEELQSRKMKMYANFARNGPNQ-----EGLPHWPLFDQEEQY 507
QY 537 KCLN-----IGDELK 546
Db 508 LQNLQPAVGRALK 521

```

```

Search completed: April 4, 2003, 09:34:03
Job time : 25.5753 secs

```


GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 10, 2003, 22:59:47 ; Search time 2938.87 Seconds

(without alignments) 16933.650 Million cell updates/sec

Title: US-09-776-910-14

Perfect score: 1710

Sequence: 1 atgaatttcgaagcaatt.....ataaagaagaattgttt 1710

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*
1: gb_da:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vt:*
15: em_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vt:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pla:*
35: em_htg_rtd:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1710	100.0	1710	ARI53445	ARI53445 Sequence
2	1657.4	96.9	2160	AF133341	AF133341 Musca dom
3	956.6	55.9	1713	AR062837	AR062837 Sequence
4	956.6	55.9	1713	ARI53438	ARI53438 Sequence
5	956.6	55.9	1713	ARI53441	ARI53441 Sequence
6	956.6	55.9	1713	ARI53442	ARI53442 Sequence
7	956.6	55.9	2240	LCU56636	LCU56636 Sequence
8	955	55.8	1713	ARI53439	ARI53439 Sequence
9	953.4	55.8	2175	AF139082	AF139082 Haematochl
10	952.2	55.7	1713	AR062838	AR062838 Sequence
11	951.8	55.7	1713	ARI53440	ARI53440 Sequence
12	646.6	37.8	2017	AY051473	AY051473 Sequence
13	353.2	20.7	2122	AY056637	AY056637 Drosophila
14	352.8	20.6	1809	AX260182	AX260182 Sequence
15	351	20.5	2820	DMU51050	DMU51050 Drosophila
16	349.4	20.4	57335	AC015272	AC015272 Drosophila
17	349.4	20.4	188459	AC008312	AC008312 Drosophila
18	349.4	20.4	197597	AC011253	AC011253 Drosophila
19	349.4	20.4	309023	AE003671	AE003671 Drosophila
20	343.2	20.1	2660	AY121675	AY121675 Drosophila
21	342	20.0	13044	AC014297	AC014297 Drosophila
22	342	20.0	117743	AC008098	AC008098 Drosophila
23	342	20.0	173373	AC008349	AC008349 Drosophila
24	342	20.0	307363	AE003457	AE003457 Drosophila
25	335	19.6	1962	AY051497	AY051497 Drosophila
26	320.6	18.7	1906	AY056345	AY056345 Drosophila
27	277	16.2	2050	AF216210	AF216210 Drosophila
28	258.6	15.1	2401	DMU51054	DMU51054 Drosophila
29	253.6	14.8	1205	AF216215	AF216215 Drosophila
30	232.2	13.6	1630	COESTR2EA	COESTR2EA Drosophila
31	224.6	13.1	1724	AY069743	AY069743 Drosophila
32	218.4	12.8	10034	AC013139	AC013139 Drosophila
33	218.4	12.8	188459	AC008312	AC008312 Drosophila
34	218.4	12.8	187597	AC011253	AC011253 Drosophila
35	218.4	12.8	309023	AE003671	AE003671 Drosophila
36	218.2	12.8	1836	COESTR1	COESTR1 Drosophila
37	215.8	12.6	3946	DMU51044	DMU51044 Drosophila
38	214	12.5	3447	DMU51052	DMU51052 Drosophila
39	205.6	12.0	3395	DMU51043	DMU51043 Drosophila
40	205.6	12.0	1331	AF216209	AF216209 Drosophila
41	204.4	12.0	2318	DMU51053	DMU51053 Drosophila
42	204.4	12.0	10034	AC013139	AC013139 Drosophila
43	204	11.9	84252	AC009207	AC009207 Drosophila
44	198	11.6	1401	CPU43544	CPU43544 Culex pipie
45	196.8	11.5	1630	COESTR2	COESTR2 C. quinquef

ALIGNMENTS

RESULT 1
LOCUS ARI53445
DEFINITION Sequence 14 from patent US 6235515.
ACCESSION ARI53445
VERSION ARI53445.1 GI:15120977
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1710)
AUTHORS Russell, R. Joyce., Newcomb, R. David., Campbell, P. Malcolm.,
Robin, G. Charlesde, Queterville., Claudianos, C., Smyth, K. A.,
Boyce, T. Mark., Oakeshott, J. Graham. and Brownlie, J. Colin.
TITLE Malathion carboxylesterase

JOURNAL Patent: US 6235515-A 14 22-MAY-2001;
 FEATURES Location/Qualifiers
 source 1. 1710
 /organism="unknown"
 BASE COUNT 498 a 369 c 394 g 449 t
 ORIGIN

Query Match 100.0%; Score 1710; DB 6; Length 1710;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1710; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACTTTTTCGAGCAATTCATATTTTCCGCGAATATGCTTTAAATGATGGTCAAT 60
 Db 1 ATGACTTTTTCGAGCAATTCATATTTTCCGCGAATATGCTTTAAATGATGGTCAAT 60
 QY 61 AATACACAACTACCGTCTGAGTACAAATGAAGAACCAATATGATGATGATGGA 120
 Db 61 AATACACAACTACCGTCTGAGTACAAATGAAGAACCAATATGATGATGATGGA 120
 QY 121 CAATTAAGGGTGTAAAGCAATGACCGTCTACGATGATTTCTTACAGTTTGGAGGT 180
 Db 121 CAATTAAGGGTGTAAAGCAATGACCGTCTACGATGATTTCTTACAGTTTGGAGGT 180
 QY 181 ATACCTATGCTAGAGCTTCAGTGGTGTAGATTCAGAGCAACCGGCGCTGTA 240
 Db 181 ATACCTATGCTAGAGCTTCAGTGGTGTAGATTCAGAGCAACCGGCGCTGTA 240
 QY 241 CCATGGGAGGAGTGTACGTGATTTGCTGAGGCGCAACAGATCGGTACAGACATTTTC 300
 Db 241 CCATGGGAGGAGTGTACGTGATTTGCTGAGGCGCAACAGATCGGTACAGACATTTTC 300
 QY 301 ATAAAGGGAACCAACAGGTTGAGAGATTTGCTATACCTGAATGTGATACCAATGAC 360
 Db 301 ATAAAGGGAACCAACAGGTTGAGAGATTTGCTATACCTGAATGTGATACCAATGAC 360
 QY 361 TTGAACCCAGACAAAAGGCGTCTGTATGTTTTCATTCATGAGGAGATTTATTTTC 420
 Db 361 TTGAACCCAGACAAAAGGCGTCTGTATGTTTTCATTCATGAGGAGATTTATTTTC 420
 QY 421 GCGAAGCAATTCGTACGTGTTTGTCCGCACTACTTATGAAACCCGCTGCTTG 480
 Db 421 GCGAAGCAATTCGTACGTGTTTGTCCGCACTACTTATGAAACCCGCTGCTTG 480
 QY 481 GTACCGTCAATATCGTTGGGTGTGTGGTTCCTTACGCTGAATCGAATAATCTC 540
 Db 481 GTACCGTCAATATCGTTGGGTGTGTGGTTCCTTACGCTGAATCGAATAATCTC 540
 QY 541 AATGTCCTCCGCAACGCTGCTCAAGATCAAGTAAATGAGTGGTCAAGAGT 600
 Db 541 AATGTCCTCCGCAACGCTGCTCAAGATCAAGTAAATGAGTGGTCAAGAGT 600
 QY 601 AATATGCAATTTTGGTGGCGATGAGCAATATTAACGCTTGGCGCAAGTCTGCT 660
 Db 601 AATATGCAATTTTGGTGGCGATGAGCAATATTAACGCTTGGCGCAAGTCTGCT 660
 QY 661 GGGGCTCAACCCATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 720
 Db 661 GGGGCTCAACCCATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 720
 QY 721 ATCATATGTCGGTAAATTCATGCTGCTCAAGGCTCTACAGAAATGCAAGTCTGCT 780
 Db 721 ATCATATGTCGGTAAATTCATGCTGCTCAAGGCTCTACAGAAATGCAAGTCTGCT 780
 QY 781 CTCACATGGCCCAAGCTGTGCTATTAAGGAGAGAGACAAATGAATATCTGGA 840
 Db 781 CTCACATGGCCCAAGCTGTGCTATTAAGGAGAGAGACAAATGAATATCTGGA 840
 QY 841 TTCTTAATGAAGCAATCCCTATGATTTGATCAAGAGAGAGAGAGAGAGAGAGAG 900
 Db 841 TTCTTAATGAAGCAATCCCTATGATTTGATCAAGAGAGAGAGAGAGAGAGAGAG 900
 QY 901 GAAAGATGCAAAATTAAGTATGTTCTTTTGGACCACTGTAACCATATCCAGACA 960
 Db 901 GAAAGATGCAAAATTAAGTATGTTCTTTTGGACCACTGTAACCATATCCAGACA 960

Db 901 GAAAGATGCAAAATTAAGTATGTTCTTTTGGACCACTGTAACCATATCCAGACA 960
 QY 961 GCGCAGTGTGTGTACCCCAACCAATCAGAGAAATGTGAGAGGCGCTGGGAAATTCG 1020
 Db 961 GCGCAGTGTGTGTACCCCAACCAATCAGAGAAATGTGAGAGGCGCTGGGAAATTCG 1020
 QY 1021 ATACCCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
 Db 1021 ATACCCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
 QY 1081 CAATATCCGAGGTTGTAAGAGGTTGGAATCCTGTGTAATTAATGATGATGATGATGAT 1140
 Db 1081 CAATATCCGAGGTTGTAAGAGGTTGGAATCCTGTGTAATTAATGATGATGATGATGAT 1140
 QY 1141 GCTGACAGTGAACGACATGCTCCCGGAAACCCCTGGAAGAGGCTCCATTTGAAAAAGGCG 1200
 Db 1141 GCTGACAGTGAACGACATGCTCCCGGAAACCCCTGGAAGAGGCTCCATTTGAAAAAGGCG 1200
 QY 1201 CATGTGATGGGGAACACCTACTCTGATTAATTTATGAGCTTGTCTATTTCTAT 1260
 Db 1201 CATGTGATGGGGAACACCTACTCTGATTAATTTATGAGCTTGTCTATTTCTAT 1260
 QY 1261 TTCTCTTTCCCATGATGCTCTCTCTACATTTGCGTTGACACACAGCTGGCACTGCC 1320
 Db 1261 TTCTCTTTCCCATGATGCTCTCTCTACATTTGCGTTGACACACAGCTGGCACTGCC 1320
 QY 1321 ATTTATTTGATATGCTTTCGATTCGATTCGAGAAATTTATTAACCCCTATGCTATTATG 1380
 Db 1321 ATTTATTTGATATGCTTTCGATTCGATTCGAGAAATTTATTAACCCCTATGCTATTATG 1380
 QY 1381 CGTTTGGCGGTGGGCTTAAAGGTGTAAGCAGTCCGATGAGTAACTATCTCTCTG 1440
 Db 1381 CGTTTGGCGGTGGGCTTAAAGGTGTAAGCAGTCCGATGAGTAACTATCTCTCTG 1440
 QY 1441 AACATTTTGTGGAAGCCCTGCAAGAGAAAGCGGCAATACAAACCATTTGAACGATG 1500
 Db 1441 AACATTTTGTGGAAGCCCTGCAAGAGAAAGCGGCAATACAAACCATTTGAACGATG 1500
 QY 1501 GTTGGCATTTTGGAGCAATTCGCGCACCCAGCAACCATATGATGATGATGATGATGAT 1560
 Db 1501 GTTGGCATTTTGGAGCAATTCGCGCACCCAGCAACCATATGATGATGATGATGATGAT 1560
 QY 1561 ATGAAAAACCTCACCTGGGATCCATAAAAATCGATATGCTATTAATGTTTAAAT 1620
 Db 1561 ATGAAAAACCTCACCTGGGATCCATAAAAATCGATATGCTATTAATGTTTAAAT 1620
 QY 1621 ATGCGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
 Db 1621 ATGCGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
 QY 1681 AGTATATTCGATTAAGAGAGATTTT 1710
 Db 1681 AGTATATTCGATTAAGAGAGATTTT 1710

RESULT 2
 AF133341 2160 bp mRNA linear INV 17-AUG-2000
 LOCUS DEFINITION Musca domestica carboxylesterase MdaE7 (mdaE7) mRNA, complete cds.
 ACCESSION AF133341
 VERSION AF133341.1 GI:4768932
 KEYWORDS
 SOURCE
 ORGANISM
 Musca domestica.
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Muscidae; Muscidae; Musca.

REFERENCE
 1 (bases 1 to 2160)
 Claudianos, C., Russell, R. J. and Oakeshott, J. G.
 The same amino acid substitution in orthologous esterases confers
 organophosphate resistance on the house fly and a blowfly
 Insect Biochem. Mol. Biol. 29 (8), 675-686 (1999)
 JOURNAL MEDLINE 99381228

Db	1760	GCATGATATAGCCGCGATGAAACCTCACTGGGATCCCATATAAAAAATCCGATGATG	1819
QY	1604	TCATATAATGTTTAAATATGCGGATGATGAAAGTTATGATTTGCCAGAAATGATAT	1663
Db	1820	TCATATAATGTTTAAATATGCGGATGATGAAAGTTATGATTTGCCAGAAATGATAT	1879
QY	1664	AAATTAACAATGAGCAAGATATATGATTAAGAAAGAAATGTTT	1710
Db	1880	AAATTAACAATGAGCAAGATATATGATTAAGAAAGAAATGTTT	1926
RESULT 3			
LOCUS	AR062837	1713 bp	DNA linear PAT 29-SEP-1999
DEFINITION	Sequence 1 from patent US 5843758.		
ACCESSION	AR062837		
VERSION	AR062837.1	GI:5990528	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 1713)		
AUTHORS	Russell, R. Joyce., Newcomb, R. David., Robin, G. Charlesde. Quetleville., Boyce, J. Mark., Campbell, P. Malcolm., Oakeshott, J. Graham. and Smyth, K. A.		
TITLE	Enzyme based bioremediation		
JOURNAL	Patent: US 5843758-A 1 01-DEC-1998;		
FEATURES	Location/Qualifiers		
source	1..1713		
BASE COUNT	516 a 305 c 370 g 522 t		
ORIGIN			
Query Match	55.9%;	Score 956.6;	DB 6; Length 1713;
Best Local Similarity	73.4%;	Pred. No. 3.8e-270;	
Matches 1223;	Conservative 0;	Mismatches 444;	Indels 0; Gaps 0;
QY	44	TTAAATGCTGTCATTAATACACAACCTACCGTCTGATGATCAAAATGAACCCCAATAA	103
Db	44	TTAAATGCTGATGAATAATAGTTTAAACTATCGTTTAACATCAATGAACCGTGATAG	103
QY	104	TCGATACGTAATATGACAAATTAAGGCTGTTAAGCGAATGACCGTCTACGATATCTT	163
Db	104	CTGAACATGAATATGGAAGAGTGAAGGCGTTTAAACGTTTAACTGTGTACATGATATCT	163
QY	164	ACTACAGTTTGAGAGTATACCCCTATGCTAGCCCTCCAGTGGGTGATGATTTCAAG	223
Db	164	ACTACAGTTTGAGAGTATACCCCTATGCTAGCCCTCCAGTGGGTGATGATTTCAAG	223
QY	224	CACCCACGCGCTTACCATTGGAGGGGTGATGATGCTGTGGGCCACCCACAGAT	283
Db	224	CACCCACGCGCAACACCCCTGGGATGGTGTGCGTATGTTGCAATCAATAAAGTAAGT	283
QY	284	CGGTACACAGATTTCTAATAGTGGCAAAACCACAGGTGGGAGGATGTTCTATACCTGA	343
Db	284	CAGTCAAGTTGATTTTATACGCGCAAAAGTGTGGCTCAGAGGATGTTCTATACCTAA	343
QY	344	ATGTGTATACCAATGACTTGAACCCAGCAAAAGCGCTCTGTTATGTTTCATCCATG	403
Db	344	GTTGCTATACCAATATCTAATCCCGAACTAAACGTCGCCGTTTATGTTATACATACATG	403
QY	404	GCGGAGATTTATTTTGGGCGAACAATGCTATCTGTTGGTCCGACTCTTATGTA	463
Db	404	GTTGCTATACCAATATCTAATCCCGAACTAAACGTCGCCGTTTATGTTATACATACATG	463
QY	464	AGAAACCGGTGCTTGTGAACCGTCAATATCGTTGGGTGTTGGTTCCTTCCATG	523
Db	464	AAAAGATGTTGCTGTTGATTAACATACATATGCTTTGGGAGCTCTAGTTTCTAAGTT	523
QY	524	TGAATGCGAAATCTCAATGTCGCCGCAACGCTGCTCAAGGATCAAGTATGAGCT	583
Db	524	TAAATTCAGAAAGCTTATATGTCGCCGTAATGCGGCTTAAAGATCAAGTATGAGCT	583

DB	1664	ACATTTAAACCAATGGGAATCGATGCTTTGAAAACCAATAGAGATTTATTT	1710
RESULT 4	ARI53438	1713 bp.	DNA
LOCUS	ARI53438	Sequence 1 from patent US 6235515.	Linear
DEFINITION	ARI53438		
ACCESSION	ARI53438		
VERSION	ARI53438.1	GI:15120970	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 1713)		
AUTHORS	Russell, R. Joyce., Newcomb, R. David., Campbell, P. Malcolm., Robin, G. Charlesde, Quetleville., Claudianos, C., Smyth, K. A., Boyce, T. Mark., Oakeshott, J. Graham. and Brownlie, J. Collin. Malathion carboxylesterase Patent: US 6235515-A 1 22-MAY-2001;		
TITLE	Location/Qualifiers		
JOURNAL	1. 1713		
FEATURES	source		
BASE COUNT	515 a 304 c 370 g 524 t		
ORIGIN			
Query Match	55.9%; Score 956.6; DB 6; Length 1713;		
Best Local Similarity	73.4%; Pred. No. 3.8e-270;		
Matches 1223;	Conservative 0; Mismatches 444; Indels 0; Gaps 0;		
OY	44	TTTAAATGCATGGTCAATAAATATACACAACCTACCGTCTGAGTACAAATGAAACCAATAA	103
DB	44	TTTAAATGCATGAAATATAGTTTAAACTATCGTTTAACTACCAATGAAACGGTGGT	103
OY	104	TGCAATACGAATATATGACAAATTAAGGGGTATACGGAATGACCGCTACATGATTCCT	163
DB	104	CTGAACATGAAATATGCAAGTGAAGGGGTAAACGTTTAACTGTGATGATGATTCCT	163
OY	164	ACTACAGTTTCAGAGATATACCCATATGCTATAGCCTCCAGTGGGTGAGTTCAAG	223
DB	164	ACTACAGTTTCAGAGATATACCCATATGCTATAGCCTCCAGTGGGTGAGTTCAAG	223
OY	224	CACCCACAGCGCTTACCATATGAGGGGTATGATGCTGTGTGGCCAGCCACAGAT	283
DB	224	CACCCACAGCGCTTACCATATGAGGGGTATGATGCTGTGTGGCCAGCCACAGAT	283
OY	284	CGGTACACAGATTTCTAATAGTGGCAAAACCCACAGGTTCCGAGAGATGCTATACCTGA	343
DB	284	CAGTCAAGTTGATTTTAAACGGGCAAAAGTGTGTGCTCAGAGATTTGCTATACCTGA	343
OY	344	ATGTGTATACCAATACATCTTGAACCCAGACAAAAGCGTCTGTATGTTTCATCATG	403
DB	344	GTGTCTATACGAATATATTAATATCCCGAAACTTAAACGTCCTTTAGTATCAATACATG	403
OY	404	GGGAGATTTTATTTTTCGGCGGAAGAAATTCGTAATCGTGGTTCGCGGACGTCTTATGA	463
DB	404	GTGTGTGTTTATTTATTCGGTGAATAATCATCGTATATATATGTGCTGTATTTTCATTA	463
OY	464	AGAAAACCCGTGTGGTGAACCGTGCAATATCGTTTGGGTGTGGTTCCTTAAGC	523
DB	464	AAAAAGATGTGTGGTGAATTAATACATACATAATATCGTTTGGAGACTCTAGTATTTCAAGT	523
OY	524	TGAATTCGAAAAATCTCAATGTCCCGGCAACGCTGCGCTCAAGATCAAGTAAGGCT	583
DB	524	TAAATTCGAAACCTTAATGTGCCCGGTAATGCGGCTTAAATCAAGTCATGAGCT	583
OY	584	TGAGATGGGTCAAGAGTATATGTCATTTTCGTTGGGATGTATAGCAATATATACGCT	643
DB	584	TGCGTTGGATTTAAATAATATGCGCAACTTTGTGTGGCAATCCGATATATATTAAGCT	643
OY	644	TGCGGGAAGTCTGTGTGGGCTCTAACCCATTTACATATGATTAACCGAGACCGCTG	703
DB	644	TTGTGGAAGTCTGTGTGGGCTCTTACCCATCATATATGTTAAACGAGAACCTTCGCG	703

QY	704	GTATTTTCATCTGCTGATACATGATGCTCCGGTAATTTTCATGCTGCTCATGCTGAGGCTCCACAG	763
Db	704	GCCTTTCCATCTGCTGATACTAATGCTGGGTAATGCTATTGTTCCATTTGCTTAATACCC	763
QY	764	AATGCCAAAGTCGTGCTGCTCACCATGAGCCAAACGTTGGCTATATAAGGAGAGAGCAATG	823
Db	764	AATGTCATACATGCTGCTTACCTTAGCCAAATTTGGCCGGCTATATAAGGCTGAGATTAAG	823
QY	824	AAAAAGATATCTGGAATTTCTTAATGAAGCCAAATTCCTATGCTATTGATCAAGAGAGC	883
Db	824	ATAAGAGATGTTTGGAAATTTCTTATGAAGCCAAAGCCACAGATATTAATAAACAATTGAGG	883
QY	884	CACAGTGTGTCACCCCGCAAGATGCAAAAATAGGTCATGTTTCCCTTTGGACCCACTG	943
Db	884	AAAAAGTTTAACTGTACAGAGCCGTACAAATAGAGTCAATGTTTCTTTGGTCCACTG	943
QY	944	TAGAACCATATCCAGACAGCCGCACTGTGTGGTATCCCAAAACCAATTCAGAGAAATGCTGAAGA	1003
Db	944	TTGAGCCATATCAGACCCGCTGATTTGTTCTTATCCCAAAATCCTCGGGAAATGTTTTAAAA	1003
QY	1004	GGCGCTGGGAAATTCGATACCCCAATTTGATAGCAATACCTTCCTACAGAGTTGCTTT	1063
Db	1004	CTGCTTGGGGTAATTCGATACCCCAATGATGATGGGTAACCTTCAATATGAGGGTCAATTTT	1063
QY	1064	CCAAATTCATTTCCCAACCAATATCCGAGAGTGTAAAGTTGGAATCTGTCGTAAT	1123
Db	1064	TGACTTCATATTTTAGCAAAATGCTATGCTTTGTTAAGGAATTTGGAATCTTGTCAAT	1123
QY	1124	ATGTGCTTTGGAGATTGGCTGTACAGTGAACGCAAGTCCCGGAAACCTCGAGAGGGCTG	1183
Db	1124	TTGTGCTCAAGTAATTTGGGTGATTTGAAGCAACGCGCCCAAGAACCTTGAAATGGGCTG	1183
QY	1184	CCATTGTGAAAAAGGCCATGTGATGGGGAACAACACTACTGTGATATTTTAATGAGC	1243
Db	1184	CTAAATTTAAAAAGGCTCATGTTTACAGGGAAGAACCAACACTGATATTTTAATGAGATC	1243
QY	1244	TTTGTGCTATTTTATTTTCTTCTTCCCATGCAATGCTTCTTACAAATGGCCTCAAC	1303
Db	1244	TTTGTCTTCACATCTATTTTCTGTTCCTCCATGCAATGCTTTGTTGCAATTTAGCTTTCATTC	1303
QY	1304	ACACAGCTGGCACTCCCATTTATTTGTATGCTTTGATTCGATTTCCGAGAAATTTATTA	1363
Db	1304	ACACCTCGGGTACACCCGCTCTACTGTGATACGCTTGACCTTGATTTGGAAGATCTTATCA	1363
QY	1364	ACCCTATGCTATTTATGCGTTTGGCCCGTGAAGGTATAGCCATGCCGATGAGC	1423
Db	1364	AACCTATGCTATTTATGCGTAGTGAGCGGAGTGAAGGTATGATCAATGCTGATGAAT	1423
QY	1424	TAACTATCTCTTTCGGAACATTTTTCGAAACGCTGCGCAAGAGAAACCCGCAATACA	1483
Db	1424	TAACTATTTCTTTCGGAATCAATTTGGCCAAACGATGCTTAAGAATGCGCTGAATACA	1483
QY	1484	AAACCATTTGAACGATGTTGGCATTTTGGACGGAATTCGCCACCAACCGGCAAAACCATACA	1543
Db	1484	AAACCATTTGAAGATGCTGATATATGATATGATATTTCCACCACTGATATCTCTTATA	1543
QY	1544	GCAATGATATACCCGCAATGGAACACCTACCTGGATGCCATTAATAAAATCCGATGATG	1603
Db	1544	GCAATGAAATTTGAAGATGGAATAATGTTTCTGGAATCCAAATTAAGAAATCCGATGAGG	1603
QY	1604	TCTATTAATTTGTTAATATTCGCGCATGGAATTAAGATTTGATTTGCGCAGAAATGATA	1663
Db	1604	TATTAAGATGTTTGAATATTTAGTGAATGATTAATAATGATTTGATGCTCGTGAATGATTA	1663
QY	1664	AAATTTAAACATGGCCAAATATTTTCGATTAATAAGAGGATTTGTTT	1710
Db	1664	AGATTTAAACAAATGGAGTGCATGTTTGAATAACATAGAGATTTATTT	1710

DEFINITION Sequence 7 from patent US 6235515.
 ACCESSION AR153441
 VERSION AR153441.1 GI:15120973
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1713)
 AUTHORS Russell, R. Joyce., Newcomb, R. David., Campbell, P. Malcolm.,
 Robin, G. Charlesde, Queteville., Claudinos, C., Smith, K., A.,
 Boyce, T. Mark., Oakeshott, J. Graham. and Brownlie, J. Colin.
 TITLE Malathion carboxylesterase
 JOURNAL Patent: US 6235515-A 7 22-MAY-2001;
 FEATURES
 source Location/Qualifiers
 1..1713
 BASE COUNT 516 a 305 c 370 g 522 t
 ORIGIN
 Query Match 55.9%; Score 956.6; DB 6; Length 1713;
 Best Local Similarity 73.4%; Pred. No. 3.8e-270;
 Matches 1223; Conservative 0; Mismatches 444; Indels 0; Gaps 0;

QY 44 TTAAATGCAATGATTAATACCAACTACCGTCTGAGTACAAATGAACCCAAATA 103
 DB 44 TTAAATGCAATGATTAATAGTTTAACTATGCTTAACTACCAATGAACCGTGTAG 103
 QY 104 TCGATTCGTAATATGACAAATTAAGGGTGTAAAGGATGACGATGACGATGATCT 163
 DB 104 CTGAATCTAATATGACAAATGAAGGCGTTAAACGTTAACTGTACGATGATCTCT 163
 QY 164 ACTAGATTCGAGATATACCTATGCTAAGCTTCAGTGGGTGAGTGAATCAAG 223
 DB 164 ACTAGATTCGAGATATACCTATGCTAAGCTTCAGTGGGTGAGTGAATCAAG 223
 QY 164 ACTAGATTCGAGATATACCTATGCTAAGCTTCAGTGGGTGAGTGAATCAAG 223
 DB 164 ACTAGATTCGAGATATACCTATGCTAAGCTTCAGTGGGTGAGTGAATCAAG 223
 QY 224 CACCCAGCGGCGCTGACATGGAGGGTGTACGATGATGCTGTGTGGCCAGCCACAT 283
 DB 224 CACCCAGCGGCGCTGACATGGAGGGTGTACGATGATGCTGTGTGGCCAGCCACAT 283
 QY 284 CAGTGAATGATTTTATTAACGGGCAAGTGTGTGGCTCAGAGATGTCTATACCTAA 343
 DB 284 CAGTGAATGATTTTATTAACGGGCAAGTGTGTGGCTCAGAGATGTCTATACCTAA 343
 QY 344 ATGTGATATCAATGATTAATGAACCCAGACAAAGGCGTCTGTATGTTTCATCATG 403
 DB 344 ATGTGATATCAATGATTAATGAACCCAGACAAAGGCGTCTGTATGTTTCATCATG 403
 QY 404 GCGGAGATTTTATTTGGCGGCAAGATCTGATGTTGGTCCGACTACTTATGA 463
 DB 404 GCGGAGATTTTATTTGGCGGCAAGATCTGATGTTGGTCCGACTACTTATGA 463
 QY 464 AGCAACCCGTGGTGGTGAACCGTGAATATGTTGGGTGTGGGTTCCTTACCC 523
 DB 464 AGCAACCCGTGGTGGTGAACCGTGAATATGTTGGGTGTGGGTTCCTTACCC 523
 QY 524 TGAATTCGCAAAATCTCAATGTCGCCGAGCAAGTGGCTCAAGATCAAGTATGGCT 583
 DB 524 TGAATTCGCAAAATCTCAATGTCGCCGAGCAAGTGGCTCAAGATCAAGTATGGCT 583
 QY 584 TGAATTCGCAAAATCTCAATGTCGCCGAGCAAGTGGCTCAAGATCAAGTATGGCT 643
 DB 584 TGAATTCGCAAAATCTCAATGTCGCCGAGCAAGTGGCTCAAGATCAAGTATGGCT 643
 QY 644 TGGGGAAGTGGTGGTGGGCTCAACCATTTACATGATGATTAACGCAAGACCGGTG 703
 DB 644 TGGGGAAGTGGTGGTGGGCTCAACCATTTACATGATGATTAACGCAAGACCGGTG 703
 QY 704 GTTATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 763
 DB 704 GTTATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 763
 QY 764 AATGCCAAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 823
 DB 764 AATGCCAAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 823

Db 764 AATGCCAAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 823
 QY 824 AAAAGATATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 883
 Db 824 AAAAGATATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 883
 QY 884 CACAGTTTGGACACCCGCAAGATGCAATGATGATGATGATGATGATGATGATGATG 943
 Db 884 CACAGTTTGGACACCCGCAAGATGCAATGATGATGATGATGATGATGATGATGATG 943
 QY 944 TAGACCATATCAAGACCGGCTGATGATGATGATGATGATGATGATGATGATGATG 1003
 Db 944 TAGACCATATCAAGACCGGCTGATGATGATGATGATGATGATGATGATGATGATG 1003
 QY 1004 GCGCTGGGGAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1063
 Db 1004 GCGCTGGGGAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1063
 QY 1064 CCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1123
 Db 1064 CCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1123
 QY 1124 ATGTCCTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1183
 Db 1124 ATGTCCTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1183
 QY 1184 CCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1243
 Db 1184 CCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1243
 QY 1244 TTTGCTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1303
 Db 1244 TTTGCTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1303
 QY 1304 ACACGCTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1363
 Db 1304 ACACGCTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1363
 QY 1364 ACCCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1423
 Db 1364 ACCCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1423
 QY 1424 TAACCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1483
 Db 1424 TAACCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1483
 QY 1484 AAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1543
 Db 1484 AAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1543
 QY 1544 GCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1603
 Db 1544 GCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1603
 QY 1604 TCTATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1663
 Db 1604 TCTATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1663
 QY 1664 AAATTAACAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1710
 Db 1664 AAATTAACAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1710

RESULT 6
 AR153442 1713 bp DNA linear PAT 08-AUG-2001
 LOCUS
 DEFINITION Sequence 9 from patent US 6235515.
 ACCESSION AR153442
 VERSION AR153442.1 GI:15120974
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 UnClassified.

REFERENCE 1 (bases 1 to 1713)
 AUTHORS Russell, R. Joyce., Newcomb, R. David., Campbell, P. Malcolim.,
 Roblin, G. Charlesde, Queteville., Claudianos, C., Smyth, K. A.,
 Boyce, T. Mark., Oakeshott, J. Graham, and Brownlie, J. Collin.
 TITLE Malathion carboxylesterase
 JOURNAL Patent: US 6235515-A 9 22-MAY-2001;
 FEATURES Location/Qualifiers
 source 1..1713
 BASE COUNT 515 a 305 c 370 g 523 t
 ORIGIN
 Query Match 55.9%; Score 956.6; DB 6; Length 1713;
 Best Local Similarity 73.4%; Pred. No. 3.8e-270;
 Matches 1223; Conservative 0; Mismatches 444; Indels 0; Gaps 0;

QY 44 TTAATGATGCTCAATTAATACACAACTACCGTCTGATACAAATGAACCAATAA 103
 DB 44 TTAATGATGCTCAATTAATACCGTCTGATACAAATGAACCGTGTAG 103
 QY 104 TCGATCTGATATGACCAATTAAGGCTTTAAGCAATGACCGTCTACGATCTT 163
 DB 104 CTGAATCTGATATGACCAATTAAGGCTTTAAGCAATGATGATGATCTT 163
 QY 164 ACTACAGTTTCGAGATATACCGTCTAAGCGTCCAGTGGGAGATGAGATTCAGG 223
 DB 164 ACTACAGTTTCGAGATATACCGTCTAAGCGTCCAGTGGGAGATGAGATTCAGG 223
 QY 224 CACCCACGCGCTGTACCATGAGGAGGTGTAGCTGTCTGAGGCGCAACAGAT 283
 DB 224 CACCCACGCGCAACACCGCTGGATGTGTGTGTGCAATCAATGAATGAAT 283
 QY 284 CGGACAGACAGATTTATAGTGAAGCCACAGCTGGGAGATGCTATACCTGA 343
 DB 284 CAGTGAAGTTGATTTATACGGGCAAGTGTGTGTGTGAGAGATGCTATACCTGA 343
 QY 344 ATGTGTATACCATGATGATGACCAACCAAGGCGCTCTGTATGTTTATCATCAG 403
 DB 344 GTGTCTATGCAATTAATCTAATACCGCAACTAAGCTCCCGTTTGTATACATACAG 403
 QY 404 GCGGAGATTTATTTTGGCGGAGCAATGCTGATGCTTTGCTCCGACTACTTATGA 463
 DB 404 GTGTGTGTTTATTTATGCGGCAAAATCATGTATGTATGCTGATTTATTTCA 463
 QY 464 AGAAGCCGCTGTGTGATACCGTGAATGCTTTGGGCTGTGGTTCCTTATGCC 523
 DB 464 AAAAGATGTGTGTATTAATACATACATATGCTTTGGGAGCTCTAGGTTTCTAAGTT 523
 QY 524 TGAATGCAAAATCTCATATGTCCTCCGCAACGCTGCTCAAGATCAATGATGCT 583
 DB 524 TAAATTCAGAAACCTTAATGTGCGGTAAATGCGGCTTAAGATCAAGTATGCGCT 583
 QY 584 TGAATGGGTGAAGATTAATTTTCCCATTTTCCGTGGCGATGTAGCAATTTACGCT 643
 DB 584 TGCCTTGGATTAATAATTAATGCGCAACTTTGTTGGCAATCCGCAATTAATTAACGCT 643
 QY 644 TCGGCGAAAGTGTGTGGGCTCTCAACCCATTCATGATGATTAACGCAACAGCCGTG 703
 DB 644 TTGGTGAAGAGTGGCGGTCTCTCTACCCATCATGATGATTTAAGCAACAGTGGCG 703
 QY 704 GTTTATTCATCGTGTATCATGATGCTCGGTAATTCATGCTGCTATGCGCTCTACAG 763
 DB 704 GTCTTTTCATCGTGTATCATGATGCTCGGTAATTCATGCTGCTATGCTGCTAATGCC 763
 QY 764 AATGCAAGTGTGCTGCTGCTCAACCATGCTGTTGGTATTAAGGAGGAGATG 823
 DB 764 AATGCAAGTGTGCTGCTGCTCAACCATGCTGTTGGTATTAAGGAGGAGATG 823
 QY 824 AAAAATATCTGGAATTTCTAATGAAGCAATCCATGATGATTTGATCAAGAGAGC 883
 DB 824 ATAAAGATGTTTGAATTTCTTATGAAGCAAGCCACAGATTTATATAAATTGAGG 883
 QY 884 CACAAGTTTGAACCCGCAAGAAATGCAAAATTAAGTCAATGTTCTTTGGACCCACTG 943

DB 884 AAAAGTTTAACTCTAGAGAGCGTACAAATTAAGCTATGCTTCTTTGGTCCACTG 943
 QY 944 TGAACCATACAGACAGCCGCTGTGTGTATCCCAACCAATCAGAGAAATGTGAGAG 1003
 DB 944 TGAACCATACAGACAGCCGCTGTGTGTATCCCAACCAATCAGAGAAATGTGAGAG 1003
 QY 1004 GGGCGGAGGAAATTCGATACCATGATGATGAGCAATACCTCTACGAGGTTGCTT 1063
 DB 1004 CTGCTTGGGATTAATTCATACCATGATGATGAGCAATACCTCTATTTATTT 1063
 QY 1064 CCAATTCATTCGCAACCAATATCCGAGGAGTTTAAAGATGGAATCTGTGTAAT 1123
 DB 1064 TCATCTCATATCTTAAGCAAAATGCTGATGCTTTAAGAAATTTGAACCTGTGCAAT 1123
 QY 1124 ATGTGCTTTGGAGTTTGGCTGTACAGTGAACGAGTGTGCGGCAACCTGAGAGGCTG 1183
 DB 1124 TGTGTCAAGTGAATGTGCTGATGCTGAACGAGTGTGCGGCAACCTGAGAGGCTG 1183
 QY 1184 CCATGTGAAAAAGGCGCATGTGATGGGGAACACACTACTGTGATTAATTTATGAGC 1243
 DB 1184 CTAAATTAATAAGCTCTCATTTACAGAGAAACACCAACAGCTGATTAATTTATGATC 1243
 QY 1244 TTTGCTCTATTTCTAATTTCTTCTTCCCATCTGCTCTTCAATTCGCTTCAAC 1303
 DB 1244 TTTGCTCTCAATCTAATTTCTTCTTCCCATCTGCTCTTCAATTCGCTTCAATC 1303
 QY 1304 ACACAGCTGGCACTCCATTTATTTGATGCTTTGATTTGATTTGATTTGATTTGATTT 1363
 DB 1304 ACACAGCTGGCACTCCATTTATTTGATGCTTTGATTTGATTTGATTTGATTTGATTT 1363
 QY 1364 ACCCTATGCTATATATGCTTTTGGCGCTGAGGCTTAAGGTTAAGTACCATGCGATGAGC 1423
 DB 1364 ATCCCTATGCTATATATGCTTTTGGCGCTGAGGCTTAAGGTTAAGTACCATGCGAT 1423
 QY 1424 TAACTATCTCTTGTGAACATTTTGTGGAACCGCTGCAAGAGAACCGCGATAC 1483
 DB 1424 TAACTATTTCTTGTGAACATTTTGTGGAACCGCTGCAAGAGAACCGCGATAC 1483
 QY 1484 AAMCATATGAGCATGATGATTTGGAGATTTGGAGATTTGGAGATTTGGAGATTTGGAGAT 1543
 DB 1484 AAMCATATGAGCATGATGATTTGGAGATTTGGAGATTTGGAGATTTGGAGATTTGGAGAT 1543
 QY 1544 GCAATGATATAGCGGCAATGAGAAACCTCAGCTGGATCCATTAATAAATCCATGATG 1603
 DB 1544 GCAATGATATGAGATGATGAGAAATGTTCCGAGATCAATTAAGAAATCCATGATG 1603
 QY 1604 TCTATTAATGTTTAATATCGCGGATGATTTGAAGTTATGATTTGCAAGAAATGATA 1663
 DB 1604 TATTAAGATGTTGAATATTAATGATGATTAAGAAATGATGATGCTGAAATGATA 1663
 QY 1664 AATTAACCAATGGCAAGATATTTGATTAATAAGAAAGAAATTTGTT 1710
 DB 1664 AGATTTAACATGGAGTGTGATGTTTGAATAAATGAGATTTATTT 1710

RESULT 7
 LCUS5636 2240 bp mRNA linear INV 10-JAN-2002
 LOCUS LCUS5636
 DEFINITION Lucilia cuprina alpha esterase (LcaEF) mRNA, implicated in
 organophosphate resistance, complete cds.
 ACCESSION U56636
 VERSION U56636.1 GI:1336079
 KEYWORDS
 SOURCE Lucilia cuprina.
 ORGANISM Lucilia cuprina.
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Oestroidea; Calliphoridae; Lucilia.
 REFERENCE 1 (bases 1 to 2240)
 AUTHORS Newcomb, R.D., East, P.D., Russell, R.J. and Oakeshott, J.G.
 TITLE Isolation of alpha cluster esterase genes associated with
 organophosphate resistance in Lucilia cuprina

JOURNAL Insect Mol. Biol. 5 (3), 211-216 (1996)
 MEDLINE 96392952
 PUBMED 8799740
 REFERENCE 2 (bases 1 to 2240)
 AUTHORS Newcomb, R.D., Campbell, P.M., Russell, R.J. and Oakeshott, J.G.
 TITLE cDNA cloning, baculovirus-expression and kinetic properties of the esterase, E3, involved in organophosphorus resistance in *Lucilia cuprina*

JOURNAL Insect Biochem. Mol. Biol. 27 (1), 15-25 (1997)
 MEDLINE 97215578
 PUBMED 9061925
 REFERENCE 3 (bases 1 to 2240)
 AUTHORS Newcomb, R.D., Campbell, P.M., Ollis, D.L., Cheah, E., Russell, R.J. and Oakeshott, J.G.
 TITLE A single amino acid substitution converts a carboxylesterase to an organophosphorus hydrolase and confers insecticide resistance on a blowfly

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (14), 7464-7468 (1997)
 MEDLINE 97352821
 PUBMED 9207114
 REFERENCE 4 (bases 1 to 2240)
 AUTHORS Campbell, P.M., Newcomb, R.D., Russell, R.J. and Oakeshott, J.G.
 TITLE Two different amino acid substitutions in the alle-esterase, E3, confer alternative types of organophosphorus insecticide resistance in the sheep blowfly

JOURNAL Unpublished
 REFERENCE 5 (bases 1 to 2240)
 AUTHORS Newcomb, R.D., Campbell, P.M., Russell, R.J. and Oakeshott, J.G.
 TITLE Direct Submission
 JOURNAL Submitted (24-APR-1996) Richard D. Newcomb, Molecular Genetics, HortResearch, Private Bag 92 169, Auckland, New Zealand

FEATURES
 SOURCE Location/Qualifiers
 1..2240
 /organism="Lucilia cuprina"
 /strain="LS2"
 /db_xref="taxon:7375"
 1..2240
 /gene="Lcae7"
 298..2010
 /gene="Lcae7"
 /note="alpha-esterase; Allele: organophosphate susceptible (LS2)"
 /codon_start=1
 /product="E3"
 /protein_id="AAB67728.1"
 /db_xref="GI:1336080"
 /translation="MNFNVSIMELKWKIKICENKPLNRYLTNETVVAETEGKYVG VKRLVVDSDYSFEGIPYAPQPYGELREFRAPQPTPMDRCCKNDKDSVOYDEIT GKNVGSFDCILSYTYNNLNDETRKPYLVYTHGGGFTIGENHNDMPDYFIKIDVYL INIYRIGALGELNSLSEDLNVPENAGLKDQVVALRWIKNNCAFGNGPNITVFES AGASTHYMMLEQTRGLFPHGILMSGNALCPVANTOCORHAFTLADLAGYKGDNDK DVEFLMKARQDILKLEFVYLTLEERTNKVMPFGPTVPEYOTADVLARKHREMK TAMGNSIPMTMGNTSYGLFETSILKQPMPLVLELTCVNESELDADARPAPELLE MGAKIKKAHTGETPTADNFMDCSHIYFWPMHRIQLRFNHTSGTPVLYAFEDDS EDLINPYRIMSGRGVGVSHADELYTFPNQILAKRMRPKSRKTERMTGTLNIDFA TTGNPYSNETIEGMENVSMDPIKSDDEVYKCLINISDELKMDVPEMDIKOWESMEFKH RDLR"
 <298..344
 /gene="Lcae7"
 345..537
 /gene="Lcae7"
 538..657
 /gene="Lcae7"
 658..808
 /gene="Lcae7"
 707
 /gene="Lcae7"
 /note="Organophosphorus insecticide resistance to diazinon"
 /replace="a"
 809..1369
 /gene="Lcae7"
 1049

/gene="Lcae7"
 /note="Organophosphorus insecticide resistance to malathion"
 /replace="t"
 /gene="Lcae7"
 1370..1539
 /gene="Lcae7"
 1540..>2010
 /gene="Lcae7"

BASE COUNT 740 a 357 c 417 g 726 t

ORIGIN

Query Match 55.9%; Score 956.6; DB 3; Length 2240;
 Best Local Similarity 73.4%; Pred. No. 3.9e-270;
 Matches 1223; Conservative 0; Mismatches 444; Indels 0; Gaps 0;

QY 44 TTAATGATGCGTCAATAAATACCAAACTACCGTGTGATACAAATGAACCAATAA 103
 |||||
 Db 341 TTAATGATGATGAATAAAGCTTTTAACTATGCTTTAACTACCAATGAACGCTGTAG 400

QY 104 TCGATGATGATATGACAAATTAAGGCTGTAAAGCAATGACCGTCTACATGATCTT 163
 |||||
 Db 401 CTGAAGTGAATATGCAAAAGTGAAGCGTTAAAGCTTTAACTGTACGATGATTCCT 460

QY 164 ACTACGTTTGCAGATATACCTTAAAGCTTCAAGCTTCAAGTGTGAGTTGATTCAGG 223
 |||||
 Db 461 ACTACGTTTGAAGGTATACCGTACGCGCCACCGCGAGGCTGAGCTGAGATTTAAAG 520

QY 224 CACCCGAGCGCGCTGTCACATGGAGGCTGTAGTATGCTGTGGGCCAGCAAGAT 283
 |||||
 Db 521 CACCCGAGCGCACACCGCTGGAGTGTGCTGATGTTTCAATCATTAAGATAGCT 580

QY 284 CGGTACAGACAGATTTTCAATAGTGGCAACCCAGGTTTCGAGATGCTATACCTGA 343
 |||||
 Db 581 CAGTCAAGTGTGATTTATTAACGGCAAAAGTGTGGCTCAGAGATGCTATACCTGA 640

QY 344 ATGCTATACCACTGATTAACCCAGCAAAAGCGCTCTGTATTAGTTTCATCATG 403
 |||||
 Db 641 GTGCTATACCACTGATTAACCTAAATCCGAAATCAAGTCCCGCTTTAGTATACATCAAG 700

QY 404 GCGAGATTTTATTTTGGGGAAGCAAAATGCTAGTGTGTTGCTCCGCTACTTATGA 463
 |||||
 Db 701 GTGCTGTTTATTTATGCGTGAATAATCATGCTATATGATGCTCTGCTGATTTATTA 760

QY 464 AGAAACCCGTGCTTGTGTAACCGTGAATATGTTGGGTGTGTTGCTTACGCT 523
 |||||
 Db 761 AAAAGATGTGCTGTTGATTAACATACATATGCTTTGGAGCTCAAGTTTCTTAAGT 820

QY 524 TGAATGGAATAATTCATATGCTCCCGGCAACGCTGCTCAAGATCAAGTATGCGCT 583
 |||||
 Db 821 TAAATTCAGAAAGACTTAATGTCGCCGTAATGCCGCGCTTTAAAGATCAAGTATGCGCT 880

QY 584 TGAATGCGGCAAGATATATGTCATTTGCTGGGCGATAGACATATTAACGCT 643
 |||||
 Db 881 TCGCTGTGATTAATAAATATGCGCAACTTGTGTGCAATCCGATATATTAACAGT 940

QY 644 TCGGCGAAAGTGTGCTGGGCGCTCAACCATTAACATGATGATTAACCAAGACAGCCGTG 703
 |||||
 Db 941 TTGCTGAAGTGTGCGGCGCTGTACCACTACATGATGATTAACCAAGACAGCTGGG 1000

QY 704 GTTATTCATGCTGTATACATGATGCTCGGTATTCATGCTATGCTATGCGCTCTACAG 763
 |||||
 Db 1001 GTCTTTCAATGCTGTATACATGATGCTGGGTAATGCTATTTGCTCATGGGCTAATACCC 1060

QY 764 AATGCCAAGTGTGCGCTACCATGCAAAAGTGTGCTATAGAGGAGAGCAATG 823
 |||||
 Db 1061 AATGTCACATGCTGCTTACCTTACCTTACCAATTTGCGCGCTATAGAGGTGAGATATG 1120

QY 824 AAAAGATATCTGTAATTCCTAATGAAGCAATCCCTATGATTTGATCAAGAGAGC 883
 |||||
 Db 1121 ATAAAGATGTTTGAATTTCTTATGAAGCAAGCAAGATTTAATAAATCTTAGG 1180

QY 884 CACAAGTTTGAACCCGAAGATCAAAATTAAGTATGTTTCTTTTGGACCACTG 943
 |||||

Db 1181 AAAAGTTTAACTAGAGAGCCAGCAATTAAGTCAATGTTCTTTGGTCCACTG 1240
 Oy 944 TAGAACCATACAGAGCCAGCGTGTGTATCCCAACCAATCAGCAAAATGGGAGCA 1003
 Db 1241 TTGAGCCATATCAGACCGCTGATGTGTCTTACCAACATCTCGGGAATGGTTAAA 1300
 Oy 1004 GCGCCCTGGGAAATTCGATACCCATGATAGGCAATACCTCTACGAGATGGCTTT 1063
 Db 1301 CTGCTGGGGTAATTCGATACCCATGATAGGCAATACCTCTACGAGATGGCTTT 1360
 Oy 1064 CCAATTCATTCGCAAAATATTCGAGGTTGTAAAGAGTTGGAATCTGTGAAT 1123
 Db 1361 TCAGTCAATTCCTTAAGCAAAATGCTATGCTTAAGCAATGGCAATCTGTCAAT 1420
 Oy 1124 ATGTCCTGGGAGTGTGCTGACATGAGCAGCAGTCCCGCAACCTGGAGAGGGTG 1183
 Db 1421 TTGTGCAAGTCAATTTGGCTGATGCTGAACGACCGCCGAGACCTTGGCAATGGTG 1480
 Oy 1184 CCATTTGAAAAAGCCCATTTGATGGGGAACACCTACTCTGATATTTTATGAGC 1243
 Db 1481 CTAAATTTAAAAAGCTCATGTTACAGAGAAACACCAAGCTGATATTTTATGATC 1540
 Oy 1244 TTGCTCCATTTCTATTTCTCTTCCCATGACATGCTCTCTCAATTTGGCTTCAAC 1303
 Db 1541 TTGCTCTCAATCTATTTCTGCTGCTCCCATGACATGCTCTCTCAATTTGGCTTCAAT 1600
 Oy 1304 ACACAGTGGCAGCTCCATTTATTTGATGCTTTCGATTTGCAATTCGAGAAATTTATTA 1363
 Db 1601 ACACCTCGGTACACCGCTCATCTTGTATGCTTGTGATTTGGAGATCTTTATTA 1660
 Oy 1364 ACCCTATGCTATTTATGCGTTTGGCGTGGCGTTAAAGGTGAAGCCATGCCATGAGC 1423
 Db 1661 ATCCCTATGCTATTTATGCGTTTGGCGTGGCGTTAAAGGTGAAGCCATGCCATGAGC 1720
 Oy 1424 TAACCTATCTCTGCGAATTTTGTGAAGCCGCTCCCAAGAAAGCCGCAATACA 1483
 Db 1721 TAACCTATCTCTGCGAATTTTGTGAAGCCGCTCCCAAGAAAGCCGCAATACA 1780
 Oy 1484 AAACCATTAAGCAATGCTGTGATTTGAGCAATTTGCGCAACCGCGCAACCATTA 1543
 Db 1781 AAACCATTAAGCAATGCTGTGATTTGAGCAATTTGCGCAACCGCGCAACCATTA 1840
 Oy 1544 GCATGATATAGCCGCGCATTTGAAAACTCACCTGGGATCCCAATAAAAATTCGATG 1603
 Db 1841 GCATGATATAGCCGCGCATTTGAAAACTCACCTGGGATCCCAATAAAAATTCGATG 1900
 Oy 1604 TCTATTAATGTTTAAATTCGCGATGTAATGAAAGTATGATTTGGCAAAATGATA 1663
 Db 1901 TATACAACTGTTTGAATATTTAGTGAAGTGAATGAAATGATTTGATGCTGAATGATA 1960
 Oy 1664 AAATTAACCAATGGGCAAGTATTTGATTAAGAAAGAGAAATTTGTT 1710
 Db 1961 AGATTAACCAATGGGCAAGTATTTGATTAAGAAAGAGAAATTTGTT 2007

RESULT 8
 AR153439 1713 bp DNA linear PAT 08-AUG-2001
 LOCUS AR153439
 DEFINITION Sequence 3 from patent US 6235515.
 ACCESSION AR153439
 VERSION AR153439.1 GI:15120971
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1713)
 AUTHORS Russell,R.,Joyce,, Newcomb,R.,David,, Campbell,,P.,Malcolm,,
 Robin,G.,Charlesde ,Queteville,, Claudianos,C., Smyth,K.,A.,
 Boyce,T.,Mark,, Oakeshott,J.,Graham, and Brownlie,J.,Colin.
 TITLE Malation carboxylesterase
 JOURNAL Patent: US 6235515-A 3 22-MAY-2001;
 FEATURES Location/Qualifiers
 1..1713

BASE COUNT 515 a 306 c 370 g 522 t
 ORIGIN
 Query Match 55.8%; Score 955; DB 6; Length 1713;
 Best Local Similarity 73.3%; Pred. No. 1.1e-269;
 Matches 1222; Conservative 0; Mismatches 445; Indels 0; Gaps 0;

Oy 44 TTAATGCTATGTCATTAATTAACCAATCTAGCTGATACCAATGAACCAATTA 103
 Db 44 TTAATGCTATGTCATTAATTAACCAATCTAGCTGATACCAATGAACCAATTA 103
 Oy 104 TCATTAATGATATGACCAATTAAGGTTGTAGCAATGACCGCTACGATGATCT 163
 Db 104 CTGAATGATATGACCAATTAAGGTTGTAGCAATGACCGCTACGATGATCT 163
 Oy 164 ACTACAGTTTCGAGAGTATACCTATGCTAAGCCTCCAGTGGGTGAGTTGAGTTCAAG 223
 Db 164 ACTACAGTTTCGAGAGTATACCTATGCTAAGCCTCCAGTGGGTGAGTTGAGTTCAAG 223
 Oy 224 CACCCAGCGGCGCTGACCATGAGGAGGTGATGATTTGCTGGGCCAGCAACAGAT 283
 Db 224 CACCCAGCGGCGCTGACCATGAGGAGGTGATGATTTGCTGGGCCAGCAACAGAT 283
 Oy 284 CGTACAGACAGATTTGATTAAGTGGCAACCAAGGTGGAGATTTGCTATACCTGA 343
 Db 284 CAGTACAGATTTGATTAAGTGGCAACCAAGGTGGAGATTTGCTATACCTGA 343
 Oy 344 ATGTGATATACCATGACTTGAACCCAGCAAAAGCGCTCTGATGTTTATCATCAGT 403
 Db 344 GTGTCTATGCAAAATTAATCTAAATCCCAATCAAGCTCCGCTTTAGTATACATCAGT 403
 Oy 404 GCGGAGTTTATTTTGGGGAAGCAATGCTGATGCTTTGGTCCCGACTACTTATGA 463
 Db 404 GCGGAGTTTATTTTGGGGAAGCAATGCTGATGCTTTGGTCCCGACTACTTATGA 463
 Oy 464 AGAAACCCGTCGCTTGTGTAACCGTGAATGATGTTGGTGGTGTCTTATAGCC 523
 Db 464 AGAAACCCGTCGCTTGTGTAACCGTGAATGATGTTGGTGGTGTCTTATAGCC 523
 Oy 524 TGAATGGAATCTCAATGTCCTGGGCAACGCTGGCTCAAGATCAAGATGATGCT 583
 Db 524 TGAATGGAATCTCAATGTCCTGGGCAACGCTGGCTCAAGATCAAGATGATGCT 583
 Oy 584 TGAATGGAATCTCAATGTCCTGGGCAACGCTGGCTCAAGATCAAGATGATGCT 583
 Db 584 TGAATGGAATCTCAATGTCCTGGGCAACGCTGGCTCAAGATCAAGATGATGCT 583
 Oy 644 TCGGCGAAGTGTGCTGTTGGGCTCAACCCATTAATGATGATTAACCAACAGCCGTG 703
 Db 644 TCGGCGAAGTGTGCTGTTGGGCTCAACCCATTAATGATGATTAACCAACAGCCGTG 703
 Oy 704 GTTATTCATCTGCTGATGATGATGCTGCTGATGATGCTGCTGATGCTGCTGATG 763
 Db 704 GTTATTCATCTGCTGATGATGATGCTGCTGATGATGCTGCTGATGCTGCTGATG 763
 Oy 764 AATGCCAAGTGTGCTGCTGATGATGATGCTGCTGATGATGCTGCTGATGATGCT 823
 Db 764 AATGCCAAGTGTGCTGCTGATGATGATGCTGCTGATGATGCTGCTGATGATGCT 823
 Oy 824 AAAAGATATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 883
 Db 824 AAAAGATATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 883
 Oy 884 CACAAGTTTGAACCCGGAAGATGCAATTAAGTATGCTTTTGGACCATCTG 943
 Db 884 CACAAGTTTGAACCCGGAAGATGCAATTAAGTATGCTTTTGGACCATCTG 943
 Oy 944 TAGACCATTCAGACAGCGGATGCTGCTGATGATGATGATGATGATGATGATGATG 1003
 Db 944 TAGACCATTCAGACAGCGGATGCTGCTGATGATGATGATGATGATGATGATGATG 1003
 Oy 1004 GCGCCTGGGGAATTTGATACCCACATGATGATGATGATGATGATGATGATGATG 1063

```

Db 1004 CCGCTGGGCTAATTCGATACCCATGATGGTAAACACTCATATGAGGTCTATTTT 1063
Oy 1064 CCAATTCATTCGCCAACAATATCCGAGGTTGTAAAGAGTGGAAATCTGTGTAAT 1123
Db 1064 TCACATCAATTCCTTAAGCAAAATGCTATGCTTAAAGAAATGGAACTTGTCTCAAT 1123
Oy 1124 ATGTGCTTGGAGTGGTGCACAGTGAACGAGTGGCCCGGAAACCCGAGAGGGCTG 1183
Db 1124 TTGTGCAAGTGAATTTGGTGTGCTGAGAACGACCGCCGACAGACCTTGAATGGGTG 1183
Oy 1184 CCATTTGCAAAAAGCCCATTTGATGGGGAACACCTACTGCTGATATTTTATGAGC 1243
Db 1184 CTAATATTTAAAGGCTCATGTTACAGGAAACCAACACAGCTGATATTTATGATC 1243
Oy 1244 TTGTGCTATTTCTATTTCTCTTCCCTGATGCTGCTCTCTCAATTTGGCTTCAAC 1303
Db 1244 TTGTGCTCATCAATTTCTGTTCTGCTCCATCATGCTTGTGCAATTTACCTTCAATC 1303
Oy 1304 ACACAGCTGGCACTCCCATTTATTTGATGCTTTGATTTGATTTGATTTGATTTATTA 1363
Db 1304 ACACCTCCGCTACACCCGCTCTACTTGTATGCTTGTGCTGCTGCTGCTGCTGCTGCT 1363
Oy 1364 ACCCTATGCTATTTATGCTTTGGCCGCTGAGGCTTAAAGTGAAGCCATGCGATGAGC 1423
Db 1364 ATCCCTATGCTATTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1423
Oy 1424 TAACCTATCTCTTCTGCAACATTTTCTGCAACGCTGCGCAAGGAAAGCCGCAATCA 1483
Db 1424 TAACCTATCTCTTCTGCAACATTTTCTGCAACGCTGCGCAAGGAAAGCCGCAATCA 1483
Oy 1484 AAACCTATGAGCATGCTTGGCATTTGGAGCAATTTGCCACCAACCGGCAACCATCA 1543
Db 1484 AAACCTATGAGCATGCTTGGCATTTGGAGCAATTTGCCACCAACCGGCAACCATCA 1543
Oy 1544 GCAATGATATGAGCATGCTTGGCATTTGGAGCAATTTGCCACCAACCGGCAACCATCA 1603
Db 1544 GCAATGATATGAGCATGCTTGGCATTTGGAGCAATTTGCCACCAACCGGCAACCATCA 1603
Oy 1604 TCTATTAATGCTTAAATGCTGAGGATTTGAAGTGAATTTGAATTTGAATTTGAATTTGA 1663
Db 1604 TATCAAGTGTGATTTGAATTTGAATTTGAATTTGAATTTGAATTTGAATTTGAATTTGA 1663
Oy 1664 AAATTAACAATGCGCAAGTATTTGATTAATTTGATTAATTTGATTAATTTGATTTGAT 1710
Db 1664 AGATTAACAATGCGCAAGTATTTGATTAATTTGATTAATTTGATTAATTTGATTTGAT 1710

RESULT 9
AF139082 2175 bp mRNA linear INV 20-OCT-2000
LOCUS Haematobia irritans irritans alpha E7 esterase (ae7) mRNA, complete
DEFINITION cds.
ACCESSION AF139082
VERSION AF139082.1 GI:6502938
KEYWORDS
SOURCE
ORGANISM Haematobia irritans irritans.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Muscoidea; Muscidae; Haematobia.
REFERENCE
1 (bases 1 to 2175)
AUTHORS Guerrero, F.D.
TITLE Cloning of a horn fly cDNA, Halpnae7, encoding an esterase whose
transcript concentration is elevated in diazinon-resistant flies
JOURNAL Insect Biochem. Mol. Biol. 30 (11), 1107-1115 (2000)
MEDLINE 20445807
PUBMED 10989298
REFERENCE
2 (bases 1 to 2175)
AUTHORS Guerrero, F.D.
TITLE Direct Submission
JOURNAL Submitted (30-MAR-1999) USDA-ARS, Knippling-Bushland U.S. Livestock
Insects Research Laboratory, 2700 Fredericksburg Rd., Kerrville, TX

```

```

FEATURES
Source 78028, USA
Location/Qualifiers
1..2175
/organism="Haematobia irritans irritans"
/strain="Camp Coolley 4/97"
/sub_species="irritans"
/db_xref="taxon:75445"
/clone="HF41C"
/notes="pyrethroid and diazinon-resistant"
1..2175
/gene="ae7"
/feature="ae7"
282..1994
/gene="ae7"
/notes="similar to Lucilia cuprina and Drosophila
melanogaster alpha E7 esterases"
CDS
/product="alpha E7 esterase"
/protein_id="AF14517.1"
/db_xref="GI:6502938"
/translation="MNFNVSFLKRLKIKVENKILNRYLTNETHTVDNEYKIKG
VKRLVYDSDSFYSEFEGIPYAKPPVGLRFRKAPORPMPMGVADCCHAARSVDIFIS
NGSGSEDCILYNVTNNLNTDTRKRVLFVPHGGFICGEANRNYGADYFIRKDVFE
ITVOYRLVGLFSLNSENLNVGNAGLKDQYMAIRWKNNCSAFSGDDCTLLFES
AGASTHMMITTEQARGLPFRVYLNSTKMCJAHATOCORRGCTYAKRIGYGENDK
DYVDFLKNAPDYLAREKHLVINEELRQVAFAPTEPEYEDCVLPKRNEMK
TAGNSIPLTIGMTSYEGLEFISVQONHLILKELEFECYVGEVLEDRSPESLE
IASILKRLVYGETPTESEFTELSDYFVYPMHRLQRFNHTVGSPIYLYRPFDS
EELINPYRIKRYRGYKASIHDELTYLFWTMLSKRMPDSREYRTIEMIGIWTQFA
TNGNPSPEINCMENMTWDSLKSDSEVYKCMNIGIDELRFDLPEMEKIKVMQSVENKK
RELFF"
BASE COUNT 690 a 365 c 435 g 685 t
ORIGIN
Query Match 55.8%; Score 953.4; DB 3; Length 2175;
Best Local Similarity 73.2%; Pred. No. 3.4e-269;
Matches 1221; Conservative 0; Mismatches 446; Indels 0; Gaps 0;
Oy 44 TTAATGCGTGCATTAATTAACAAACTGCTGAGTACAAATGAACCAATTA 103
Db 325 TTAAGTGTGTAATAAATTTAAACCTTATTAACCAAGAAACCAATATG 384
Oy 104 TCGATACGATTAAGCAATTTAAGGTGTGAAGCAAGCTGATGATTTCT 163
Db 385 TCGATACGATTAAGCAATTTAAGGTGTGAAGGTGTTAAGCTGATGATTTCT 444
Oy 164 ACTACAGTTTGCAGATATACCTATGCTTAAGCCTCCAGTGGTGAATTAAG 223
Db 445 TCTACAGTTTGAAGATATACCATATGCCAAACCTCCTGAGGAGATTAAG 504
Oy 224 CACCCAGCGGCTGTACATGGAGGGTGTACGTGATTTGCTGTGGCCAGCAACAT 283
Db 505 CTCCACAAACGTCCTGCTGCTGAGTGAAGATTTGTCATGCTGCCCTCCGTT 564
Oy 284 CGGTACAGACAGATTTCAATTAAGTGAACCAACCCACAGTGTGAGATTTCTATAC 343
Db 565 CGGTTCAAACAGATTTCAATTAAGTGAACCAACCCACAGTGTGAGATTTCTATTA 624
Oy 344 ATGTATACCAATGACTTGAACCCAGACAAAGGCTCTGTTATGTTTCAATCATG 403
Db 625 ATGTATACCAATGACTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTA 684
Oy 404 GCGAGATTTTATTTTGGCGCAACCAATCTAATCGTTTGTCCGACCTACTTTGA 463
Db 685 GTGTGCTTATTTTGGCGCAACCAATCTAATCGTTTGTCCGACCTACTTTGA 744
Oy 464 AGAACCCTGCTCTGTTGATGCAATATCTTTGGGTGTGTGGTTTCTTATGACC 523
Db 745 AGAAGAGCTTGTCTTCAATCTGCAATATCTTTAGGGGTGTGTGGTTTCTTATG 804
Oy 524 TGAATTCGAAATCTCAATGCTCCCGCAACGCTGAGCTTCAGATCAAGTAATGCGCT 583
Db 805 TAAATTCGAAATCTCAATGCTGATATGCTGCTTAAAGATCAAGTATGCGCT 864

```

GenCore version 5.1.4-p5_4578
Copyright (c) 1993 - 2003 Compen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2003, 09:08:22 ; Search time 15.9846 seconds

(without alignments)
1725.596 Million cell updates/sec

Title: us-09-776-910-43

Perfect score: 1095

Sequence: 1 QVDFITGKVCSEDCXLYSLV.....KAKPDILIKLEKVLIEER 207

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: /SID52/gcgcdata/geneseq/geneseq-emb1/AA1980.DAT:*
2: /SID52/gcgcdata/geneseq/geneseq-emb1/AA1981.DAT:*
3: /SID52/gcgcdata/geneseq/geneseq-emb1/AA1982.DAT:*
4: /SID52/gcgcdata/geneseq/geneseq-emb1/AA1983.DAT:*
5: /SID52/gcgcdata/geneseq/geneseq-emb1/AA1984.DAT:*
6: /SID52/gcgcdata/geneseq/geneseq-emb1/AA1985.DAT:*
7: /SID52/gcgcdata/geneseq/geneseq-emb1/AA1986.DAT:*
8: /SID52/gcgcdata/geneseq/geneseq-emb1/AA1987.DAT:*
9: /SID52/gcgcdata/geneseq/geneseq-emb1/AA1988.DAT:*
10: /SID52/gcgcdata/geneseq/geneseq-emb1/AA1989.DAT:*
11: /SID52/gcgcdata/geneseq/geneseq-emb1/AA1990.DAT:*
12: /SID52/gcgcdata/geneseq/geneseq-emb1/AA1991.DAT:*
13: /SID52/gcgcdata/geneseq/geneseq-emb1/AA1992.DAT:*
14: /SID52/gcgcdata/geneseq/geneseq-emb1/AA1993.DAT:*
15: /SID52/gcgcdata/geneseq/geneseq-emb1/AA1994.DAT:*
16: /SID52/gcgcdata/geneseq/geneseq-emb1/AA1995.DAT:*
17: /SID52/gcgcdata/geneseq/geneseq-emb1/AA1996.DAT:*
18: /SID52/gcgcdata/geneseq/geneseq-emb1/AA1997.DAT:*
19: /SID52/gcgcdata/geneseq/geneseq-emb1/AA1998.DAT:*
20: /SID52/gcgcdata/geneseq/geneseq-emb1/AA1999.DAT:*
21: /SID52/gcgcdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SID52/gcgcdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SID52/gcgcdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1095	100.0	570	18	AAW17768
2	1090	99.5	570	18	AAW17766
3	1089	99.5	570	16	AAW17765
4	1089	99.5	570	18	AAW17767
5	819	74.8	570	18	AAW17767
6	812.5	74.2	572	22	ABB57850
7	653.5	59.7	567	22	ABB57857
8	610	55.7	554	22	ABB57866
9	591	54.0	572	22	ABB57867
10	590	53.9	530	22	ABB57868

11	578	52.8	565	22	ABB57746	Drosophila melanog
12	573	52.3	554	22	ABB59161	Drosophila melanog
13	561	51.2	542	22	ABB57790	Drosophila melanog
14	546.5	49.9	566	22	ABB51983	Drosophila melanog
15	530.5	48.4	602	23	AAW17598	Drosophila cell cy
16	499.5	45.6	541	22	ABB57789	Drosophila melanog
17	498	45.5	568	22	ABB57831	Drosophila melanog
18	496.5	45.3	513	19	AAW57863	C. felis esterase,
19	496.5	45.3	528	19	AAW57862	Ctenocephalides fe
20	496.5	45.3	528	22	AAE12916	Drosophila melanog
21	470	42.9	551	22	ABB57788	C. felis esterase,
22	434	39.6	530	19	AAW57866	Drosophila melanog
23	434	39.6	530	19	AAW57867	C. felis esterase,
24	432	39.5	495	19	AAW57869	C. felis esterase,
25	432	39.5	530	19	AAW57855	C. felis esterase,
26	432	39.5	530	19	AAW57877	C. felis esterase,
27	432	39.5	530	22	AAE12911	Ctenocephalides fe
28	432	39.5	550	19	AAW57853	C. felis esterase,
29	432	39.5	550	19	AAW57854	C. felis esterase,
30	432	39.5	550	22	AAE12910	Ctenocephalides fe
31	429	39.2	505	19	AAW57851	C. felis esterase,
32	429	39.2	505	22	AAW57852	C. felis esterase,
33	429	39.2	505	22	AAE12909	Ctenocephalides fe
34	429	39.2	550	19	AAW57864	Drosophila melanog
35	429	39.2	550	19	AAW57865	C. felis esterase,
36	429	39.2	550	22	AAE12923	Ctenocephalides fe
37	426.5	38.9	527	22	ABB62353	Drosophila melanog
38	413.5	37.8	576	22	ABB64915	Carboxylesterase c
39	401.5	36.7	575	23	ABB79538	Drosophila melanog
40	397.5	36.3	562	22	ABB64708	Carboxylesterase d
41	393.5	35.9	584	23	ABB07676	C. felis esterase,
42	391.5	35.8	570	19	AAW57857	C. felis esterase,
43	391.5	35.8	570	19	AAW57858	Ctenocephalides fe
44	391.5	35.8	570	22	AAE12913	C. felis esterase,
45	391.5	35.8	596	19	AAW57856	C. felis esterase,

ALIGNMENTS

RESULT 1
ID AAW17768 standard; Protein; 570 AA.
AC AAW17768;
XX
XX 08-AUG-1997 (first entry)
DE Malathion carboxylesterase RM6Con.
XX
XX Malathion carboxylesterase; organophosphate; insecticide;
KW pesticide; remediation; bioremediation; decontamination; esterase;
KW Lucilia cuprina.
XX
XX Lucilia cuprina.
OS
XX
XX WO9719176-A1.
PN
XX
XX 29-MAY-1997.
PD
XX
XX 22-NOV-1996; 96WO-A000746.
PF
XX
XX 23-NOV-1995; 95AU-0006751.
PR
XX
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
PA
XX
XX Boyce T, Brownlie JC, Campbell PM, Claudianos C;
PI Newcomb KD, Oakeshott JG, Robin GC, Russell RJ, Smyth K;
PL WPI; 1997-298113/27.
DR
XX
XX DNA encoding enzyme that degrades organophosphate pesticides -
PT useful for decontamination of soil, water, food etc

```

XX
PS Claim 6; Fig 1; 52bp; English.
CC A malathion carboxylesterase (AAW17768), designated RM-8Con, differs
CC from the esterase (AAW17765) of a malathion susceptible clone of
CC Lucilia cuprina by a substn. of the tryptophan residue at amino
CC acid position 251 by a leucine residue. This mutation from the active
CC site at the base of the active site gorge, 6.5 Angstroms from the active
CC site serine. The RM8Con amino acid sequence is a consensus deduced
CC from the DNA sequences of 3 resistant clones (RM8 A-C) and their
CC comparison to reference susceptible clone Lc743 (AA168596) of
CC Lc-alpha-E7. The enzyme is capable of hydrolysing carboxylester
CC and/or dimethylloxon organophosphates and can be formulated for use
CC in bioremediation strategies for treatment of soil or water.
XX
SQ Sequence 570 AA;
XX
Query Match 100.0%; Score 1095; DB 18; Length 570;
Best Local Similarity 100.0%; Pred. No. 1.2e-116; Indels 0; Gaps 0;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 QVDFITGKVCSEDCILSVYTNLNPETKRPVLYIHGGFTIGENHRDMYGPDYFIKK 60
DB 97 QVDFITGKVCSEDCILSVYTNLNPETKRPVLYIHGGFTIGENHRDMYGPDYFIKK 156
OY 61 DVLINIOYRLGALGFLSLNSEDLVNPGNAGLKQVYALRMWKNNKCNFGNPDNITVFG 120
DB 157 DVLINIOYRLGALGFLSLNSEDLVNPGNAGLKQVYALRMWKNNKCNFGNPDNITVFG 216
OY 121 ESAGASTHYMMLTEQRTGFLHRIILMSGNAICPLANTQCOHRAFTLAKLAGYGEDNDK 180
DB 217 ESAGASTHYMMLTEQRTGFLHRIILMSGNAICPLANTQCOHRAFTLAKLAGYGEDNDK 276
OY 181 DYLEFLMKAKPQDLIKLEKVLTLER 207
DB 277 DYLEFLMKAKPQDLIKLEKVLTLER 303
XX
RESULT 2
AAW17766
ID AAW17766 standard; Protein; 570 AA.
XX
AC AAW17766;
XX
DT 08-AUG-1997 (first entry)
XX
DE Malathion carboxylesterase.
XX
KW Malathion carboxylesterase; organophosphate; insecticide;
KW pesticide; remediation; bioremediation; decontamination; esterase;
KW Lucilia cuprina.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT MISC-difference 251 /label= Leu, Ser, Ala, Ile, Val, Thr, Cys, Met, Gly
ET /note= "pref. Leu or Ser"
XX
XX WO9719176-A1.
XX
XX 29-MAY-1997.
XX
XX 22-NOV-1996; 96WO-AU00746.
XX
XX 23-NOV-1995; 95AU-0006751.
XX
XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX
XX Boyce T, Brownlie JC, Campbell PM, Claudianos C;
XX Newcomb RD, Oakeshott JG, Robin GC, Russell RJ, Smyth K;
XX WPI, 1997-298113/27.
XX

```

```

XX
PS DNA encoding enzyme that degrades organophosphate pesticides -
XX useful for decontamination of soil, water, food etc
XX
XX Claim 1; Fig 1; 52bp; English.
CC A malathion carboxylesterase (AAW17766) differs from the esterase
CC (AAW17765) of a malathion susceptible clone of Lucilia cuprina by
CC a substn. of the tryptophan residue at amino acid position 251.
CC The enzyme is capable of hydrolysing carboxylester and/or
CC dimethylloxon organophosphates and can be formulated for use in
CC bioremediation strategies for treating soil or water.
XX
SQ Sequence 570 AA;
XX
Query Match 99.5%; Score 1090; DB 18; Length 570;
Best Local Similarity 99.5%; Pred. No. 4.4e-116; Indels 0; Gaps 0;
Matches 206; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 QVDFITGKVCSEDCILSVYTNLNPETKRPVLYIHGGFTIGENHRDMYGPDYFIKK 60
DB 97 QVDFITGKVCSEDCILSVYTNLNPETKRPVLYIHGGFTIGENHRDMYGPDYFIKK 156
OY 61 DVLINIOYRLGALGFLSLNSEDLVNPGNAGLKQVYALRMWKNNKCNFGNPDNITVFG 120
DB 157 DVLINIOYRLGALGFLSLNSEDLVNPGNAGLKQVYALRMWKNNKCNFGNPDNITVFG 216
OY 121 ESAGASTHYMMLTEQRTGFLHRIILMSGNAICPLANTQCOHRAFTLAKLAGYGEDNDK 180
DB 217 ESAGASTHYMMLTEQRTGFLHRIILMSGNAICPXANTQCOHRAFTLAKLAGYGEDNDK 276
OY 181 DYLEFLMKAKPQDLIKLEKVLTLER 207
DB 277 DYLEFLMKAKPQDLIKLEKVLTLER 303
XX
RESULT 3
AAR78142
ID AAR78142 standard; Protein; 570 AA.
XX
AC AAR78142;
XX
DT 22-DEC-1995 (first entry)
XX
DE OP-sensitive esterase E3.
XX
KW Esterase; E3; bioremediation; organophosphate; carbamate;
KW insecticide; pesticide; water decontamination; meat decontamination.
XX
OS Lucilia cuprina.
XX
XX WO9519440-A1.
XX
XX 20-JUL-1995.
XX
XX 13-JAN-1995; 95WO-AU00016.
XX
XX 13-JAN-1994; 94AU-0003347.
XX
XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX
XX Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;
XX Parker AG, Robin GC, Russell RJ, Smyth K;
XX WPI, 1995-263870/34.
XX
XX N-P-SDB; AAQ91561.
XX
XX Pure E3 esterase from Lucilia cuprina and related DNA - used to
XX eliminate residues of organo:phosphate and carbamate pesticides from
XX water, meat etc.
XX
XX Example 3; Page 12-17; 38pp; English.
XX

```

CC cDNA from organophosphate (OP)-sensitive *L. cuprina* pupa cDNA
 CC library was amplified using cluster-specific esterase primers.
 CC Isolated clone Lc743, a probable full-length cDNA, was expressed
 CC using a baculovirus vector in insect cells and shown to encode
 CC an OP-susceptible E3 esterase useful in bioremediation.

XX Sequence 570 AA;

Query Match 99.5%; Score 1089; DB 16; Length 570;
 Best Local Similarity 99.5%; Pred. No. 5.7e-116;
 Matches 206; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVPEITGKVGSEDCILSYVTNNLNPEKRPVLYIHGGFIIENHRDMPDYFIKK 60
 |||||||
 Db 97 QVPEITGKVGSEDCILSYVTNNLNPEKRPVLYIHGGFIIENHRDMPDYFIKK 156
 QY 61 DVLINIQIRLALGFLSLNSEDLPNGNGLKDYMALRWIKNNCANFGNPDIYFVG 120
 |||||||
 Db 157 DVLINIQIRLALGFLSLNSEDLPNGNGLKDYMALRWIKNNCANFGNPDIYFVG 216
 QY 121 ESAGASTHYWMLTEQTRGLFHRGILMSGNAICPLANTOCQHRAPFLAKLAGYKGEDNDK 180
 |||||||
 Db 217 ESAGASTHYWMLTEQTRGLFHRGILMSGNAICPMANTOCQHRAPFLAKLAGYKGEDNDK 276
 QY 181 DYLEFLMKAKPQDLIKLEKVLTEER 207
 |||||||
 Db 277 DYLEFLMKAKPQDLIKLEKVLTEER 303

RESULT 4
 AAM17765
 ID AAM17765 standard; Protein: 570 AA.

XX AAM17765;

DT 08-AUG-1997 (first entry)

DE Lc-alpha-E7 malathion susceptible clone Lc743 esterase E3.

XX Malathion carboxylesterase; organophosphate; insecticide;

KW pesticide; remediation; bioremediation; decontamination; esterase.

OS *Lucilia cuprina*.

XX Key Location/Qualifiers

FT Misc-difference 251 /note= "amino acid 251 is Leu in resistant

FT mutants"

XX WO9719176-A1.

XX 29-MAY-1997.

XX 22-NOV-1996; 96WO-AU00746.

XX 23-NOV-1995; 95AU-0006751.

XX (CSIR) COMMONWEALTH SCI & IND RES ORG.

XX Boyce T, Brownlie JC, Campbell PM, Claudianos C, Smyth K;

PI Newcomb RD, Oakeshott JG, Robin GC, Russell RJ, Smyth K;

XX WPI: 1997-298113/27.

DR N-PSDB; AAT68596.

XX DNA encoding enzyme that degrades organophosphate pesticides -

XX useful for decontamination of soil, water, food etc

XX Disclosure; Fig 1; 52pp; English.

XX Esterase E3 (AAM17765) from a malathion susceptible strain of

CC *Lucilia cuprina* differs from an esterase enzyme (see also

CC AAM17768) from malathion resistant RM8 strains by a Trp for Leu

CC substr. at amino acid position 251, owing to a mutation in the
 CC encoding DNA sequence (see also AAT68596). The resistant enzyme,
 CC termed malathion carboxylesterase, can be formulated for use in
 CC degrading environmental carboxylester or dimethyl general
 CC organophosphates.

XX Sequence 570 AA;

Query Match 99.5%; Score 1089; DB 18; Length 570;
 Best Local Similarity 99.5%; Pred. No. 5.7e-116;
 Matches 206; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVPEITGKVGSEDCILSYVTNNLNPEKRPVLYIHGGFIIENHRDMPDYFIKK 60
 |||||||
 Db 97 QVPEITGKVGSEDCILSYVTNNLNPEKRPVLYIHGGFIIENHRDMPDYFIKK 156
 QY 61 DVLINIQIRLALGFLSLNSEDLPNGNGLKDYMALRWIKNNCANFGNPDIYFVG 120
 |||||||
 Db 157 DVLINIQIRLALGFLSLNSEDLPNGNGLKDYMALRWIKNNCANFGNPDIYFVG 216
 QY 121 ESAGASTHYWMLTEQTRGLFHRGILMSGNAICPLANTOCQHRAPFLAKLAGYKGEDNDK 180
 |||||||
 Db 217 ESAGASTHYWMLTEQTRGLFHRGILMSGNAICPMANTOCQHRAPFLAKLAGYKGEDNDK 276
 QY 181 DYLEFLMKAKPQDLIKLEKVLTEER 207
 |||||||
 Db 277 DYLEFLMKAKPQDLIKLEKVLTEER 303

RESULT 5
 AAM17767
 ID AAM17767 standard; Protein: 570 AA.

XX AAM17767;

DT 08-AUG-1997 (first entry)

DE Md-alpha-E7 malathion resistant mutant.

XX Malathion carboxylesterase; organophosphate; insecticide;

KW pesticide; remediation; bioremediation; decontamination.

OS *Musca domestica* Rutgers strain.

XX Key Location/Qualifiers

FT Misc-difference 251 /note= "Ser-251 is tryptophan in the susceptible

FT allele expression product"

XX WO9719176-A1.

XX 29-MAY-1997.

XX 22-NOV-1996; 96WO-AU00746.

XX 23-NOV-1995; 95AU-0006751.

XX (CSIR) COMMONWEALTH SCI & IND RES ORG.

XX Boyce T, Brownlie JC, Campbell PM, Claudianos C, Smyth K;

PI Newcomb RD, Oakeshott JG, Robin GC, Russell RJ, Smyth K;

XX WPI: 1997-298113/27.

DR N-PSDB; AAT68597.

XX DNA encoding enzyme that degrades organophosphate pesticides -

XX useful for decontamination of soil, water, food etc

XX Disclosure; Fig 3; 52pp; English.

XX A polypeptide (AAM17767) is the expression product of a malathion

CC resistant allele of the *Musca domestica* Md-alpha-E7 gene, and

CC contains a Ser for Trp substr. at amino acid position 251. The

CC enzyme is capable of hydrolysing carboxylester and/or
CC dimethylxylon organophosphates and can be formulated for use
CC in bioremediation strategies for treatment of soil or water.
XX
SQ Sequence 570 AA:

Query Match 74.8%; Score 819; DB 18; Length 570;
Best Local Similarity 73.7%; Pred. No. 6,1e-85;
Matches 151; Conservative 27; Mismatches 27; Indels 0; Gaps 0;

QY 1 QVDFITGVGSEDCYLYSYTNNLNPTKRPVLYYIHGGFIFIGENHDMYGPDIYFKK 60
DB 97 QTFDISGPTSEDCYLYSYTNNLNPTKRPVLYYIHGGFIFIGENHDMYGPDIYFKK 156
QY 61 DVLINIQYRLGALGFLSLNSEDVNPVGNAGLKDQVALRWIKNNCANFGNPDNITVFG 120
DB 157 DVLINIQYRLGALGFLSLNSEDVNPVGNAGLKDQVALRWIKNNCANFGNPDNITVFG 216
QY 121 ESAGASTHYMMLEQTRGFLHRIILMSGNALCPANTOCQHRAPFLAKLAGYKGEDNDK 180
DB 217 ESAGASTHYMMLEQTRGFLHRIILMSGNALCPANTOCQHRAPFLAKLAGYKGEDNDK 276
QY 181 DYLEFLMKAKPDLIKLEKVLTEER 205
DB 277 DYLEFLMKANPYDLIKPEQVLTPE 301

RESULT 6

ABB57850
ID ABB57850 standard; Protein; 572 AA.

AC ABB57850;

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 342.

KW Drosophila; developmental biology; cell signalling; insecticide;
pharmaceutical.

OS Drosophila melanogaster.

PN WO200171042-A2.

PD 27-SEP-2001.

PF 23-MAR-2001; 2001WO-US09231.

PR 23-MAR-2000; 2000US-191637P.

PR 11-JUL-2000; 2000US-0614150.

PA (PEKE) PE CORP NY.

PI Venter JC, Adams M, Li PWD, Myers EW;

DR WPI: 2001-656860/75.

DR N-PSDB; ABL01953.

PT New isolated nucleic acid detection reagent for detecting 1000 or more
genes from Drosophila and for elucidating cell signalling and cell-cell
interactions -

PS Disclosure; SEQ ID NO 342; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
CC sequences (AB101840-AB16175) and the encoded proteins
CC (ABB57737-ABB72072).

CC The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 572 AA:

Query Match 74.2%; Score 812.5; DB 22; Length 572;
Best Local Similarity 73.1%; Pred. No. 3.4e-84;
Matches 152; Conservative 26; Mismatches 29; Indels 1; Gaps 1;

QY 1 QVDFITGVGSEDCYLYSYTNNLNPTKRPVLYYIHGGFIFIGENHDMYGPDIYFKK 60
DB 97 QVDFITGVGSEDCYLYSYTNNLNPTKRPVLYYIHGGFIFIGENHDMYGPDIYFKK 156
QY 61 DVLINIQYRLGALGFLSLNSEDVNPVGNAGLKDQVALRWIKNNCANFGNPDNITVFG 120
DB 157 DVLINIQYRLGALGFLSLNSEDVNPVGNAGLKDQVALRWIKNNCANFGNPDNITVFG 216
QY 121 ESAGASTHYMMLEQTRGFLHRIILMSGNALCPANTOCQHRAPFLAKLAGYKGEDND 179
DB 217 ESAGASTHYMMLEQTRGFLHRIILMSGNALCPANTOCQHRAPFLAKLAGYKGEDND 276
QY 180 KDYLEFLMKAKPDLIKLEKVLTEER 207
DB 277 KDYLEFLQNVKAKDLIRVENVLTLEER 304

RESULT 7

ABB57857
ID ABB57857 standard; Protein; 567 AA.

AC ABB57857;

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 363.

KW Drosophila; developmental biology; cell signalling; insecticide;
pharmaceutical.

OS Drosophila melanogaster.

PN WO200171042-A2.

PD 27-SEP-2001.

PF 23-MAR-2001; 2001WO-US09231.

PR 23-MAR-2000; 2000US-191637P.

PR 11-JUL-2000; 2000US-0614150.

PA (PEKE) PE CORP NY.

PI Venter JC, Adams M, Li PWD, Myers EW;

DR WPI: 2001-656860/75.

DR N-PSDB; ABL01960.

PT New isolated nucleic acid detection reagent for detecting 1000 or more
genes from Drosophila and for elucidating cell signalling and cell-cell
interactions -

PS Disclosure; SEQ ID NO 363; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
CC sequences (AB101840-AB16175) and the encoded proteins
CC (ABB57737-ABB72072).

CC The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO

[illegible]

RESULT 10
ABB57868
ID ABB57868 standard; Protein; 530 AA.
XX
AC ABB57868;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 396.
XX
KW Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P. 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI: 2001-655860/75.
DR N-PSDB; ABLO1971.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
XX
PS Disclosure; SEQ ID NO 396; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (AHL16176-AHL30511), expressed DNA sequences (ABLO1840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
CC
XX
SQ Sequence 530 AA;

[illegible]

XX	RESULT 11
XX	ABB57746
ID	ABB57746 standard; Protein; 565 AA.
AC	ABB57746;
XX	
DT	26-MAR-2002 (first entry)
XX	
DE	Drosophila melanogaster polypeptide SEQ ID NO 30.
XX	
KW	Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
XX	
OS	Drosophila melanogaster.
XX	
PN	WO20011042-A2.
XX	
PD	27-SEP-2001.
XX	
PF	23-MAR-2001; 2001WO-US09231.
XX	
PR	23-MAR-2000; 2000US-191637P. 11-JUL-2000; 2000US-0614150.
XX	
PA	(PEKE) PE CORP NY.
XX	
PI	Venter JC, Adams M, Li PMD, Myers EW;
DR	WPI: 2001-656860/75.
DR	N-PSTDB; ABL01849.
XX	
PT	New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
XX	
PS	Disclosure; SEQ ID NO 30; 21pp + Sequence Listing; English.
XX	
CC	The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (AB16176-AB130511), expressed DNA sequences (AB101840-AB16175) and the encoded proteins (ABB57737-ABB72072).
CC	The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX	
Sequence	565 AA:

Matches 105; Conservative 36; Mismatches 66; Indels 1; Gaps 1;

Matches	99;	Conservative	38;	Mismatches	54;	Indels	9;	Gaps	1;
---------	-----	--------------	-----	------------	-----	--------	----	------	----

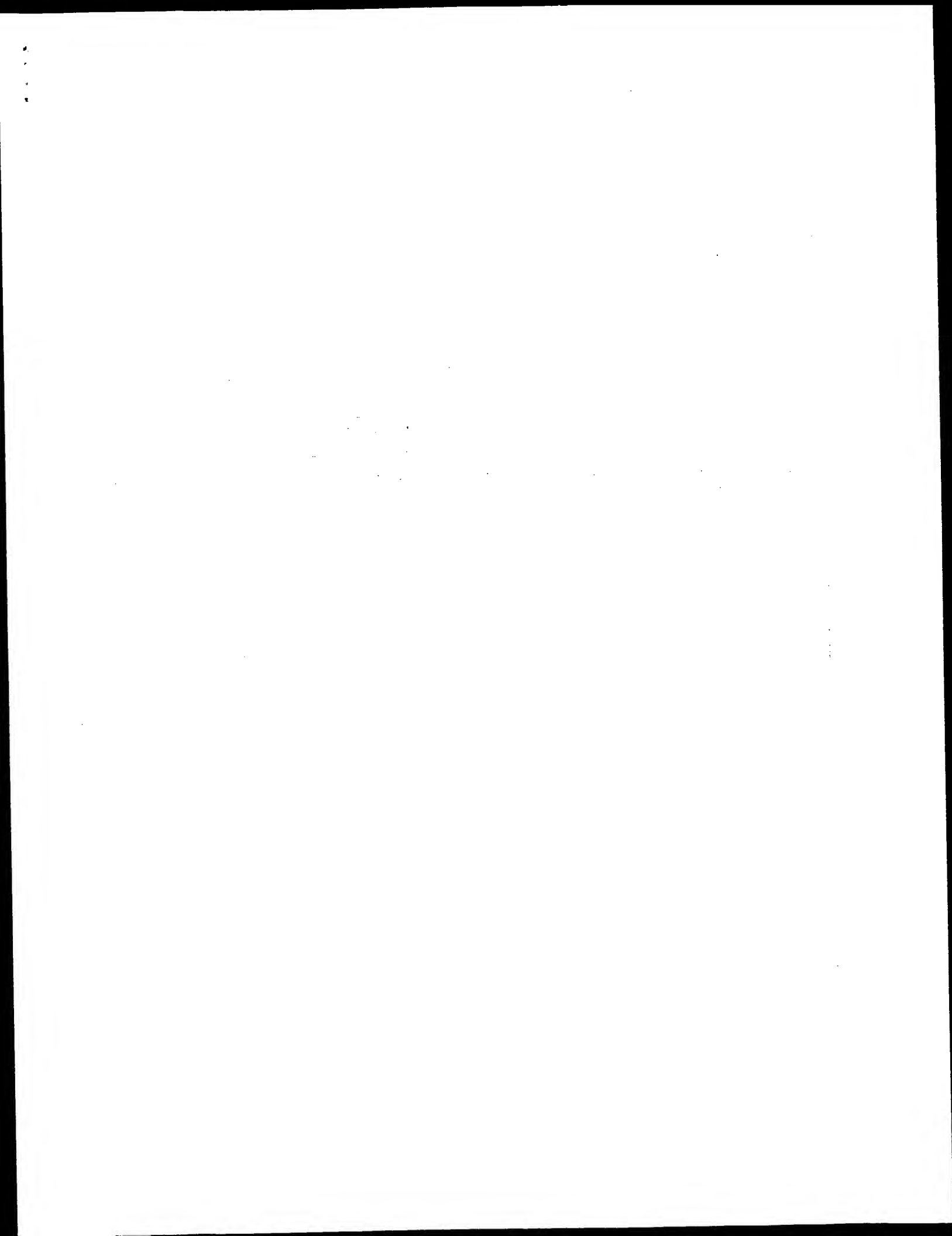
Mon Apr 14 10:18:20 2003

us-09-776-910-43.rag

Page 9

[illegible]

Search completed: April 4, 2003, 09:13:06
Job time : 17.9846 secs



GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2003, 09:10:33 ; Search time 6.92664 Seconds
(without alignments)
2872.940 Million cell updates/sec

Title: US-09-776-910-43

Perfect score: 1095

Sequence: 1 QVDFITGKVGSGEDCLYLSV.....KAKPDLIKLEKVLLEER 207

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR_73:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	483	44.1	540	2 A35986	esterase B1 - sout
2	475	43.4	540	2 S53370	carboxylesterase (
3	464	42.4	503	2 S53372	carboxylesterase (
4	463	42.3	540	2 S53371	carboxylesterase (
5	395	36.1	564	2 A34325	juvenile-hormone e
6	373	34.1	583	2 S10712	acetylcholinestera
7	370	33.6	614	2 A39256	acetylcholinestera
8	365.5	33.5	596	1 ACRYE	acetylcholinestera
9	366	33.4	614	2 JH0811	acetylcholinestera
10	365.5	33.4	564	2 A38868	carboxylesterase (
11	364.5	33.3	599	1 A38868	acetylcholinestera
12	362	33.1	614	2 JH0314	acetylcholinestera
13	358.5	32.7	584	2 S48724	acetylcholinestera
14	357.5	32.6	552	2 S36786	carboxylesterase (
15	356.5	32.6	603	2 S70849	carboxylesterase (
16	353.5	32.3	602	1 ACHU	cholinesterase (EC
17	349	31.9	544	2 B34089	carboxylesterase (EC
18	348.5	31.8	767	2 S47639	acetylcholinestera
19	347.5	31.7	547	2 S55233	juvenile hormone e
20	346.5	31.6	545	2 S58972	carboxylesterase (
21	345.5	31.6	545	2 S58980	carboxylesterase (
22	345.5	31.6	581	2 C39768	cholinesterase (EC
23	344.5	31.5	545	2 S58978	carboxylesterase (
24	344.5	31.5	545	2 S58970	carboxylesterase (
25	344.5	31.5	545	2 S58975	carboxylesterase (
26	344.5	31.5	545	2 S58982	carboxylesterase (
27	344.5	31.5	545	2 S58983	carboxylesterase (
28	344.5	31.5	545	2 S58977	carboxylesterase (
29	344.5	31.5	545	2 S58973	carboxylesterase (

30	344.5	31.5	612	2 A34967	sterol esterase (E
31	343.5	31.4	545	2 S58976	carboxylesterase (
32	343	31.3	548	2 T32907	hypothetical prote
33	343	31.3	599	2 A57701	sterol esterase (E
34	342.5	31.3	545	2 S58979	carboxylesterase (
35	341.5	31.2	545	2 S58969	carboxylesterase (
36	341.5	31.2	545	2 S58981	carboxylesterase (
37	340.5	31.1	545	2 S58974	carboxylesterase (
38	340.5	31.1	545	2 S58968	carboxylesterase (
39	337	30.8	544	2 A34089	carboxylesterase (
40	337	30.8	544	2 C41426	carboxylesterase (
41	337	30.8	544	2 A41426	carboxylesterase (
42	337	30.8	544	2 B40122	carboxylesterase (
43	337	30.8	544	2 A28022	carboxylesterase (
44	336	30.7	548	2 A40122	carboxylesterase (
45	335.5	30.6	545	2 S58971	carboxylesterase (

ALIGNMENTS

RESULT 1

A35986

esterase B1 - southern house mosquito

C:Species: Culex pipiens quinquefasciatus (southern house mosquito)

C>Date: 16-Nov-1990 #sequence_revision 13-Jan-1993 #text_change 21-Jul-2000

C/Accession: A35986

R;Kouches, C.; Pauplin, Y.; Agarwal, M.; Lemieux, L.; Herzog, M.; Abdon, M.; Beyssat

Proc. Natl. Acad. Sci. U.S.A. 87, 2574-2576, 1990

A>Title: Characterization of an amplification core and esterase B1 gene responsible for

A:Reference number: A35986; MWID:90207238; PMID:2320576

A:Accession: A35986

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-540 <MOU>

A:Cross-references: GB:M32328; NID:9156687; PIDN:AA28289.1; PID:9156688

A>Note: the authors translated the codon CGT for residue 213 as Ala, and CGT for resi

C;Superfamily: cholinesterase; cholinesterase homology

Query Match 44.1%; Score 483; DB 2; Length 540;

Best Local Similarity 44.9%; Pred. No. 6.4e-38;

Matches 88; Conservative 45; Mismatches 63; Indels 0; Gaps 0;

QY	8	KVCGSEDCLYVYNNLNPEKRPVLVYIHGGFTIGENHRMGYPDYFIKKVVLINI	67
DB	77	KIVCEESLKLINFAKINPSTPLPVLVYGGFEGTGTGLGPDPLVQDIYVSP	136
QY	68	QYRIGALGFLSLSNEDLVNPGNAGLKDQVALRWIKNNCANEGNDPNTVFEESGAAS	127
DB	137	NYRIGALGFLCSOEDDGPVGNAGLKDQDLIRWVLEINIAAFGDPKRYTLAHSAGAAS	196
QY	128	THYVMLLEQTRGLFHRGILMSGNALICPLANTQCOHRAFLTAGYKGEINDVLEFLM	187
DB	197	VQYHLISDASKDLFRIRIVSGSYSSWLSLROKNMYEKLAIGMDGGEGSALRFLR	256
QY	188	KAKPDLIKLEKVL 203	
DB	257	RAKPDIVAHQEKLT 272	

RESULT 2

S53370

carboxylesterase (EC 3.1.1.1) B2 - southern house mosquito

C:Species: Culex pipiens quinquefasciatus (southern house mosquito)

C>Date: 15-Jul-1995 #sequence_revision 08-Sep-1995 #text_change 21-Jul-2000

C/Accession: S53370; S44211

R;Vaughan, A.; Rodriquez, M.; Hemingway, J.

Biochem. J. 305, 651-658, 1995

A>Title: The independent gene amplification of electrophoretically indistinguishable

A:Reference number: S53370; MWID:95134253; PMID:7530448

A:Accession: S53370

A:Molecule type: mRNA

A:Residues: 1-540 <VAU>

OY 170 LAGYKEDND 179
Db 268 LQILGNORD 277

RESULT 6

10712

acetylcholinesterase (EC 3.1.1.7) - bovine

C:Species: Bos primigenius taurus (cattle)

C>Date: 21-Nov-1993 #sequence_revision 23-Mar-1995 #text_change 12-May-1995

C:Accession: S10712; A39734; B39734; B25650

R:Doctor, B.P.; Chapman, T.C.; Christner, C.E.; Deal, C.D.; de la Hoz, D.M.; Gentry, M.K.

FEBS Lett. 266, 123-127, 1990

A:Title: Complete amino acid sequence of fetal bovine serum acetylcholinesterase and its

A:Reference number: S10712; MUID:90306335; PMID:2365060

A:Accession: S10712

A:Molecule type: protein

A:Residues: 1-583 <DOC>

A:Experimental source: fetal serum

R:Roberts, W.L.; Doctor, B.P.; Foster, J.D.; Rosenberry, T.L.

J. Biol. Chem. 266, 7481-7487, 1991

A:Title: Bovine brain acetylcholinesterase primary sequence involved in intersubunit dis

A:Reference number: A39734; MUID:91210255; PMID:2019579

A:Accession: A39734

A:Molecule type: protein

A:Residues: 1-15, 'R', 17-38, 225-235, 'X', 237-244, 248-264, 'X', 266-273, 365-380, 396-404, 'X', 4

A:Experimental source: brain, erythrocyte

A:Accession: B39734

A:Molecule type: protein

A:Residues: 1-38 <RO>

A:Experimental source: fetal serum

R:Bon, S.; Chang, J.Y.; Strosberg, A.D.

FEBS Lett. 209, 206-212, 1986

A:Title: Identical N-terminal peptide sequences of asymmetric forms and of low-salt-sol

A:Reference number: A91370; MUID:87080761; PMID:3792544

A:Accession: B25650

A:Molecule type: protein

A:Residues: 'XS', 3-12 <BON>

A:Experimental source: caudate nucleus

C:Superfamily: cholinesterase; cholinesterase homology

C:Keywords: carboxylic ester hydrolase; glycoprotein

F:32-538/Domain: cholinesterase homology <CH>

F:61,265,350,464,541/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:203/Active site: Ser #status predicted

Query Match 34.1%; Score 373; DB 2; Length 583;
Best Local Similarity 42.3%; Pred. No. 2, 1e-27;
Matches 85; Conservative 36; Mismatches 72; Indels 8; Gaps 4;

OY 12 SEDCLYISVTNNLNPEKRPVLYIHGGFTIGENHRDMGDPYFIKKD-VVLTIOYR 70
Db 93 SEDCLYLVWTPYPRSPPTVLYWITGGFGYSASSLDVDFGLVQAEVTVLSMNYR 152
OY 71 LGALGFLSLNSEDLVNPGNAGLKDVVALRWIKNKGNGPNDITVFGESGASASTHY 130
Db 153 VGAFGLALPG-SREAPGNVGLLDQRLALQSVGNVAFAFGDPTSVTLFGESGASASTHY 211
OY 131 MMLTEQTRGLFHRGILMSGNAICPLANT--QCQHRAPFLAKLAGYK--GEDNDKYLE 184
Db 212 HLSPSPSGFLHRAVLQSGAPNGPMAVGVGEARRRATLLARLVGCPGAGNDTEIVA 271
OY 185 FLMAKAPDILKLEKVTLE 205
Db 272 CLRARPADLDVHEMVLPOE 292

RESULT 7

A39256

acetylcholinesterase (EC 3.1.1.7) precursor, brain splice form - human

C:Species: Homo sapiens (man)

C>Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 18-Jun-1999

C:Accession: A39256; S03959

R:Soreq, H.; Ben-Aziz, R.; Prody, C.A.; Seidman, S.; Gnatt, A.; Neville, L.; Lieberman-H

Proc. Natl. Acad. Sci. U.S.A. 87, 9688-9692, 1990

A:Title: Molecular cloning and construction of the coding region for human acetylchol

A:Reference number: A39256; MUID:91088577; PMID:2263619

A:Accession: A39256

A:Molecule type: DNA

A:Residues: 1-614 <SOR>

A:Cross-references: GB:M55040; NID:q177974; PIDN:AA68151.1; PID:q177975

A>Note: this sequence represents composite of clones including clone ABGACHE from adu

nce should represent an authentic brain splice form

R:Chajin, V.; Derr, D.; Charles, B.; Schnell, E.; August, T.

FEBS Lett. 247, 279-282, 1989

A:Title: Purification and partial amino acid sequence analysis of human erythrocyte a

A:Reference number: S03959; MUID:89232136; PMID:2714437

A:Accession: S03959

A:Molecule type: protein

A:Residues: 256-266, 'Y', 268-273, 306-308, 'X', 310-313, 'X', 315-316, 'D', 318-323, 'D', 325-3

Y', 532-551 <CH>

A:Experimental source: erythrocytes

C:Note: this form was a disulfide-linked homodimer

C:Gene: GDB:ACHE; YF

A:Cross-references: GDB:118746; OMIM:100740

A:Map position: 7q22-7q22

C:Superfamily: cholinesterase; cholinesterase homology

C:Keywords: alternative splicing; carboxylic ester hydrolase; glycoprotein; phosphati

F:63-569/Domain: cholinesterase homology <CH>

Query Match 33.8%; Score 370; DB 2; Length 614;
Best Local Similarity 42.3%; Pred. No. 4, 2e-27;
Matches 85; Conservative 34; Mismatches 74; Indels 8; Gaps 4;

OY 12 SEDCLYISVTNNLNPEKRPVLYIHGGFTIGENHRDMGDPYFIKKD-VVLTIOYR 70
Db 124 SEDCLYLVWTPYPRSPPTVLYWITGGFGYSASSLDVDFGLVQAEVTVLSMNYR 183
OY 71 LGALGFLSLNSEDLVNPGNAGLKDVVALRWIKNKGNGPNDITVFGESGASASTHY 130
Db 184 VGAFGLALPG-SREAPGNVGLLDQRLALQSVGNVAFAFGDPTSVTLFGESGASASTHY 242
OY 131 MMLTEQTRGLFHRGILMSGNAICPLANT--QCQHRAPFLAKLAGYK--GEDNDKYLE 184
Db 243 HLSPSPSGFLHRAVLQSGAPNGPMAVGVGEARRRATLLARLVGCPGAGNDTEIVA 302
OY 185 FLMAKAPDILKLEKVTLE 205
Db 303 CLRARPADLDVHEMVLPOE 323

RESULT 8

acetylcholinesterase (EC 3.1.1.7) precursor, 11S form [validated] - Pacific electric

N:Alternate names: acetylcholinesterase, asymmetric form

C:Species: Torpedo californica (Pacific electric ray)

C>Date: 17-Mar-1987 #sequence_revision 08-Nov-1996 #text_change 15-Sep-2000

C:Accession: A00773; A60820; B31962; A23902; B41117; S15677

R:Schumacher, M.; Camp, S.; Mauler, Y.; Newton, M.; Machee-quigley, K.; Taylor, S.S.

Nature 319, 407-409, 1986

A:Title: Primary structure of Torpedo californica acetylcholinesterase deduced from 1

A:Reference number: A00773; MUID:86118676; PMID:3753747

A:Accession: A00773

A:Molecule type: mRNA

A:Residues: 'NS', 11-596 <SCH>

A:Cross-references: GB:X03439; NID:964389

A:Experimental source: electric organ

A:Note: parts of this sequence, including the amino and carboxyl ends of the mature p

R:Schumacher, M.; Camp, S.; Mauler, Y.; Newton, M.; Machee-quigley, K.; Taylor, S.S.

Fed. Proc. 45, 2976-2981, 1986

A:Title: Primary structure of acetylcholinesterase: implications for regulation and f

A:Accession: A60820

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA
 A:Residues: 22-596 <SC2>
 R:Schumacher, M.; Maulet, Y.; Camp, S.; Taylor, P.
 J. Biol. Chem. 263, 18979-18987, 1988
 A:Title: Multiple messenger RNA species give rise to the structural diversity in acetylcholine
 A:Reference number: A92701; MUID:89066695; PMID:3198606
 A:Accession: A31962
 A:Molecule type: mRNA
 A:Residues: 1-23 <SC3>
 A:CROSS-references: EMBL:X03439; NID:964389
 A:Experimental source: clones ACHE-11 and ACHE-18
 A:Note: revision to sequence A00773
 A:Accession: B31962
 A:Molecule type: DNA
 A:Residues: 499-565 <SC4>
 A:CROSS-references: GB:X03439; NID:964389
 A:Experimental source: clone ACHE-1
 R:Macphée-Quigley, K.; Taylor, P.; Taylor, S.
 J. Biol. Chem. 260, 12185-12189, 1985
 A:Title: Primary structures of the catalytic subunits from two molecular forms of acetylcholine
 A:Reference number: A23902; MUID:86008285; PMID:2900071
 A:Accession: A23902
 A:Molecule type: protein
 A:Residues: 22, B, 24-45; 214-237 <MAC>
 A:Note: active site Ser identification
 R:Kreienkamp, H.J.; Weise, C.; Raba, R.; Aaviksaar, A.; Hucho, F.
 Proc. Natl. Acad. Sci. U.S.A. 88, 6117-6121, 1991
 A:Title: Amino acid residues of the catalytic center of acetylcholinesterase from Torpedo
 A:Reference number: M1117; MUID:91296772; PMID:2068091
 A:Accession: B4117
 A:Molecule type: protein
 A:Residues: 100-108 <KRE>
 A:Note: substrate binding site
 R:Maulet, Y.; Camp, S.; Gihney, G.; Rachinsky, T.L.; Ekstrom, T.J.; Taylor, P.
 Neuron 4, 289-301, 1990
 A:Title: Single gene encodes glycopospholipid-anchored and asymmetric acetylcholinesterase
 A:Reference number: PS0113; MUID:90166618; PMID:2306366
 A:Accession: S15677
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 557-596 <MAN>
 A:CROSS-references: EMBL:X56516
 R:Macphée-Quigley, K.; Vedvick, T.S.; Taylor, P.; Taylor, S.S.
 J. Biol. Chem. 261, 13565-13570, 1986
 A:Title: Profile of the disulfide bonds in acetylcholinesterase.
 A:Reference number: A43099; MUID:87008586; PMID:3759980
 A:Contents: annotation: disulfide bonds
 R:Sussman, J.L.; Harel, M.; Silman, I.
 submitted to the Brookhaven Protein Data Bank, October 1991
 A:Reference number: A50061; PDB:1ACE
 A:Contents: annotation: X-ray crystallography, 2.8 angstroms, residues 26-481, 511-555 of
 R:Sussman, J.L.; Harel, M.; Frolow, F.; Oefner, C.; Goldman, A.; Tokier, L.; Silman, I.
 Science 253, 872-879, 1991
 A:Title: Atomic structure of acetylcholinesterase from Torpedo californica: a prototypic
 A:Reference number: A43099; MUID:91439328; PMID:1678899
 A:Contents: annotation: X-ray crystallography, 2.8 angstroms, residues 26-481, 511-555 of
 C:Comment: Synapses usually contain this 11S (asymmetric) form of cholinesterase with a
 cholinesterase occurs on the outer surfaces of cell membranes, including those of erythrocytes
 C:Complex: 11S form is disulfide linked homodimer; 18S form is homotetramer, a dimer of
 C:Function:
 A:Description: hydrolyzes acetylcholine to choline and acetate
 A:Pathway: neurotransmitter degradation
 C:Superfamily: cholinesterase; cholinesterase homology
 C:Keywords: alternative splicing; carboxylic ester hydrolase; glycoprotein; membrane protein
 F:1-21/Domain: signal sequence #status predicted <SC2>
 F:22-596/Product: acetylcholinesterase, 11S form #status experimental <MAN>
 F:51-551/Domain: cholinesterase homology <CHE>
 F:80, 478, 554/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:88-115, 275-286, 423-542/Disulfide bonds: #status experimental
 F:105/Binding site: substrate (Trp) #status experimental
 F:221/Active site: Ser #status experimental
 F:348, 461/Active site: Glu, His #status predicted
 F:437/Binding site: carbohydrate (Asn) (covalent) #status experimental

F:593/Disulfide bonds: interchain #status experimental
 Query Match 33.5%; Score 366.5; DB 1; Length 596;
 Best Local Similarity 40.4%; Pred. No. 8, 8e-27;
 Matches 80; Conservative 43; Mismatches 68; Indels 7; Gaps 5;
 12 SEDCLYLVYTNLNPETRPVLYTHGGFLLGEGHRRMDYGPDPY-IRKDVYLINIOXR 70
 112 SEDCLYLVNTPSPRRKS-TYVWVWITGGFYSGSSSTLDVYNKYLATYEVLVLSYR 170
 71 LGALGFLSLNSEDLPVGNAGLKDYVALRWIKNNCANFGNPDNTITVGEASGAATHY 130
 171 VGAFGFLALHGSQ-EAPGVNGLDQRMALQWVDNTOFGGPKVTYITGEASGASVGM 229
 131 MMEETGRGLFHFGILMSGNAICPLANT--TQCHRAFLTLAKYAGKEDNDKVDLEFLM 187
 230 HILSPGSRDLFRRAITLQSSSPNCMAVSVAEERRRAVELGRNLNC-NLNSDELHCLR 288
 188 KAKPDILKLEKVTLE 205
 289 EKKPDELIVENVLPFD 306
 RESULT 9
 JH0811
 acetylcholinesterase (EC 3.1.1.7) catalytic chain precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 18-Jun-1999
 C:Accession: JH0811
 R:LeMay, C.; Bon, S.; Vernier, P.; Cousens, F.; Massoulie, J.
 J. Neurochem. 60, 337-346, 1993
 A:Title: Cloning and expression of a rat acetylcholinesterase subunit: generation of
 A:Reference number: JH0811; MUID:93107932; PMID:8417155
 A:Accession: JH0811
 A:Molecule type: mRNA
 A:Residues: 1-614 <LEG>
 A:CROSS-references: GB:S50879; NID:9262092; PIDN:AAB24586.1; PID:9262093
 A:Experimental source: striatum
 C:Comment: This protein is responsible for hydrolysis of acetylcholine at cholinergic
 C:Superfamily: cholinesterase; cholinesterase homology
 C:Keywords: carboxylic ester hydrolase; glycoprotein; membrane protein; muscle; nerve
 F:1-31/Domain: signal sequence #status predicted <SC2>
 F:32-614/Product: acetylcholinesterase catalytic chain #status predicted <MAN>
 F:63-569/Domain: cholinesterase homology <CHE>
 F:100-127, 288-303, 440-560/Disulfide bonds: #status predicted
 F:234, 365, 478/Active site: Ser, Glu, His #status predicted
 F:296, 381, 495/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 33.4%; Score 366; DB 2; Length 614;
 Best Local Similarity 41.3%; Pred. No. 1e-26;
 Matches 83; Conservative 35; Mismatches 75; Indels 8; Gaps 4;
 12 SEDCLYLVYTNLNPETRPVLYTHGGFLLGEGHRRMDYGPDPY-IRKDVYLINIOXR 70
 124 SEDCLYLVNTPSPRRKS-TYVWVWITGGFYSGASLDVDRFLAQVGGTVALVGMNR 183
 71 LGALGFLSLNSEDLPVGNAGLKDYVALRWIKNNCANFGNPDNTITVGEASGAATHY 130
 184 VGAFGFLALPG-SREAPGVNGLDQRMALQWVDNTOFGGPKVTYITGEASGASVGM 242
 131 MMEETGRGLFHFGILMSGNAICPLANT--TQCHRAFLTLAKYAGK---GEINDVDLE 184
 243 HILSPGSRDLFRRAITLQSSSPNCMAVSVAEERRRAVELGRNLNC-NLNSDELHCLR 302
 185 FLMKAKPDILKLEKVTLE 205
 303 CLKTRPADLDVHEHVLPOE 323
 RESULT 10
 S36787
 carboxylesterase (EC 3.1.1.1) F64 precursor - green peach aphid
 C:Species: Myzus persicae (green peach aphid)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: S36787
 R:Field: L.M.; Williamson, M.S.; Moores, G.D.; Devonshire, A.L.
 Biochem. J. 294, 569-574, 1993
 A>Title: Cloning and analysis of the esterase genes conferring insecticide resistance in
 A:Reference number: S36786; MUID:93384534; PMID:8373371
 A:Accession: S36787
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-564 <FTE>
 A:Cross-references: EMBL:X74555; NID:9397512; PIDN:CAA52649.1; PID:9397513
 C:Keywords: cholinesterase; cholinesterase homology
 C:Keywords: carboxylic ester hydrolase
 F:52-552/Domain: cholinesterase homology <CHE>

Query Match 33.4%; Score 365.5; DB 1; Length 564;
 Best Local Similarity 40.8%; Pred. No. 1e-26;
 Matches 82; Conservative 42; Mismatches 64; Indels 13; Gaps 8;

QY 2 VDFITG-KVCGSEDCIYVYTNLNLPETK----RPVLVYIHGGGFIIGENHRDMYGPDPY 56
 Db 92 IEFSGSKITIQEDCLFNTVTPKLPQENSAGDLMNVYVHIGGGYFGBS--ILYGFHY 149
 QY 57 FI-KKDVLLINIOYRGLGALGFLSLNSEDLPVGNAGLKDQVVALRWIKNCGNFGNPDN 115
 Db 150 LLDNDFYVYSINRSLVGLFAS--TGQGVLPGNNGLKQVVALKQIDQNIYVAFGSDPS 207
 QY 116 ITVEGSAAGASTHYMMLTEQTRGLFHRGILMSGNAICPLANTQ:COHRAFTLAKIAGYK 174
 Db 208 VITGMSAGSSVHNHLLISPMKSGFENRAITQSGSACFCHMSTAEVAKTXYIANLLGCP 267
 QY 175 GEDNDKDLVEFLMKAKKPDLLI 195
 Db 268 -TNSVETVECL-RSRPAKAI 286

RESULT 11

A38868
 acetylcholinesterase (EC 3.1.1.7) precursor - marbled electric ray
 C:Species: Torpedo marmorata (marbled electric ray)
 C>Date: 23-Apr-1993 #sequence_revision 15-Nov-1996 #text_change 11-Jun-1999
 C:Accession: A38868; A29682; S15696; A25650
 R:Massoulié, J.; Bon, S.
 Submitted to the EMBL Data Library, June 1992
 A:Reference number: A38868
 A:Accession: A38868
 A:Molecule type: mRNA
 A:Residues: 1-599 <MAS>
 A:Cross-references: EMBL:X05497; NID:964414; PIDN:CAA29047.1; PID:964415
 R:Storav, J.L.; Krejci, E.; Massoulié, J.
 EMBL J. 6, 1865-1873, 1967
 A>Title: cDNA sequences of Torpedo marmorata acetylcholinesterase: primary structure of
 A:Reference number: A29682; MUID:88004392; PMID:2820709
 A:Accession: A29682
 A:Molecule type: mRNA
 A:Residues: 1-40, 'G', 42-226, 'G', 228-272, 'G', 274-284, 'E', 286-420, 'N', 422-599 <SIK>
 A:Cross-references: EMBL:X05497
 R:Storav, J.L.; Duval, N.; Anselmet, A.; Bon, S.; Krejci, E.; Legay, C.; Osterlund, M.;
 EMBL J. 7, 2983-2993, 1988
 A>Title: Complex alternative splicing of acetylcholinesterase transcripts in Torpedo eide
 A:Reference number: S01293; MUID:89030590; PMID:3181125
 A:Accession: S15696
 A:Molecule type: mRNA
 A:Residues: 526-599 <SI2>
 A:Cross-references: EMBL:X13172; NID:964416; PIDN:CAA31570.1; PID:964417
 A:Experimental source: clone pACHE2
 R:Bon, S.; Chang, J.Y.; Stroberg, A.D.
 PNAS Lett. 209, 206-212, 1986
 A>Title: Identical N-terminal peptide sequences of asymmetric forms and of low-salt-sol
 inesterase.
 A:Reference number: A91370; MUID:87080761; PMID:3792544
 A:Accession: A25650
 A:Molecule type: protein

A:Residues: 25-40, 'G', 42-47 <BON>

A:Gene: Ache
 C:Genetics:
 C:Function: hydrolyzes acetylcholine to choline and acetate
 A:Description: neurotransmitter degradation
 C:Pathway: cholinesterase; cholinesterase homology
 C:Superfamily: cholinesterase; carboxylic ester hydrolase; glycoprotein; neurotran
 C:Keywords: alternative splicing; carboxylic ester hydrolase; glycoprotein; neurotran
 F:25-559/Domain: signal sequence #status predicted <SIG>
 F:25-559/Product: acetylcholinesterase #status predicted <MAT>
 F:24-554/Domain: cholinesterase homology <CHE>
 F:34-440, 481, 557/Binding site: carbohydrate (asn) (covalent) #status predicted
 F:91-118, 278-289, 426-545/Disulfide bonds: #status predicted
 F:224, 351, 464/Active site: Ser, Glu, His #status predicted
 F:596/Disulfide bonds: interchain #status predicted

Query Match 33.3%; Score 364.5; DB 1; Length 599;
 Best Local Similarity 40.4%; Pred. No. 1.4e-26;
 Matches 80; Conservative 44; Mismatches 67; Indels 7; Gaps 5;

QY 12 SEDCIYVYTNLNLPETKRPVLYIHGGGFIIGENHRDMYGPDPY-IKKDVLLINIOYR 70
 Db 115 SEDCIYVYTNLNLPETKRPVLYIHGGGFIIGENHRDMYGPDPY-ILYEVVLSLSTR 173
 QY 71 LGALGFLSLNSEDLPVGNAGLKDQVVALRWIKNCGNPDNITVEGSAAGASTHY 130
 Db 174 VGAFGLALHGSQ-EAPGNMGLLDQNRALQWVADNIOFGGDPKTYTLTGESAGRASVGM 232
 QY 131 MMLTEQTRGLFHRGILMSGNAICPLAN--TQCQHRAFTLAKIAGYKGEDNDKDLVEFLM 187
 Db 233 HILSPGSRDLFRRAILLQSGSPNCPMASVYAEGRRAVELRRMLNC-NLNSDEDLIOCLR 291
 QY 188 KAKPDILKLEEKVYTLTE 205
 Db 292 EKRPQELIDVEWVLPED 309

RESULT 12

AJ0314
 acetylcholinesterase (EC 3.1.1.7) precursor - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 18-Jun-1999
 C:Accession: JH0314
 R:Rechinsky, T.L.; Camp, S.; Li, Y.; Ekstrom, T.J.; Newton, M.; Taylor, P.
 Neuron 5, 317-327, 1990
 A>Title: Molecular cloning of mouse acetylcholinesterase: tissue distribution of alte
 A:Reference number: JH0314; MUID:90380429; PMID:2400605
 A:Accession: JH0314
 A:Molecule type: mRNA
 A:Residues: 1-614 <RAC>
 A:Cross-references: EMBL:X56518; NID:949844; PIDN:CAA39867.1; PID:949845
 A:Experimental source: Brain
 C:Superfamily: cholinesterase; cholinesterase homology
 C:Keywords: carboxylic ester hydrolase; glycoprotein; membrane protein; muscle; nerve
 F:1-314/Domain: signal sequence #status predicted <SIG>
 F:1-614/Product: acetylcholinesterase #status predicted <MAT>
 F:63-559/Domain: cholinesterase homology <CHE>
 F:100-127, 288-303, 440-560/Disulfide bonds: #status predicted
 F:224/Active site: Ser #status predicted
 F:296, 381, 495/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 33.1%; Score 362; DB 2; Length 614;
 Best Local Similarity 41.3%; Pred. No. 2.4e-26;
 Matches 83; Conservative 34; Mismatches 76; Indels 8; Gaps 4;

QY 12 SEDCIYVYTNLNLPETKRPVLYIHGGGFIIGENHRDMYGPDPYK-KDVLLINIOYR 70
 Db 124 SEDCIYVYTNLNLPETKRPVLYIHGGGFIIGENHRDMYGPDPYK-KDVLLINIOYR 183
 QY 71 LGALGFLSLNSEDLPVGNAGLKDQVVALRWIKNCGNPDNITVEGSAAGASTHY 130
 Db 184 VGFGLALPQ-SREAPGNVGLLDQRLALQWVADNIOFGGDPKTYTLTGESAGRASVGM 242

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2003, 09:09:07 ; Search time 3.86293 Seconds

(without alignments)
2222.555 Million cell updates/sec

Title: US-09-776-910-43

Perfect score: 1095

Sequence: 1 QVDFITGKVGSGEDCLYLSV.....KAKPDILKLEKVLLEER 207

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match Length	ID	Description
1	483	44.1	540	EST1_CULPI	P16854 culex pipie
2	390.5	35.7	564	EST1_HELVI	P12992 heliothis v
3	383	35.0	613	ACES_BOVIN	P23795 bos taurus
4	381	34.8	357	CHL1_BRALA	Q95000 brachiolesto
5	380	34.7	611	ACES_FELCA	Q62763 felis silve
6	370	33.8	614	ACES_HUMAN	P23203 homo sapien
7	369	33.7	584	ACES_RABIT	Q29499 oryctolagus
8	369	33.7	634	ACES_BRARE	Q94653 brachydanio
9	367	33.5	633	ACES_ELEEL	Q42275 electrophor
10	366.5	33.5	586	ACES_TORCA	P40588 torpeda cal
11	366	33.4	614	ACES_RAT	P31936 rattus norv
12	365.5	33.4	564	EST1_MYAPE	P35502 myzus persi
13	365.5	33.4	581	ACES_BUNFA	Q92035 bungarus fa
14	364.5	33.3	590	ACES_TORMA	P07692 torpeda mar
15	362	33.0	574	ACES_MOUSE	P21836 mus musculu
16	361.5	33.0	614	CHLE_HORSE	P81908 equus cabal
17	357.5	32.6	552	EST1_MOUSE	P35501 myzus persi
18	356.5	32.6	603	CHLE_MOUSE	Q03311 mus musculu
19	353.5	32.3	602	CHLE_HUMAN	P06276 homo sapien
20	349	31.9	544	EST1_DROME	P18167 drosophila
21	348.5	31.8	767	ACES_CHICK	P36196 gallus gall
22	345.5	31.6	581	CHLE_RABIT	P21937 oryctolagus
23	344.5	31.5	545	EST1_DROME	P25726 drosophila
24	344.5	31.5	612	EST1_DROME	P07882 rattus norv
25	343.5	31.4	547	EST1_DROME	P25727 drosophila
26	343	31.3	599	BAL_MOUSE	Q64285 mus musculu
27	341.5	31.2	545	EST1_DROME	P25725 drosophila
28	339	31.0	542	EST1_DROME	P47982 drosophila
29	337	30.8	744	EST1_DROME	P08171 drosophila
30	331.5	30.3	542	BAL_HUMAN	P19835 homo sapien
31	331	30.2	542	EST1_DROME	Q08662 drosophila
32	327	29.9	629	ACES_LEPDE	Q27677 leptinotars
33	324	29.6	566	EST1_PIG	Q29550 sus scrofa

34	322.5	29.5	565	EST10_RAT	P16303 rattus norv
35	321.5	29.4	597	BAL_BOVIN	P30122 bos taurus
36	320.5	29.3	338	ACES_MYXGL	Q92081 myxine glut
37	319	29.1	489	PBNA_BACST	P37967 bacillus su
38	318.5	29.1	532	EST12_RABIT	P14943 oryctolagus
39	318.5	29.1	561	EST1_MESAU	Q64419 mesocricetu
40	318.5	29.1	567	EST1_HUMAN	P23141 homo sapien
41	317.5	29.0	561	EST14_RAT	Q64573 rattus norv
42	314	28.7	620	ACES1_CAEBR	Q27459 caenorhabdi
43	313.5	28.6	337	CHL2_BRALA	P10959 brachiolesto
44	313.5	28.6	349	EST1_RAT	P10959 rattus norv
45	313	28.6	554	EST1_MOUSE	Q63880 mus musculu

ALIGNMENTS

RESULT 1	ID	EST1_CULPI	STANDARD	PRT	540 AA.
AC	P16854:	01-AUG-1990 (Rel. 15, Created)			
DT	01-AUG-1990 (Rel. 15, Last sequence update)				
DT	01-FEB-1994 (Rel. 28, Last annotation update)				
DE	Esterase B1 precursor (EC 3.1.1.1).				
GN	Bl.				
OS	Culex pipiens (House mosquito).				
OC	Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;				
OC	Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;				
OC	Culicoidae; Culex.				
OX	NCBI_TaxID=7175;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=TEM-R;				
RX	MEDLINE=90207238; PubMed=2320576;				
RA	Mouches C., Pauplin Y., Agarwal M., Lemieux L., Herzog M.,				
RA	Abadon C., Baysat-Arnaouty V., Hylien O., de Saint Vincent B.R.,				
RA	Georgiou G.P., Pasteur N.;				
RT	Characterization of amplification core and esterase B1 gene				
RT	responsible for insecticide resistance in Culex.;				
RL	Proc. Natl. Acad. Sci. U.S.A. 87:2574-2578(1990).				
CC	- FUNCTION: OVERPRODUCTION OF NONSPECIFIC ESTERASES IS A COMMON				
CC	MECHANISM OF RESISTANCE TO ORGANOPHOSPHATE INSECTICIDES.				
CC	- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a				
CC	carboxylic anion.				
CC	- MISCELLANEOUS: THERE ARE TWO SUCH ESTERASES: A AND B. ALLELES OF				
CC	BOTH A AND B ARE KNOWN.				
CC	- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.				
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	EMBL: M32328; AAA28289.1; -				
DR	PIR: A35986; A35986.				
DR	HSSP: P21836; IMAA.				
DR	InterPro: IPR002018; Carboxylesterase.				
DR	InterPro: IPR000379; Ser_esterase_site.				
DR	Pfam: PF00135; Coesterase; 1.				
DR	PROSITE: PS00412; CARBOXYLESTERASE_B_1; 1.				
DR	PROSITE: PS00411; CARBOXYLESTERASE_B_2; FALSE_NEG.				
KW	Hydrolase; Serine esterase; Glycoprotein; Multigene family; Signal.				
FT	CHAIN	1	540		
FT	ACT_SITE	191	191		
FT	ACT_SITE	442	442		
FT	DISULFID	68	81		
FT	CARBOHYD	452	452		
SQ	SEQUENCE	540 AA;	60806 MW;	F73B253A7157C95 CRC64;	

Query Match 44.1%; Score 483; DB 1; Length 540;
 Best Local Similarity 44.9%; Pred. No. 1.6e-37;
 Matches 88; Conservative 45; Mismatches 63; Indels 0; Gaps 0;

QY 8 KYCGSEDCILYLSVYNNLNDETRKPVLYVYHGGGFTIGENHNDMGDDYFIKKDVLVINT 67
 1
 77 KIVCGCDSTFKINFAKINPSTPLPYMLYIGGGEGTSGTELYGPDPLVQKDIYLVSR 136
 68 QYRIGALGFLSINSEDLNPGNAGLKDQVMALEMINNANPCGNPDNITVPEESGAAS 127
 1
 137 NTRIGALGFLCCQSEODGVPNAGLKDQVMALEMINNANPCGNPDNITVPEESGAAS 196
 128 THYMLTEQTRGIFHRGILMSGNAICPLANTOCQHRATFLAKYKGEDNDKQVLEFLM 187
 1
 197 VQYHLSDASKDLFORRYIMSSGTSYSSWLTQRNNVETLAKAIGMDGGEGSALRFLR 256
 QY 188 KAKPDILKLEKVL 203
 1
 DB 257 RAKPEDIVAHQEKLT 272

RESULT 2
 ESTD_HELVY STANDARD; PRT; 564 AA.
 AC P12992;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Juvenile hormone esterase precursor (EC 3.1.1.59) (JH esterase).
 OS Heliothis virescens (Noctuid moth) (Owlet moth).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;
 OC Ditrysia; Noctuoidea; Noctuidae; Heliothinae; Heliothis.
 NCBI_TaxID=7102;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 20-54.
 RA MEDLINE=89308671; PubMed=2745451;
 RA Hanzlik T.N., Yehia A.I.A.-A., Harshman L.G., Hammock B.D.;
 RT "Isolation and sequencing of cDNA clones coding for juvenile hormone
 esterase from *Heliothis virescens*. Evidence for a catalytic mechanism
 for the serine carboxylsterases different from that of the serine
 proteases.";
 RT J. Biol. Chem. 264:12419-12425(1989).
 RL [2]
 RN REVISIONS.
 RA Hanzlik T.N.;
 RL Submitted (DEC-1997) to the EMBL/Genbank/DBS databases.
 CC -I- FUNCTION: JH ESTERASE PLAYS A CRUCIAL ROLE IN THE DECREASE OF
 JH ACTIVITY IN LEPIDOPTERAN INSECTS, BY HYDROLYZING THE METHYL
 ESTER OF JH. IT IS ALSO INVOLVED IN THE TRANSPORT OF JH.
 CC -I- CATALYTIC ACTIVITY: Methyl (2E,6E)-(10R,11S)-10,11-epoxy-3,7,11-
 trimethyltrideca-2,6-dienate + H(2)O = (2E,6E)-(10R,11S)-10,11-
 epoxy-3,7,11-trimethyltrideca-2,6-dienate + methanol.
 CC -I- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL ESTERASE/LIPASE FAMILY.
 CC -----
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: J04955; AAB88629.1; -
 DR PIR: A34325; A34325.
 DR HSR: P37967; I0E3.
 DR InterPro: IPR002018; Carboxylase.
 DR InterPro: IPR000379; Ser-estrs.site.
 DR Pfam: PF00135; Coesterase.1.
 DR PROSITE: PS00122; CARBOXYL ESTERASE_B.1; 1.
 DR PROSITE: PS00941; CARBOXYL ESTERASE_B.2; FALSE_NEG.
 KW Hydrolase; Serine esterase; Glycoprotein; Signal.

FT SIGNAL 1 19
 FT CHAIN 20 564
 FT ACT_SITE 220 220
 FT ACT_SITE 351 351
 FT ACT_SITE 465 465
 FT DISULFID 89 109
 FT CARBOHYD 81 81
 FT CARBOHYD 180 180
 FT CARBOHYD 402 402
 FT CARBOHYD 515 515
 FT VARIANT 29 29
 FT VARIANT 52 52
 SQ SEQUENCE 564 AA; 62614 MW; D140E5DD91914E8D CRC64;

Query Match 35.7%; Score 390.5; DB 1; Length 564;
 Best Local Similarity 38.4%; Pred. No. 7.3e-29;
 Matches 84; Conservative 42; Mismatches 76; Indels 17; Gaps 7;

QY 1 QVDFITGKYCG-----SEDCILYLSVY--NNLNDETRK-----RPLVYVYHGGGFTIGENHR 49
 1
 DB 91 QTVYLGRLMAASEMSEACIYANIHVPMQSL-PRVHGTPPLRLIVFIHGGGAFPSGHE 149
 QY 50 DMGPDYFIKKDVLVINTQYRIGALGFLSINSEDLNPGNAGLKDQVMALEMINNANPCGNPDNITVPEESGAAS 109
 1
 DB 150 DLHGPEYLVTKVYVITFVNFVFGFLSMNT--TKIPGNAGHLDQVTLIRVQRAKNE 207
 QY 110 GGNPDNITVPEESGAASASHYMLTEQTRGIFHRGILMSGNAICPLANTOCQHRATFLAK 169
 1
 DB 208 GGSPSITTAGSAGSAHALTLTKATBGLFRALIMSGTSYFTTSPLEAFATYSKO 267
 QY 170 LAGYKG-EDNDKDLVLEFLMKAKPDILKLEKVL 207
 1
 DB 268 LQILGILNFTDPEIRHQLDIPAE--KLINEANAVLIEQ 304

RESULT 3
 ACES_BOVIN STANDARD; PRT; 613 AA.
 ID ACES_BOVIN
 AC P23795; 097579;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Acetylcholinesterase precursor (EC 3.1.1.7) (ACHE).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RA TISSUE=Kidney;
 RC MEDLINE=98359754; PubMed=9693127;
 RA Mendelson I., Kromman C., Ariel N., Shafferman A., Velan B.;
 RT "Bovine acetylcholinesterase: cloning, expression and
 characterization.";
 RT Biochem. J. 334:251-259(1998).
 RL [2]
 RP SEQUENCE OF 31-613 (ISOFORM H).
 RC TISSUE=Retal serum;
 RX MEDLINE=90306335; PubMed=2365060;
 RA Doctor B.P., Chapman T.C., Christner C.E., Deal C.D., de la Hoz D.M.,
 RA Gentry M.K., Ogert R.A., Rush R.S., Smyth K.K., Wolfe A.D.;
 RT "Complete amino acid sequence of fetal bovine serum
 acetylcholinesterase and its comparison in various regions with other
 cholinesterases.";
 RL FEBS Lett. 266:123-127(1990).
 CC -I- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.
 CC -I- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
 CC -I- SUBUNIT: ISOFORM H GENERATES GPI-ANCHORED DIMERS; DISULFIDE
 CC LINKED. ISOFORM T GENERATES MULTIPLE STRUCTURES, RANGING FROM
 CC MONOMERS AND DIMERS TO COLLAGEN-TAILED AND HYDROPHOBIC-TAILED
 CC FORMS, IN WHICH CATALYTIC TETRAMERS ARE ASSOCIATED WITH ANCHORING

CC PROTEINS THAT ATTACH THEM TO THE BASAL LAMINA OR TO CELL
 CC MEMBRANES. IN THE COLLAGEN-TAILED FORMS, ISOFORM T SUBUNITS ARE
 CC ASSOCIATED WITH A SPECIFIC COLLAGEN, COL1, WHICH TRIGGERS THE
 CC FORMATION OF ISOFORM T TRIMERS, FROM MONOMERS AND DIMERS.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS, H AND T (SHOWN HERE); ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL: AF061815; AAC64270.1; -
 DR EMBL: AF061813; AAC64270.1; JOINED.
 DR EMBL: AF061814; AAC64270.1; JOINED.
 DR PIR: S10712; S10712.
 DR HSSP: P2303; ZCUL.
 DR GlycoSuiteDB: P23795; -
 DR InterPro: IPR002018; Carboxylesterase.
 DR InterPro: IPR000997; Cholinesterase.
 DR InterPro: IPR000379; Ser_ests_site.
 DR Pfam: PF00135; Coesterase; 1.
 DR PRINTS: PR00878; CHOLINESTRASE.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B.1; 1.
 DR PROSITE: PS00941; CARBOXYLESTERASE_B.2; 1.
 KM Hydrolyase: Serine esterase; Synapse; Membrane; Nerve; Muscle; Signal;
 KM Neurotransmitter degradation; Glycoprotein; Alternative splicing.

FT SIGNAL 1 30
 FT CHAIN 31 613
 FT ACT_SITE 233 233
 FT ACT_SITE 364 364
 FT ACT_SITE 477 477
 FT DISULFID 99 126
 FT DISULFID 287 302
 FT DISULFID 439 559
 FT DISULFID 610 610
 FT CARBOHYD 91 91
 FT CARBOHYD 295 295
 FT CARBOHYD 380 380
 FT CARBOHYD 494 494
 FT VARSPLIC 574 613

CONFLICT 46 46
 CONFLICT 169 169
 CONFLICT 212 212
 CONFLICT 323 323
 CONFLICT 352 352
 CONFLICT 424 424
 CONFLICT 524 524
 CONFLICT 554 554
 CONFLICT 571 571

SEQUENCE 613 AA; 67663 MW; 698D4F0DF8624B12 CRC64;
 S -> N (IN REF. 2).
 R -> E (IN REF. 2).
 T -> V (IN REF. 2).
 W -> S (IN REF. 2).
 S -> H (IN REF. 2).
 H -> V (IN REF. 2).
 L -> W (IN REF. 2).
 D -> A (IN REF. 2).
 EVRRGL -> GYPOAS (IN REF. 2).
 -> ASDAPCTGSPAHGAEAPRRGLPLPLLLLSRL
 LRL (IN ISOFORM H).
 R -> E (IN REF. 2).
 T -> V (IN REF. 2).
 W -> S (IN REF. 2).
 S -> H (IN REF. 2).
 H -> V (IN REF. 2).
 L -> W (IN REF. 2).
 D -> A (IN REF. 2).
 EVRRGL -> GYPOAS (IN REF. 2).
 -> ASDAPCTGSPAHGAEAPRRGLPLPLLLLSRL

Query Match 35.0%; Score 383; DB 1; Length 613;
 Best Local Similarity 42.8%; Pred. No. 4.1e-28;
 Matches 86; Conservative 35; Mismatches 72; Indels 8; Gaps 4;

QY 12 SEDCLYLSYNNLNINPETKRPVLYVYHGGFTIGENHRDMYGPDYFKD-VLLINIOYR 70
 DB 123 SEDCLYLNWVOPSPAP-PGATVLYVWYGGFGFSGLSDYDGRYLARMEDEVVYVSNMR 182

QY 71 LGALGFLSLNSEDLVNPNAGLKDQVMAIRKKNKNCANFGNPNNTVFGESAGASTHY 130
 DB 183 VGAFGLTSGE--AAPNAGLIDQHLALQWQONISFGGDPKVTYIFESAGASVNF 241

QY 131 MMLTEQRTGLFHRGILMSGNAICPLANT---OCQRAFTLAKLAGYGEQNDQVLE-EFL 186
 DB 242 HILSPSRDLQFRMMHMSASALAPWATPSPQARQSRKALALIDIGSADDEMDVYVACL 301

QY 185 FLMAKRPQDLIKLEEVLTLE 205
 DB 302 CLRARPAQDLVDHEWVLPQE 322

RESULT 4
 CHIL_BRLA
 ID CHIL_BRLA STANDARD; PRT; 357 AA.
 AC Q95000;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Cholinesterase 1 (EC 3.1.1.8) (Fragment).
 GN CHEL
 OS Branchiostoma lanceolatum (Common lancelet) (Amphioxus).
 OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
 OC Branchiostoma.
 OX NCBI_TaxID=7740;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-97216845; PubMed-9062997;
 RA Sutherland D., McClellan J.S., Milner D., Soong W., Axon N.,
 RA Sanders M., Hester A., Kao Y.H., Poczatek T., Routt S.,
 RA Pezzementi L.;
 RT "Two cholinesterase activities and genes are present in amphioxus.";
 RL J. Exp. Zool. 277:213-229(1997).
 CC -1- CATALYTIC ACTIVITY: An acetylcholine + H(2)O = choline + a
 CC carboxylic acid anion.
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL: U74378; AB18262.1; -
 DR HSSP: P21836; IMAA.
 DR InterPro: IPR002018; Carboxylesterase.
 DR InterPro: IPR000379; Ser_ests_site.
 DR Pfam: PF00135; Coesterase; 1.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B.1; 1.
 DR PROSITE: PS00941; CARBOXYLESTERASE_B.2; 1.
 KM Hydrolyase; Serine esterase; Glycoprotein; Multigene family.

FT NON_TER 1 1
 FT ACT_SITE 112 112
 FT ACT_SITE 244 244
 FT ACT_SITE 357 357
 FT DISULFID 166 179
 FT NON_TER 357 357

SEQUENCE 357 AA; 39462 MW; A2CBDE841704DCDF CRC64;
 S -> N (IN REF. 2).
 R -> E (IN REF. 2).
 T -> V (IN REF. 2).
 W -> S (IN REF. 2).
 S -> H (IN REF. 2).
 H -> V (IN REF. 2).
 L -> W (IN REF. 2).
 D -> A (IN REF. 2).
 EVRRGL -> GYPOAS (IN REF. 2).
 -> ASDAPCTGSPAHGAEAPRRGLPLPLLLLSRL

Query Match 34.8%; Score 381; DB 1; Length 357;
 Best Local Similarity 43.5%; Pred. No. 3.3e-28;
 Matches 87; Conservative 38; Mismatches 67; Indels 8; Gaps 5;

QY 12 SEDCLYLSYNNLNINPETKRPVLYVYHGGFTIGENHRDMYGPDYFKD-KDYVLLINIOYR 70
 DB 4 SEDCLYLNWVOPSPAP-PGATVLYVWYGGFGFSGLSDYDGRYLARMEDEVVYVSNMR 62

QY 71 LGALGFLSLNSEDLVNPNAGLKDQVMAIRKKNKNCANFGNPNNTVFGESAGASTHY 130
 DB 63 LGALGFLTSGE--AAPNAGLIDQHLALQWQONISFGGDPKVTYIFESAGASVNF 120

QY 131 MMLTEQRTGLFHRGILMSGNAICPLANT---OCQRAFTLAKLAGYGEQNDQVLE-EFL 186
 DB 121 HILSPSRDLQFRMMHMSASALAPWATPSPQARQSRKALALIDIGSADDEMDVYVACL 180

QY 187 FLMAKRPQDLIKLEEVLTLE 206


```

0C Cyprinidae: Danio.
0X NCBI_TaxID=7955.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20576389; PubMed=11016933;
RA Bertrand C., Chettonet A., Takke C., Van Y., Postlethwait J.,
RT Toulant J.-P., Cousin X.;
RT "Zebrafish acetylcholinesterase is encoded by a single gene localized
RT on linkage group 7, gene structure and polymorphism; molecular forms
RT and expression pattern during development.";
RL J. Biol. Chem. 276:464-474(2001).
CC -1- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.
CC -1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
CC -1- SUBUNIT: DIMERS AND COLLAGEN-TAILED FORMS, IN WHICH CATALYTIC
CC TERMEMES ARE ASSOCIATED WITH ANCHORING PROTEINS THAT ATTACH THEM
CC TO THE BASAL LAMINA OR TO CELL MEMBRANES. IN THE COLLAGEN-TAILED
CC FORMS, SUBUNITS ARE ASSOCIATED WITH A SPECIFIC COLLAGEN, COL1,
CC WHICH TRIGGERS THE FORMATION OF ISOFORM T TETRAMERS FROM DIMERS.
CC -1- MISCELLANEOUS: NO OTHER ISOFORMS EXIST. THIS PROTEIN CORRESPONDS
CC TO THE T ISOFORM IN OTHER SPECIES.
CC -1- SIMILARITY: BELONGS TO THE CARBOXYLESTERASE TYPE-B FAMILY.
CC
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboratio
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on it
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercia
CC CC entities requires a license agreement (See http://www.isb-sdb.ch/announce
CC or send an email to license@isb-sdb.ch).
CC
CC EMBL: AJ251640; CAC19790.1; -.
CC HSSP: P04058; ISOM.
CC ZFIN: ZDB-GENE-010906-1; ache.
CC InterPro: IPR002018; Carbesterase.
CC DR InterPro: IPR000997; Cholinesterase.
CC DR InterPro: IPR000379; Ser-estr- site.
CC Pfam: PF00135; Coesterase; 1.
CC PRINTS: PRO0878; CHOLINESTRASE.
CC DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
CC DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
CC KW Hydrolase; Serine esterase; Synapse; Membrane; Nerve; Muscle; Signal;
CC Neurotransmitter degradation; Glycoprotein.
CC FT SIGNAL 1 23
CC FT CHAIN 1 634
CC FT ACT_SITE 225 225 ACETYLCHOLINESTERASE.
CC FT ACT_SITE 352 352 BY SIMILARITY.
CC FT ACT_SITE 495 495 BY SIMILARITY.
CC FT DISULFID 91 118 BY SIMILARITY.
CC FT DISULFID 279 290 BY SIMILARITY.
CC FT DISULFID 427 580 BY SIMILARITY.
CC FT DISULFID 631
CC FT CARBOHYD 133 133 INTERCHAIN (BY SIMILARITY).
CC FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 283 283 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 368 368 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 512 512 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 592 592 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 634 AA; 71998 MW; 47F348EA8AVCI0E52 CRC64;
SO
Query Match 33.7%; Score 369; DB 1; Length 634;
Best Local Similarity 43.2%; Pred. No. 8.5e-27;
Matches 86; Conservative 32; Mismatches 67; Indels 14; Gaps 6;
OY 12 SEDCLLYSVYTNNNINPETKRP---VLVTYHGGGFIIGENHRDMYGPDYF-IRKDDVILIN 66
DB 115 SEDCLLYLVWV-----PPTPRPONTLVWMIWYGGGFYSSSSLDVYDGRYLAITYEKVYVS 170
OY 67 IGYVGLGLGFLSINSEDLNPNGANGLKDQVWALFWINNCANFGCNPNDITVGEESAGAA 126
DB 171 MNKRVGAFGLALNGSS-DAPGNVGLDQRIALOWQENIHFFGNGNKQVYIFGEESAGAA 229
OY 127 STRHYMTEEDTRGLFHGIIIMSGNAICPLANT--QCQHAFTLAKIAGKGEINDQVIL 183

```

FT CARBOHYD	591	591	N-LINKED (GLCNAC. . .) (POTENTIAL).
-------------	-----	-----	-------------------------------------

RT "Profile of the disulfide bonds in acetylcholinesterase"

RL J. Biol. Chem. 261:13565-13570(1986).
 RN [6]
 RP STRUCTURE OF THE GPI-ANCHOR.
 RX MEDLINE-94079692; PubMed=8257440;
 RA Mehler A., Varon L., Silman I., Homans S.W., Ferguson M.A.;
 RT "Structure of the glycosyl-phosphatidylinositol membrane anchor of
 acetylcholinesterase from the electric organ of the electric-fish,
 Torpedo californica.";
 RL Biochem. J. 296:473-479(1993).
 RN [7]
 RP GPI-ANCHOR.
 RX MEDLINE-96176849; PubMed=8597567;
 RA Bucht G., Hjalmarsson K.;
 RT "Residues in Torpedo californica acetylcholinesterase necessary for
 processing to a glycosyl phosphatidylinositol-anchored form.";
 RL Biochim. Biophys. Acta 1292:223-232(1996).
 RN [8]
 RP MUTAGENESIS.
 RX MEDLINE-91017542; PubMed=2217185;
 RA Gibney G., Camp S., Dionne M., McPhee-Quigley K., Taylor P.;
 RT "Mutagenesis of essential functional residues in
 acetylcholinesterase.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:7546-7550(1990).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
 RX MEDLINE-91343928; PubMed=1678899;
 RA Sussman J.L., Harel M., Frolow F., Oefner C., Goldman A., Tokar L.,
 Silman I.;
 RT "Atomic structure of acetylcholinesterase from Torpedo californica: a
 prototypic acetylcholine-binding protein.";
 RL Science 253:872-879(1991).
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF COMPLEX WITH FASCICULIN.
 RX MEDLINE-96363673; PubMed=8747462;
 RA Harel M., Kleywegt G.J., Ravelli R.B., Silman I., Sussman J.L.;
 RT "Crystal structure of an acetylcholinesterase-fasciculin complex:
 interaction of a three-fingered toxin from snake venom with its
 target.";
 RL Structure 3:1355-1366(1995).
 RN [11]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE-97143314; PubMed=8989325;
 RA Raves M.L., Harel M., Pang Y.P., Silman I., Kozikowski A.P.,
 Sussman J.L.;
 RT "Structure of acetylcholinesterase complexed with the nootropic
 alkaloid, (-)-huperzine A.";
 RL Nat. Struct. Biol. 4:57-63(1997).
 RN [12]
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
 RX MEDLINE-99249780; PubMed=10231521;
 RA Barcolucci C., Perola E., Cellai L., Brufani M., Lamba D.;
 RT "Back door" opening implied by the crystal structure of a
 carbamoylated acetylcholinesterase.";
 RL Biochemistry 38:5714-5719(1999).
 RN [13]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RX MEDLINE-99282167; PubMed=10353814;
 RA Millard C.B., Kryger G., Orendtlich A., Greenblatt H.M., Harel M.,
 Raves M.L., Segall Y., Barak D., Shaffer A., Silman I.,
 Sussman J.L.;
 RT "Crystal structures of aged phosphorylated acetylcholinesterase:
 nerve agent reaction products at the atomic level.";
 RL Biochemistry 38:7032-7039(1999).
 RN [14]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RX MEDLINE-20074924; PubMed=10606746;
 RA Greenblatt H.M., Kryger G., Lewis T., Silman I., Sussman J.L.;
 RT "Structure of acetylcholinesterase complexed with (-)-galanthamine at
 2.3-A resolution.";
 RL FEBS Lett. 463:321-326(1999).
 RN [15]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE-99197295; PubMed=10368299;

RA Kryger G., Silman I., Sussman J.L.;
 RT "Structure of acetylcholinesterase complexed with E2020 (Arlcept(R)):
 RT implications for the design of new anti-alzheimer drugs.";
 RL Structure 7:297-307(1999).
 CC -1- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.
 CC MAY BE INVOLVED IN CELL-CELL INTERACTIONS.
 CC -1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
 CC -1- SUBUNIT: THE H FORM IS AN HOMODIMER; THE ASYMMETRIC FORM IS A
 CC DISULFIDE-BONDED OLIGOMER COMPOSED OF A COLLAGENIC SUBUNIT (C) AND
 CC A VARIABLE NUMBER OF T CATALYTIC SUBUNITS.
 CC -1- SUBCELLULAR LOCATION: THE H FORM IS ATTACHED TO THE MEMBRANE BY A
 CC GPI-ANCHOR.
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOMERIS: H/GLOBULAR (SHOWN HERE)
 CC AND T; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: AChE IS FOUND IN THE SYNAPSES AND TO A LOWER
 CC EXTENT IN EXTRAJUNCTIONAL AREAS OF MUSCLE AND NERVE, AND ON
 CC ERYTHROCYTE MEMBRANES.
 CC -1- PTM: AN INTERCHAIN DISULFIDE BOND IS PRESENT IN WHAT BECOMES
 CC POSITION 593 OF THE T ISOFORM.
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X03439; CA27169.1;
 DR EMBL; X56516; -; NOT_ANNOTATED_CDS.
 DR EMBL; X56517; -; NOT_ANNOTATED_CDS.
 DR PIR; A00773; ACRYE.
 DR PIR; A34026; A34026.
 DR PIR; A31962; A31962.
 DR PDB; 2ACE; 08-NOV-96.
 DR PDB; 3ACE; 16-DEC-98.
 DR PDB; 4ACE; 16-DEC-98.
 DR PDB; 1ACJ; 31-AUG-94.
 DR PDB; 2ACK; 11-FEB-98.
 DR PDB; 1ACK; 11-AUG-94.
 DR PDB; 1AMN; 03-APR-96.
 DR PDB; 1FSS; 03-SEP-97.
 DR PDB; 1VOT; 16-JUN-97.
 DR PDB; 1AX9; 11-FEB-98.
 DR PDB; 1EVE; 22-MAR-99.
 DR PDB; 1CFJ; 01-APR-99.
 DR PDB; 1OCE; 18-MAY-99.
 DR PDB; 2DFP; 28-JUN-99.
 DR PDB; 1SOM; 25-JUN-99.
 DR PDB; 1DX6; 02-JAN-00.
 DR InterPro: IPR002018; Carboxylesterase.
 DR InterPro: IPR000997; Cholinesterase.
 DR InterPro: IPR000379; Ser-estrs_site.
 DR Pfam; PF00135; Cholinesterase_1.
 DR PRINTS; PR00878; CHOLNESTRASE.
 DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
 KW Hydrolyase: Serine esterase; Synapse; Membrane; Nerve; Muscle; Signal;
 KW Neurotransmitter degradation; Glycoprotein; GPI-anchor; 3D-structure;
 KW Alternative splicing.
 FT SIGNAL 1 21
 FT CHAIN 22 564
 FT PROPEP 565 586
 FT ACT_SITE 221 221
 FT ACT_SITE 348 348
 FT ACT_SITE 461 461
 FT DISULFID 88 115
 FT DISULFID 275 286
 FT DISULFID 423 542
 FT DISULFID 558 558
 FT CARBOHYD 80 80
 FT CARBOHYD 437 437
 ACETYLCHOLINESTERASE.
 REMOVED IN MATURE FORM.
 INTERCHAIN.
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).

[1]
 RN SEQUENCE FROM N.A., AND SEQUENCE OF 24-63.
 RP STRAIN-Isolate 800F.
 RC MEDLINE-93384534; PubMed-83733731.
 RX Field L.M., Williamson M.S., Moores G.D., Devonshire A.L.;
 RA "Cloning and analysis of the esterase genes conferring insecticide
 RT resistance in the peach-potato aphid, Myzus persicae (Sulzer).";
 RL Biochem. J. 294:569-574(1993).
 CC -1- FUNCTION: OVERPRODUCTION OF NONSPECIFIC ESTERASES IS A COMMON
 CC MECHANISM OF RESISTANCE TO ORGANOPHOSPHATE INSECTICIDES.
 CC -1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
 CC carboxylic anion.
 CC -1- MISCELLANEOUS: THIS ESTERASE CONFERS INSECTICIDE RESISTANCE.
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X74555; CAAS2649.1; -.
 DR PIR: S36787; S36787.
 DR HSSP: P21836; 1MAA.
 DR InterPro: IPR002018; Carboxylesterase.
 DR InterPro: IPR000379; Ser_estrs_site.
 DR Pfam: PF00135; Coesterase_1.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B.1; 1.
 DR PROSITE: PS00941; CARBOXYLESTERASE_B.2; FALSE_NEG.
 KM Hydrolyase; Serine esterase; Glycoprotein; Signal.
 FT SIGNAL 1 23
 FT CHAIN 24 564 ESTERASE PE4.
 FT ACT_SITE 214 214 BY SIMILARITY.
 FT ACT_SITE 339 339 BY SIMILARITY.
 FT ACT_SITE 463 463 BY SIMILARITY.
 FT DISULFID 89 106 BY SIMILARITY.
 FT DISULFID 266 277 BY SIMILARITY.
 FT CARBOHYD 81 81 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 269 269 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 371 371 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 443 443 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SO SEQUENCE 564 AA; 62757 MW; 128CC0EC3F2D9F1A CRC64;
 Query Match 33.4%; Score 365.5; DB 1; Length 564;
 Best Local Similarity 40.8%; Pred. No. 1.6e-26;
 Matches 82; Conservative 42; Mismatches 64; Indels 13; Gaps 8;

DT 16-OCT-2001 (rel. 40, last annotation update)
 DE Acetylcholinesterase precursor (EC 3.1.1.7) (AChE).
 OS Bungarus fasciatus (Banded Krait).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Bungarinae; Bungarus.
 ON NBI_TaxID=8613;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Venom gland;
 RX MEDLINE-96279007; PubMed-8662867;
 RA Cousin X., Bon S., Duval N., Massoulie J., Bon C.;
 RA "Cloning and expression of acetylcholinesterase from Bungarus
 RT fasciatus venom. A new type of COOH-terminal domain; involvement of a
 RT positively charged residue in the peripheral site.";
 RL J. Biol. Chem. 271:15099-15108(1996).
 RN [2]
 RP SEQUENCE OF 206-220; 253-272; 321-340; 347-372 AND 503-511.
 RC TISSUE-Venom;
 RX MEDLINE-96244524; PubMed-8674549;
 RA Cousin X., Cremonin C., Grassi J., Meflah K., Cornu G., Sallou B.,
 RA Bon S., Massoulie J., Bon C.;
 RA "Acetylcholinesterase from Bungarus venom: a monomeric species.";
 RL FEBS Lett. 387:196-200(1996).
 CC -1- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.
 CC -1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: THE N-TERMINUS IS BLOCKED.
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-9 IS THE INITIATOR.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U54591; AAC59905.1; -.
 DR HSSP: P04058; 1SOM.
 DR InterPro: IPR002018; Carboxylesterase.
 DR InterPro: IPR000997; Cholinesterase.
 DR InterPro: IPR000379; Ser_estrs_site.
 DR Pfam: PF00135; Coesterase_1.
 DR PRINTS: PR00878; CHOLINESTRASE.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B.1; 1.
 DR PROSITE: PS00941; CARBOXYLESTERASE_B.2; 1.
 KM Hydrolyase; Serine esterase; Synapse; Membrane; Signal; Glycoprotein;
 KW Neurotransmitter degradation.
 FT SIGNAL 1 28
 FT CHAIN 29 573 ACETYLCHOLINESTERASE.
 FT PROPEP 574 581 BY SIMILARITY.
 FT ACT_SITE 231 231 BY SIMILARITY.
 FT ACT_SITE 358 358 BY SIMILARITY.
 FT ACT_SITE 471 471 BY SIMILARITY.
 FT DISULFID 98 125 BY SIMILARITY.
 FT DISULFID 285 296 BY SIMILARITY.
 FT DISULFID 433 552 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 374 374 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 484 484 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 564 564 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT MORGAN 101 101 BINDING.
 FT MORGAN 316 316 K->D: INCREASES PERIPHERAL SITE LIGAND
 FT BINDING.
 FT CONFLICT 268 268 T -> S (IN REF. 2).
 FT CONFLICT 350 350 V -> L (IN REF. 2).
 SO SEQUENCE 581 AA; 64722 MW; 436C3CB8457E399F CRC64;
 Query Match 33.4%; Score 365.5; DB 1; Length 581;

QY 131 MMLTEQRTGLFHRGILMSGNAICPLAN---TQCQRAFTLAKIAGYKGDNDKDVLEFIM 187
 DB 233 HILSGSHDLFRRAILDSGSPNCWASVSAEGRRAVELRNINC-NLNSDEDLIQCLR 291
 QY 188 KAKPDLLKLEKVTLE 205
 DB 292 EKKPDLLIDEMVNPFPD 309

RESULT 15
 ACES_MOUSE STANDARD: PRT: 614 AA.

ID ACES_MOUSE STANDARD: PRT: 614 AA.

AC P21836: 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Acetylcholinesterase precursor (EC 3.1.1.7) (Ache).
 GN Ache.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN 11
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90380429; PubMed=2400605;
 RA Rachinsky T.L., Camp S., Li Y., Ekstrom T.J., Newton M., Taylor P.;
 RT "Molecular cloning of mouse acetylcholinesterase: tissue distribution
 of alternatively spliced mRNA species.";
 RL Neuron 5:317-327(1990).
 RN 12
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SV;
 RX MEDLINE=21136439; PubMed=11239002;
 RA Wilson M.D., Riemer C., Matindale D.W., Schnupf P., Boright A.P.,
 RA Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Tsui L.-C.,
 RA Miller W., Koop B.F.;
 RT "Comparative analysis of the gene-dense Ache/TFR2 region on human
 chromosome 7q22 with the orthologous region on mouse chromosome 5.";
 RL Nucleic Acids Res. 29:1352-1365(2001).
 RN 13
 RP X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS) OF COMPLEX WITH FASCICULIN.
 RX MEDLINE=96067648; PubMed=8521480;
 RA Bourne Y., Taylor P., Marchot P.;
 RT "Acetylcholinesterase inhibition by fasciculin: crystal structure of
 the complex.";
 RL Cell 83:503-512(1995).
 RN 14
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE=99115643; PubMed=9915834;
 RA Bourne Y., Taylor P., Bougis P.E., Marchot P.;
 RT "Crystal structure of mouse acetylcholinesterase. A peripheral site-
 occluding loop in a tetrameric assembly.";
 RL J. Biol. Chem. 274:2963-2970(1999).
 CC 1- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.
 CC 1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
 CC 1- SUBUNIT: ISOMER H GENERATES MULTIPLE STRUCTURES, RANGING FROM
 LINKED, ISOMER T GENERATES MULTIPLE STRUCTURES, RANGING FROM
 MONOMERS AND DIMERS TO COLLAGEN-TAILED AND HYDROPHOBIC-TAILED
 FORMS, IN WHICH CATALYTIC TETRAMERS ARE ASSOCIATED WITH ANCHORING
 PROTEINS THAT ATTACH THEM TO THE BASAL LAMINA OR TO CELL
 MEMBRANES. IN THE COLLAGEN-TAILED FORMS, ISOMER T SUBUNITS ARE
 ASSOCIATED WITH A SPECIFIC COLLAGEN, COLO, WHICH TRIGGERS THE
 FORMATION OF ISOMER T TETRAMERS, FROM MONOMERS AND DIMERS (BY
 SIMILARITY).
 CC 1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: H AND T (SHOWN HERE); MAY BE
 PRODUCED BY ALTERNATIVE SPLICING.
 CC 1- TISSUE SPECIFICITY: PREDOMINATES IN MOST EXPRESSING TISSUES
 EXCEPT ERYTHROCYTES WHERE A GLYCOPHOSPHOLIPID-ATTACHED FORM OF
 Ache PREDOMINATES.
 CC 1- MISCELLANEOUS: SYNAPSES USUALLY CONTAIN ASYMMETRIC MOLECULES OF
 CHOLINESTERASE, WITH A COLLAGEN-LIKE PART DISULFIDE-BONDED TO THE
 CATALYTIC PART. A DIFFERENT, GLOBULAR TYPE OF CHOLINESTERASE
 OCCURS ON THE OUTER SURFACES OF CELL MEMBRANES, INCLUDING THOSE OF

CC ERYTHROCYTES.
 CC MISCELLANEOUS: THIS IS THE CATALYTIC SUBUNIT OF AN ASYMMETRIC OR
 SOLUBLE FORM OF Ache.
 CC 1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL ESTERASE/LIPASE FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC EMBL: X56518; CAA39867.1; -
 DR EMBL: AF312033; AAK28816.1; -
 DR PIR: JH0314; JH0314.
 DR PDB: 1MAH; 03-APR-96.
 DR PDB: 1MAA; 20-APR-99.
 DR MGD: MGI:87876; Ache.
 DR InterPro: IPR002018; Carboxylesterase.
 DR InterPro: IPR000997; Cholinesterase.
 DR InterPro: IPR000379; Ser-estr-ase.
 DR Pfam: PF00135; Coesterase_1.
 DR PRINTS: PR0078; CHOLINESTERASE.
 DR PROSITE: PS00122; CARBOXYL ESTERASE-B_1; 1.
 DR PROSITE: PS00941; CARBOXYL ESTERASE-B_2; 1.
 KW Hydrolase; Serine esterase; Synapse; Membrane; Nerve; Muscle; Signal;
 KW Neurotransmitter degradation; Glycoprotein; Alternative splicing;
 KW 3D-structure. 1
 FT SIGNAL 32 31
 FT CHAIN 32 614 ACETYLCHOLINESTERASE.
 FT ACT_SITE 234 234
 FT ACT_SITE 365 365
 FT ACT_SITE 478 478
 FT DISULFID 100 127
 FT DISULFID 288 303
 FT DISULFID 440 560
 FT DISULFID 611 611
 FT CARBOHYD 296 296 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 381 381 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 495 495 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 614 AA: 66E168 MW: 66E2512463C21172 CR664;

Query Match 33.18; Score 362; DB 1; Length 614;
 Best Local Similarity 41.3%; Pred. No. 3; 76-76; Indels 8; Gaps 4;
 Matches 83; Conservative 34; Mismatches 76;

QY 12 SEDCLYLSVYNNINNPETKRPVLYIHGGFIIIGENHRDMYGPDYFIK-KDVLINIOYR 70
 DB 124 SEDCLYLNWMTPTPRPASPTPLWITGGGFYSASLDVYDGRFLAOGVGAIVGMNTR 183
 QY 71 LGALGFLNSLSEDLNVPNGNLKDQVNAIRKNNCANFGNDNITVEGESAASSTHY 130
 DB 184 VGTGFLALPG-SREAPGNVGLDQRLALQWQENIAAFGSDPMSTVTLFEGESAASVGM 242
 QY 131 MMLTEQRTGLFHRGILMSGNAICPLAN---TQCQRAFTLAKIAGYK---GEQNDVYLE 184
 DB 243 HILSPSSSLFHRVAVLDSGTPNGPMTATVSAEARRATTLARLVGPPGGAGNDTELLA 302
 QY 185 FLMAKAPDILLKLEKVTLE 205
 DB 303 CLTRPPADIVDEHVNLPDE 323

Search completed: April 4, 2003, 09:13:42
 Job time : 5.86293 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2003, 09:09:58 ; Search time 20.6467 Seconds
(without alignments)
2065.788 Million cell updates/sec

Title: US-09-776-910-43

Perfect score: 1095

Sequence: 1 QVDFTRKVCSEDCLYLV.....KAKPDLIKLEKVTLEER 207

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_21.*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mmc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1089	99.5	570	5	Q25252 lucilia cup
2	843	77.0	570	5	Q9U4U9 haematobia
3	836	76.3	570	5	Q9XZ70 musca domes
4	812.5	74.2	556	5	Q24201 drosophila
5	812.5	74.2	572	5	Q9VIB5 drosophila
6	802.5	73.3	345	5	Q9VIB3 drosophila
7	653.5	59.7	567	5	Q9VIB3 drosophila
8	652.5	59.6	558	5	Q24202 drosophila
9	640	58.4	286	5	Q9N152 drosophila
10	612	55.9	297	5	Q9N151 drosophila
11	610	55.7	554	5	Q9VIB0 drosophila
12	605	55.3	565	5	Q9N159 drosophila
13	596	54.4	572	5	Q24203 drosophila
14	591	54.0	572	5	Q9VIB1 drosophila
15	590	53.9	570	5	Q91715 drosophila
16	590	53.9	549	5	Q24204 drosophila

17	589	53.8	401	5	Q9N160 drosophila
18	588	53.7	564	5	Q9N161 drosophila
19	578	52.8	553	5	Q24194 drosophila
20	578	52.8	565	5	Q9VIC3 drosophila
21	573	52.3	554	5	Q9VIC2 drosophila
22	573	52.3	566	5	Q9VIC2 drosophila
23	569	52.0	554	5	Q24195 drosophila
24	561	51.2	542	5	Q9U300 drosophila
25	561	51.2	542	5	Q24198 drosophila
26	561	51.2	542	5	Q9V109 drosophila
27	546.5	49.9	566	5	Q9W243 drosophila
28	544	49.7	446	5	Q9N155 drosophila
29	528	48.2	540	5	Q8W088 culex pipie
30	526	48.0	540	5	Q8W088 culex pipie
31	524	47.9	467	5	P91597 culex pipie
32	523	47.8	467	5	P91596 culex pipie
33	523	47.8	540	5	Q23733 culex quin
34	523	47.8	540	5	P92025 culex quin
35	518	47.3	467	5	P91598 culex pipie
36	499.5	45.6	541	5	Q24197 drosophila
37	499.5	45.6	541	5	Q9VIC0 drosophila
38	498	45.5	568	5	Q9VIB6 drosophila
39	497	45.4	540	5	Q9G095 culex tarsa
40	495	45.2	540	5	P91920 culex tarsa
41	494.5	45.2	360	5	Q9U9R1 drosophila
42	493	45.0	463	5	Q96137 drosophila
43	480	43.8	532	5	Q91726 anisoplerom
44	479	43.7	568	5	Q24200 drosophila
45	478	43.7	532	5	Q61727 anisoplerom

ALIGNMENTS

RESULT 1

Q25252 PRELIMINARY; PRT; 570 AA.
ID Q25252
AC Q25252; Q25247;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Alpha esterase (LCAE7) (Carboxylesterase).
GN Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
OS Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Oestroidea; Calliphoridae; Lucilia.
OX NCBI_TaxID=7375;
RN [1]
RP SEQUENCE FROM N.A.
RA Newcomb R.D., East P.D., Russell R.J., Oakeshott J.G.;
RC STRAIN=LS2;
RN Insect Mol. Biol. 5:0-0(0).
RN [2]
RP SEQUENCE OF 70-181 FROM N.A.
RA Newcomb R.D., East P.D., Russell R.J., Oakeshott J.G.;
RC STRAIN=LS2;
RN Insect Mol. Biol. 0:0-0(0).
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL: U56636; AAB67728.1; -;
DR EMBL: U49421; AAA92012.1; -;
DR HSSP: P37967; IOE3.
DR InterPro: IPR002018; Carboxylesterase.
DR InterPro: IPR000379; Ser. esters. site.
DR Pfam: PF00135; Coesterase.1.
DR PROSITE: PS00122; CARBOXYLESTERASE_B.1; 1.
KW Hydrolase.
SQ SEQUENCE 570 AA: 65416 MW: 399D72B3A0F338FD CRC64;

Query Match 99.5%; Score 1089; DB 5; Length 570;
Best Local Similarity 99.5%; Pred. No. 1.2e-96;
Matches 206; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 QVDFITGKVCSEDCLYLSVTNNLNPEKRPVLYIHGGGFIIGENHRDMGPDYFIKK 60
DB 97 QVDFITGKVCSEDCLYLSVTNNLNPEKRPVLYIHGGGFIIGENHRDMGPDYFIKK 156
QY 61 DVLVNIQYRLGALGFLSLNSEDNLVPGNAGLKDQVMALEKNNKNCANFGNPDNITVFG 120
DB 157 DVLVNIQYRLGALGFLSLNSEDNLVPGNAGLKDQVMALEKNNKNCANFGNPDNITVFG 216
QY 121 ESAGAASTHYMMLTEQIRGLFHRGILMSGNALICPLANTQCOHRAFTLAKLAGYKGEDNDK 180
DB 217 ESAGAASTHYMMLTEQIRGLFHRGILMSGNALICPLANTQCOHRAFTLAKLAGYKGEDNDK 276
QY 181 DYLEFLMKAKPODLIKLEEKVLTLEE 207
DB 277 DYLEFLMKAKPODLIKLEEKVLTLEE 303

RESULT 2
Q9U4U9 PRELIMINARY; PRT; 570 AA.
ID Q9U4U9
AC Q9U4U9
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Alpha E7 esterase.
GN AE7.
OS Haematobia irritans irritans.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Muscoidea; Muscidae; Haematobia.
OX NCBI_TaxID=75445;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CAMP COOLEY 4/97;
RX MEDLINE=20445807; PubMed=10989298;
RA Guerrero F.D.;
RT "Cloning of a horn fly cDNA, H1alphaE7, encoding an esterase whose
transcript concentration is elevated in diazinon-resistant flies.";
RL Insect Biochem. Mol. Biol. 30:1107-1115(2000).
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
EMBL: AF139082; AAF14517.1;
DR HSSP: P37967; 1OE3.
DR InterPro: IPR002018; CarbesteraseB.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF00135; Coesterase; 1.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
KM Hydrolyase.
SQ SEQUENCE 570 AA; 65613 MW; 18DA0A9A94AB970D CRC64;

Query Match 77.0%; Score 843; DB 5; Length 570;
Best Local Similarity 76.2%; Pred. No. 7,1e-73;
Matches 157; Conservative 20; Mismatches 29; Indels 0; Gaps 0;

```

```

AC Q9X270;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Carboxylesterase MdaE7 (Ec 3.1.1.1).
GN MDAE7.
OS Musca domestica (House fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Muscoidea; Muscidae; Musca.
OX NCBI_TaxID=7370;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RUTGERS DIAZINON-R;
RX MEDLINE=99381228; PubMed=10451921;
RA Claudianos C.; Russell R.J.; Oakeshot J.G.;
RT "The same amino acid substitution in orthologous esterases confers
organophosphate resistance on the house fly and a blowfly.";
RL Insect Biochem. Mol. Biol. 29:675-686(1999).
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
EMBL: AF133341; AAD29685.1;
DR HSSP: P37967; 1OE3.
DR InterPro: IPR002018; CarbesteraseB.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF00135; Coesterase; 1.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
KM Hydrolyase.
SQ SEQUENCE 570 AA; 65421 MW; 08AFEBFE284003BB CRC64;

Query Match 76.3%; Score 836; DB 5; Length 570;
Best Local Similarity 74.8%; Pred. No. 3,4e-72;
Matches 154; Conservative 26; Mismatches 26; Indels 0; Gaps 0;

```

```

QY 1 QVDFITGKVCSEDCLYLSVTNNLNPEKRPVLYIHGGGFIIGENHRDMGPDYFIKK 60
DB 97 QVDFITGKVCSEDCLYLSVTNNLNPEKRPVLYIHGGGFIIGENHRDMGPDYFIKK 156
QY 61 DVLVNIQYRLGALGFLSLNSEDNLVPGNAGLKDQVMALEKNNKNCANFGNPDNITVFG 120
DB 157 DVLVNIQYRLGALGFLSLNSEDNLVPGNAGLKDQVMALEKNNKNCANFGNPDNITVFG 216
QY 121 ESAGAASTHYMMLTEQIRGLFHRGILMSGNALICPLANTQCOHRAFTLAKLAGYKGEDNDK 180
DB 217 ESAGAASTHYMMLTEQIRGLFHRGILMSGNALICPLANTQCOHRAFTLAKLAGYKGEDNDK 276
QY 181 DYLEFLMKAKPODLIKLEEKVLTLEE 206
DB 277 DYLEFLMKAKPODLIKLEEKVLTLEE 302

RESULT 4
Q24201 PRELIMINARY; PRT; 556 AA.
ID Q24201
AC Q24201
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Alpha esterase (Fragment).
GN ALPHA-EST7 OR AE7 OR CG1112.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC Rodin C.; Medvedzky K.M.; Russell R.J.; Oakeshot J.G.;
RL J. Mol. Evol. 0:0-0(0).
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
EMBL: U51050; AAB01149.1;
DR HSSP: P21836; 1MAA.
DR Pfam: PF0015575; alpha-Est7.
DR InterPro: IPR002018; CarbesteraseB.

```


DR InterPro: IPR000379; Ser_estrs_site.
 DR Pfam: PF00135; Coesterase_1.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
 KW Hydrolase.
 FT NON_TER 1 1
 FT NON_TER 556 556
 SQ SEQUENCE 556 AA; 63397 MW; AFOF80AID3C34425 CRC64;
 Query Match
 Best local similarity 74.2%; Score 812.5; DB 5; Length 556;
 Matches 152; Conservative 26; Mismatches 29; Indels 1; Gaps 1;
 QY 1 QVDFITGKVCSEDCILYLYVTNNINLPETKRPVLYIHGGGFIIGENHMDGPDYFIKK 60
 DB 81 QVGFVDEKVESEDCILYLYVTNNINLPETKRPVLYIHGGGFIIGENHMDGPDYFIKK 140
 QY 61 DVLVLIQYRLGALGFLSLNSEDLPNGNAGLKDOVALRMKNNKNCANFGNPDNITVFG 120
 DB 141 DVLVLIQYRLGALGFLSLNSEDLPNGNAGLKDOVALRMKNNKNCANFGNPDNITVFG 200
 QY 121 ESAGASTHYMMLTEQTRGLFHRGILMSGNAICPLA-NTQCQHRAPFLTLAKGYGEND 179
 DB 201 ESAGASTHYMMLTEQTRGLFHRGILMSGNAICPLA-NTQCQHRAPFLTLAKGYGEND 260
 QY 180 KDVEFLMKAKPODLIKLEKVTLEER 207
 DB 261 KDVEFLMKAKPODLIKLEKVTLEER 288
 RESULT 5
 Q9VIB5 PRELIMINARY; PRT; 572 AA.
 AC Q9VIB5;
 DT 01-MAY-2000 (TRENBLREL. 13, Created)
 DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
 DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
 DE Alpha-EST7 protein (GH13950P).
 GN ALPHA-EST7 OR CG1112.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RX MEDLINE-20196006; PubMed-10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bernier B.P., Bhandari D., Bolshakov S.,
 RA Borova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
 RA Burks K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrelia S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Goddek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.J.,
 RA Jajala M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laake P., Lei Y., Levine S.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mallet B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclebo J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Sidenklamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "the genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nunoo J., Paclebo J., Paragas V., Park S., Phouanavong S., Wan K.,
 RA Yu C., Lewis S.F., Rubin G.M., Celniker S.,
 RL submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 DE EMBL: AE003671; AAF54010.1; -;
 DR EMBL: AY051473; AAK92897.1; -;
 DR HSSP: P21836; IMAA.
 DR FLYBASE: FBgn0015575; alpha-EST7.
 DR InterPro: IPR002016; CarbesteraseB.
 DR InterPro: IPR000379; Ser_estrs_site.
 DR Pfam: PF00135; Coesterase_1.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
 DR Hydrolase.
 SQ SEQUENCE 572 AA; 65435 MW; 693D9360DA18AEZ7 CRC64;
 Query Match
 Best local similarity 74.2%; Score 812.5; DB 5; Length 572;
 Matches 152; Conservative 26; Mismatches 29; Indels 1; Gaps 1;
 QY 1 QVDFITGKVCSEDCILYLYVTNNINLPETKRPVLYIHGGGFIIGENHMDGPDYFIKK 60
 DB 97 QVGFVDEKVESEDCILYLYVTNNINLPETKRPVLYIHGGGFIIGENHMDGPDYFIKK 156
 QY 61 DVLVLIQYRLGALGFLSLNSEDLPNGNAGLKDOVALRMKNNKNCANFGNPDNITVFG 120
 DB 157 DVLVLIQYRLGALGFLSLNSEDLPNGNAGLKDOVALRMKNNKNCANFGNPDNITVFG 216
 QY 121 ESAGASTHYMMLTEQTRGLFHRGILMSGNAICPLA-NTQCQHRAPFLTLAKGYGEND 179
 DB 217 ESAGASTHYMMLTEQTRGLFHRGILMSGNAICPLA-NTQCQHRAPFLTLAKGYGEND 276
 QY 180 KDVEFLMKAKPODLIKLEKVTLEER 207
 DB 277 KDVEFLMKAKPODLIKLEKVTLEER 304
 RESULT 6
 Q9NT53 PRELIMINARY; PRT; 345 AA.
 AC Q9NT53;
 DT 01-OCT-2000 (TRENBLREL. 15, Created)
 DT 01-OCT-2000 (TRENBLREL. 15, Last sequence update)
 DT 01-MAR-2002 (TRENBLREL. 20, Last annotation update)
 DE Alpha-esterase 7 (Fragment).
 GN AE7A OR AE7.
 OS Drosophila buzzatii (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7264;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Robin C., Claudianos C., Russell R.J., Oakeshott J.G.;
 RA "the alpha-esterase cluster of Drosophila buzzatii";
 RT Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 DR EMBL: AF216215; AAF26729.1; -
 DR HSSP: P21836; IMAA.
 DR FLYBASE: FBgn0029447; Dbuz\ae7a.
 DR InterPro: IPR002018; CarbesteraseB.
 DR InterPro: IPR000379; Ser_estrs_site.
 DR Pfam: PF00135; Coesterase.1.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B.1; 1.
 KM Hydrolyase.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 345 AA; 38472 MW; C08564A34E4EC87A CRC64;
 Query Match 73.3%; Score 802.5; DB 5; Length 345;
 Best Local Similarity 74.9%; Pred. No. 3e-69;
 Matches 155; Conservative 23; Mismatches 28; Indels 1; Gaps 1;
 QY 1 QVDFITGKVCSEDCILSYVTNNLNPETKRPVLVYHGSGFTIGENHRDMGPDYFIKK 60
 DB 28 QVHFVDFRVEGSEDCILSYVTNNLNPETKRPVLVYHGSGFTIGENHRDMGPDYFIKE 87
 QY 61 DVLVLTIOYRIGALGFLSLNSFDLNPVGNAGLKQDYMALRMKNNKCANFGNPDITVFG 120
 DB 88 DVLVLTIOYRIGALGFLSLKTPGVLNPGNAGLKQDYMALRMKNNKCANFGSDPDITVFG 147
 QY 121 ESAGASTHYMMLTQOTGFLFRGILMSGNAICPLA-NTQCOHRAFTLAKIAGYGEDND 179
 DB 148 ESAGASTHYMMLTQOTGFLFRGILMSGNAICPLA-NTQCOHRAFTLAKIAGYGEDND 207
 QY 180 KDVEFLMKAKPODLIKLEKVLTLER 206
 DB 208 KDVLQFLQVVARADLRIVEQVLTPEE 234
 RESULT 7
 QVYIB3 PRELIMINARY; PRT; 567 AA.
 AC 09VIB3:
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE ALPHA-EST8 protein.
 GN ALPHA-EST8 OR CG1121.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RX MEDLINE=20196606; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amaniatis P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H.C., Blake J.R., Champé M., Pfeiffer B.D.,
 RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abrell J.F., Abmayyan A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Bendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borliva D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Burris K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster L., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz L.B., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Maitel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy J., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Ruskern D.R., Racle J.M.,
 RA Palazolo M., Pitman G.S., Pan S., Pollard J., Pui Y., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Sytkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 DR EMBL: AE003671; AAF34012.1; -
 DR HSSP: P37967; 10E3.
 DR FLYBASE: FBgn0015576; alpha-Est8.
 DR InterPro: IPR002018; CarbesteraseB.
 DR InterPro: IPR000379; Ser_estrs_site.
 DR Pfam: PF00135; Coesterase.1.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B.1; 1.
 DR PROSITE: PS00941; CARBOXYLESTERASE_B.2; 1.
 KM Hydrolyase.
 FT NON_TER
 SQ SEQUENCE 567 AA; 64831 MW; 07D6ACG72786F14A CRC64;
 Query Match 59.7%; Score 653.5; DB 5; Length 567;
 Best Local Similarity 59.1%; Pred. No. 1.4e-54;
 Matches 123; Conservative 34; Mismatches 50; Indels 1; Gaps 1;
 QY 1 QVDFITGKVCSEDCILSYVTNNLNPETKRPVLVYHGSGFTIGENHRDMGPDYFIKK 60
 DB 90 QVNTLVKQVGSSEDCILSYVTNNLNPETKRPVLVYHGSGFTIGENHRDMGPDYFIKE 149
 QY 61 DVLVLTIOYRIGALGFLSLNSFDLNPVGNAGLKQDYMALRMKNNKCANFGNPDITVFG 120
 DB 150 HVLVLTISYRIGALGFLSLADELDVGNAGLKQDYMALRMKNNKCANFGSDPDITVFG 209
 QY 121 ESAGASTHYMMLTQOTGFLFRGILMSGNAICPLA-NTQCOHRAFTLAKIAGYGEDND 179
 DB 210 ESAGASTHYMMLTQOTGFLFRGILMSGNAICPLA-NTQCOHRAFTLAKIAGYGEDND 269
 QY 180 KDVEFLMKAKPODLIKLEKVLTLER 207
 DB 270 RDIHAHLKCKKASSMLKVAEDITMEER 297
 RESULT 8
 Q24202 PRELIMINARY; PRT; 558 AA.
 ID 024202:
 AC 024202:
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Alpha esterase (Fragment).
 GN ALPHA-EST8 OR CG1121.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Robin C., Medveczky K.M., Russell R.J., Oakeshott J.G.;
 RL J. Mol. Evol. 0:0-0(0).
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 DR EMBL: U51052; AAB01151.1; -
 DR HSSP: P37967; 10E3.
 DR FLYBASE: FBgn0015576; alpha-Est8.
 DR InterPro: IPR002018; CarbesteraseB.

DR InterPro; IPR000379; Ser-estrs_-site.
 DR Pfam; PF00135; Coesterase; 1.
 DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
 KW Hydrolase.
 FT NON_TER 1
 SQ SEQUENCE 558 AA; 63916 MW; BF6F62C8FF212720 CRC64;

Query Match 59.6%; Score 652.5; DB 5; Length 558;
 Best Local Similarity 58.7%; Pred. No. 1.8e-54;
 Matches 122; Conservative 35; Mismatches 50; Indels 1; Gaps 1;

QY 1 QVDFITGKVCSEDCILYSVYTNINLPETKRPVLYIHGGFFIIGENHRDMYGPDIYFK 60
 DB 81 QVNIYLVKVOGSEDCILYVYTRRELPHRPLVLYWYGGFGOMGEASRDLYSPDIYME 140
 QY 61 DVLINIQYRLGALGFLSLNSIEDLVNPGNAGIKQDVMLRWIKNNCANFGNPNITVFG 120
 DB 141 HVLVIVISYRIGALGFLSLADELDVPGNAGIKQDVMLRWYKRCNCOFGGDDPDNITVFG 200
 QY 121 ESAGASTHYMMLTEQTRGLFHRGLIMSGNAICPLANTOCO-HRAFTLAKLAGYGEEDND 179
 DB 201 ESAGASTHYMMLTDQAGLGHKTYIMSGSALAPWAGTPHINPRLAQTGTGDAND 260
 QY 180 KDVEFLMKAKPDLIKLEEKVLTLEER 207
 DB 261 RDIFAHLKKCKASSMLKVAEDITITWEER 288

RESULT 9
 Q9NT52 PRELIMINARY; PRT; 286 AA.

DR 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DE 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Alpha-esterase 8 (Fragment).
 GN AE8A OR AE8.
 OS Drosophila buzzatii (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7264;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Robin C., Claudianos C., Russell R.J., Oakeshott J.G.;
 RT "The alpha-esterase cluster of Drosophila buzzatii."
 RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 DR EMBL; AF216216; AAF26730.1; -.
 DR HSSP; P21836; IMAA.
 DR FlyBase; FBgn0029446; DpuzaAE8A.
 DR InterPro; IPR002018; Carbesteraseb.
 DR InterPro; IPR000379; Ser-estrs_-site.
 DR Pfam; PF00135; Coesterase; 1.
 DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; UNKNOWN_1.
 KW Hydrolase.
 FT NON_TER 1
 FT NON_TER 286
 SQ SEQUENCE 286 AA; 32409 MW; ADCCAFD124D2A953 CRC64;

Query Match 58.4%; Score 640; DB 5; Length 286;
 Best Local Similarity 56.5%; Pred. No. 1.2e-53;
 Matches 117; Conservative 38; Mismatches 52; Indels 0; Gaps 0;

QY 1 QVDFITGKVCSEDCILYSVYTNINLPETKRPVLYIHGGFFIIGENHRDMYGPDIYFK 60
 DB 28 QVNIYLVKVOGSEDCILYVYTRRELPHRPLVLYWYGGFGOMGEASRDLYSPDIYME 87
 QY 61 DVLINIQYRLGALGFLSLNSIEDLVNPGNAGIKQDVMLRWIKNNCANFGNPNITVFG 120
 DB 88 HVLVIVISYRIGALGFLSLADELDVPGNAGIKQDVMLRWYKRCNCOFGGDDPDNITVFG 147

QY 121 ESAGASTHYMMLTEQTRGLFHRGLIMSGNAICPLANTOCOCHRAFTLAKLAGYGEEDND 180
 DB 148 ESAGASTHYMMLTEQTRGLFHRGLIMSGNAICPLANTOCOCHRAFTLAKLAGYGEEDND 180
 QY 181 DVEFLMKAKPDLIKLEEKVLTLEER 207
 DB 208 EIFKHLQCKASSMLRMAEGIVTWEER 234

RESULT 10

Q9NT51 PRELIMINARY; PRT; 297 AA.
 AC Q9NT51;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DE 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Alpha-esterase 9 (Fragment).
 GN AE9A OR AE9.
 OS Drosophila buzzatii (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7264;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Robin C., Claudianos C., Russell R.J., Oakeshott J.G.;
 RT "The alpha-esterase cluster of Drosophila buzzatii."
 RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 DR EMBL; AF216217; AAF26731.1; -.
 DR HSSP; P37967; 10E3.
 DR FlyBase; FBgn0029445; DpuzaAE9A.
 DR InterPro; IPR002018; Carbesteraseb.
 DR InterPro; IPR000379; Ser-estrs_-site.
 DR Pfam; PF00135; Coesterase; 1.
 DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
 KW Hydrolase.
 FT NON_TER 297
 FT NON_TER 297
 SQ SEQUENCE 297 AA; 33635 MW; 89CF7761871B362D CRC64;

Query Match 55.9%; Score 612; DB 5; Length 297;
 Best Local Similarity 55.6%; Pred. No. 6.2e-51;
 Matches 115; Conservative 35; Mismatches 57; Indels 0; Gaps 0;

QY 1 QVDFITGKVCSEDCILYSVYTNINLPETKRPVLYIHGGFFIIGENHRDMYGPDIYFK 60
 DB 81 QHFFVEMTDSGEDCLYVYTRKLYPVKPMVWYVWYGGFGOMGEASRECYSPDIYRE 140
 QY 61 DVLINIQYRLGALGFLSLNSIEDLVNPGNAGIKQDVMLRWIKNNCANFGNPNITVFG 120
 DB 141 DVLVIVISYRIGALGFLSLADELDVPGNAGIKQDVMLRWYKRCNCOFGGDDPDNITVFG 200
 QY 121 ESAGASTHYMMLTEQTRGLFHRGLIMSGNAICPLANTOCOCHRAFTLAKLAGYGEEDND 180
 DB 201 DSASASVHYMMLTEQTRGLFHRGLIMSGNLTSPWAVTPQNMWYRLAVAGYIGENTER 260
 QY 181 DVEFLMKAKPDLIKLEEKVLTLEER 207
 DB 261 EWFELMKAKSDILIKANGELCIXEEK 287

RESULT 11

Q9VTB0 PRELIMINARY; PRT; 554 AA.
 AC Q9VTB0;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DE 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Alpha-EST9 protein.
 GN ALPHA-EST9 OR CG1128.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxId=7227;
 [1]
 RP SQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sluton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Branton R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abell J.F., Agbayan A., An H.-J., Andrews-Pfannkoch L., Basley E.M.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bernan B.P., Brokstein P., Brotler P.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu L.B., Davies P.,
 RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies I.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Doudin K.J., Evangelista C.C., Garg N.S., Gelbart W.M., Glasser K.,
 RA Foster C., Gabrielian A.E., Garg N.S., Guan P., Harris M.,
 RA Fostek A., Gong F., Gottrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lal Z.,
 RA Li X., Matel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pauley J.M., Reese M.G.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svikas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao X., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*."
 RL Science 287:2185-2195(2000)
 CC EMBL: AEO03671; AAF54014.1; -
 DR HSSP: P37967; 1OE3.
 DR FLYBASE: FBgn0015577; alpha-Est9.
 DR InterPro: IPR002018; Cholinesterase.
 DR InterPro: IPR000997; Cholinesterase.
 DR InterPro: IPR000379; Ser-estrs_site.
 DR Pfam: PF00135; Coesterase.1.
 DR PRINTS: PR00878; CHOLINESTERASE.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B_1.1.
 KM Hydrolyase.
 SO SEQUENCE 554 AA; 63670 MW; 0A72368389DFEC2B CRC64;

Query Match 55.7%; Score 610; DB 5; Length 554;
 Best Local Similarity 56.0%; Pred. No. 2.2e-50;
 Matches 116; Conservative 34; Mismatches 57; Indels 0; Gaps 0;

QY 1 QVDFITGVCSSEDLVSYVYNNINLPETKRPVLYIHGGFFITGENHMDYGYDITK 60
 DB 81 OKHEVFEWTDSEDLVYNNITKNTKPKPVMVWVWYIGGFGFGEASRECYSDYLRE 140
 QY 61 DVLINIOYRIGALGFLSLNSEDLVNPGNAGIKQVVALRKIKNNKANGPNITVFG 120
 DB 141 DVVVISINRILGFLGLDIDPELDVPGNAGIKQVVALRKWKAKCSFGGDSANITTFG 200
 QY 121 ESAGASTHYMMLTEOTRGLFHRGILMSGNAICPLANTQCOHRAFTLAKLAGYGEDNDK 180
 DB 201 DSAGSASVHYMMLTEOTRGLFHRGILMSGNAICPLANTQCOHRAFTLAKLAGYGEDNDK 260

QY 181 DVEFLMKAKPODLIKLEKVLTEER 207
 DB 261 DVEFLMKAKPODLIKLEKVLTEER 287
 RESULT 12
 ID Q9N159 PRELIMINARY; PRT: 565 AA.
 AC Q9N159; 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, last annotation update)
 DE Alpha-esterase 2.
 GN AE2A OR AE2.
 OS *Drosophila buzzatii* (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxId=7264;
 [1]
 RP SQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sluton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Branton R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abell J.F., Agbayan A., An H.-J., Andrews-Pfannkoch L., Basley E.M.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bernan B.P., Brokstein P., Brotler P.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu L.B., Davies P.,
 RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies I.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Doudin K.J., Evangelista C.C., Garg N.S., Gelbart W.M., Glasser K.,
 RA Foster C., Gabrielian A.E., Garg N.S., Guan P., Harris M.,
 RA Fostek A., Gong F., Gottrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwan C.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lal Z.,
 RA Li X., Matel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pauley J.M., Reese M.G.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svikas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao X., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*."
 RL Science 287:2185-2195(2000)
 CC EMBL: AEO03671; AAF54014.1; -
 DR HSSP: P37967; 1OE3.
 DR FLYBASE: FBgn0029452; DbuzAE2a.
 DR InterPro: IPR002018; Cholinesterase.
 DR InterPro: IPR000997; Cholinesterase.
 DR InterPro: IPR000379; Ser-estrs_site.
 DR Pfam: PF00135; Coesterase.1.
 DR PRINTS: PR00878; CHOLINESTERASE.
 KM Hydrolyase.
 SO SEQUENCE 565 AA; 64618 MW; 0BC92E956B23006E CRC64;

Query Match 55.3%; Score 605; DB 5; Length 565;
 Best Local Similarity 55.8%; Pred. No. 7e-50;
 Matches 115; Conservative 39; Mismatches 52; Indels 0; Gaps 0;

QY 1 QVDFITGVCSSEDLVSYVYNNINLPETKRPVLYIHGGFFITGENHMDYGYDITK 60
 DB 97 QNNMVGILSESEDLVYNNITKNTKPKPVMVWVWYIGGFGFGEASRECYSDYTMKQ 156
 QY 61 DVLINIOYRIGALGFLSLNSEDLVNPGNAGIKQVVALRKIKNNKANGPNITVFG 120
 DB 157 NVVLVYINRIGALGFLSLNSEDLVNPGNAGIKQVVALRKIKNNKANGPNITVFG 216
 QY 121 ESAGASTHYMMLTEOTRGLFHRGILMSGNAICPLANTQCOHRAFTLAKLAGYGEDNDK 180
 DB 217 ESAGASTHYMMLTEOTRGLFHRGILMSGNAICPLANTQCOHRAFTLAKLAGYGEDNDK 276
 QY 181 DVEFLMKAKPODLIKLEKVLTEER 206
 DB 277 DILRYLTRKASARQIASHDEIVTLDE 302
 RESULT 13
 ID Q24203 PRELIMINARY; PRT: 572 AA.
 AC Q24203; 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, last annotation update)
 DE Alpha-esterase.
 GN ALPHA-EST9 OR AE9 OR CG1128.
 OS *Drosophila melanogaster* (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxId=7227;
 [1]

RP SEQUENCE FROM N.A.
 RA Robin C., Medveczky K.M., Russell R.J., Oakeshott J.G.:
 RL J. Mol. Evol. 0:0-0(0).
 CC -1 SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 DR EMBL: 051053; AAB01152.1; -.
 DR HSSP: P37967; 10E3.
 DR FlyBase: FBgn0015577; alpha-Est9.
 DR InterPro: IPR002018; Carboxylesterase.
 DR Pfam: PF000379; Ser_estrs_site.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
 KW Hydrolase.
 SQ SEQUENCE 572 AA: 65660 MW: 37F1440F86AD2BD8 CRC64:
 Query Match 54.4%; Score 596; DB 5; Length 572;
 Best Local Similarity 52.0%; Pred. No. 5,2e-49;
 Matches 117; Conservative 34; Mismatches 56; Indels 18; Gaps 1;
 QY 1 QVDFTTGKVGSGEDCLLYSYNNLNPEKRPVLYIHGGFTIGENHRMGDPDTFKK 60
 DB 81 QKTFEEMTDGSEDCLYLNVYTKMLPTKPMEMVWYIGGFGFGEASRECYSPDYLLRE 140
 QY 61 DVLINIOYRLGAL-----GFLSNSEDLVNPGNAGLKQVMAIRMI 102
 DB 141 DVVVISINRRLGRLGNDTDMKKKHITFNISLPGFLCLDPELDVPGNAGLKQVIALRW 200
 QY 103 KNNCANFGNPDNITVFGESAGASTHYMMLTEQTRGLFHRCILMSGNAICPLANTQCOH 162
 DB 201 KANCSRFSGDSANITIFGDSAGSASVHYMMITEQTRGLFHKAICMSGNTLSPMAVTPQRN 260
 QY 163 RAFLTLAKLAGKGDNDKVDLEFLMKAKPODLIKLEKVTLEER 207
 DB 261 WPRYLAVQAGYAGENNTRDWEFLKNAKGSIIKANGELCIDEEK 305
 RESULT 14
 QYVIBI PRELIMINARY: PRT: 572 AA.
 AC 09VIBI.
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Alpha-Est9 protein.
 GN ALPHA-EST9 OR CG1128.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton R.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.T., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
 RA Borova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Burlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Churly J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Dudin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Mei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Mekulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nussken D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinelt K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shee B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers R.W., Rubin G.M., Venter J.C.:
 "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 CC -1 SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 DR EMBL: AEO03671; AAF54015.1; -.
 DR HSSP: P37967; 10E3.
 DR FlyBase: FBgn0015577; alpha-Est9.
 DR InterPro: IPR002018; Carboxylesterase.
 DR InterPro: IPR000997; Cholinesterase.
 DR InterPro: IPR000379; Ser_estrs_site.
 DR Pfam: PF00135; Coesterase; 1.
 DR PRINTS: PR00878; CHOLINESTRASE.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 2.
 KW Hydrolase.
 SQ SEQUENCE 572 AA: 65767 MW: 9138FB95713DF350 CRC64:
 Query Match 54.0%; Score 591; DB 5; Length 572;
 Best Local Similarity 51.6%; Pred. No. 1.6e-48;
 Matches 116; Conservative 34; Mismatches 57; Indels 18; Gaps 1;
 QY 1 QVDFTTGKVGSGEDCLLYSYNNLNPEKRPVLYIHGGFTIGENHRMGDPDTFKK 60
 DB 81 QKHFVFEEMTDGSEDCLYLNVYTKMLPTKPMVWYIGGFGFGEASRECYSPDYLLRE 140
 QY 61 DVLINIOYRLGAL-----GFLSNSEDLVNPGNAGLKQVMAIRMI 102
 DB 141 DVVVISINRRLGRLGNDTDMKKKHITFNISLPGFLCLDPELDVPGNAGLKQVIALRW 200
 QY 103 KNNCANFGNPDNITVFGESAGASTHYMMLTEQTRGLFHRCILMSGNAICPLANTQCOH 162
 DB 201 KANCSRFSGDSANITIFGDSAGSASVHYMMITEQTRGLFHKAICMSGNTLSPMAVTPQRN 260
 QY 163 RAFLTLAKLAGKGDNDKVDLEFLMKAKPODLIKLEKVTLEER 207
 DB 261 WPRYLAVQAGYAGENNTRDWEFLKNAKGSIIKANGELCIDEEK 305
 RESULT 15
 QYVIBI PRELIMINARY: PRT: 530 AA.
 AC 09VIBI.
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Alpha-Est10 protein.
 GN ALPHA-EST10 OR CG1131.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

nm hydrolase. 530 AA; 59739 MW; FF9011F52DEA07F1 CRC64;
SQ SEQUENCE

Matches 106; Conservative 39; Mismatches 55; Indels

```

Db      249  SMSG EIVKATATVLSNDEK  268

```

GenCore version 5.1.4-p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2003, 09:10:57 ; Search time 5.7278 Seconds
(without alignments)
1063.331 Million cell updates/sec

Title: US-09-776-910-43

Perfect score: 1095

Sequence: 1 QVDFITGKVGSEDCILYVY.....KAKFQDLIKLEKVLTEER 207

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1095	100.0	207	4	US-09-068-960-43
2	1095	100.0	570	4	US-09-068-960-2
3	1095	100.0	570	4	US-09-068-960-4
4	1095	100.0	570	4	US-09-068-960-6
5	1095	100.0	570	4	US-09-068-960-10
6	1089	99.5	570	4	US-08-669-524-3
7	1089	99.5	570	4	US-09-068-960-8
8	1072	97.9	570	2	US-08-668-524-4
9	826	75.4	207	4	US-09-068-960-15
10	819	74.8	570	4	US-09-068-960-13
11	812.5	74.2	572	2	US-08-669-524-8
12	496.5	45.3	528	3	US-08-747-221B-37
13	496.5	45.3	528	4	US-09-005-051-37
14	432	39.5	530	3	US-08-747-221B-53
15	432	39.5	530	4	US-09-005-051-53
16	432	39.5	550	3	US-08-747-221B-19
17	432	39.5	550	4	US-09-005-051-19
18	429	39.2	505	3	US-08-747-221B-14
19	429	39.2	505	4	US-09-005-051-14
20	429	39.2	550	3	US-08-747-221B-58
21	429	39.2	550	4	US-09-005-051-58
22	391.5	35.8	570	4	US-08-747-221B-54
23	391.5	35.8	570	4	US-09-005-051-54
24	391.5	35.8	596	3	US-08-747-221B-25
25	391.5	35.8	596	4	US-09-005-051-25
26	390.5	35.7	570	4	US-08-747-221B-55
27	390.5	35.7	570	4	US-09-005-051-55

28	390.5	35.7	595	3	US-08-747-221B-31	Sequence 31, Appl
29	390.5	35.7	595	4	US-09-005-051-31	Sequence 31, Appl
30	370	33.8	600	2	US-08-370-156-4	Sequence 4, Appl
31	370	33.8	600	3	US-08-814-095-4	Sequence 4, Appl
32	370	33.8	600	4	US-08-975-084-1	Sequence 1, Appl
33	370	33.8	614	1	US-07-732-962A-2	Sequence 2, Appl
34	370	33.8	614	2	US-08-370-156-2	Sequence 2, Appl
35	370	33.8	614	3	US-08-446-100-19	Sequence 19, Appl
36	370	33.8	614	3	US-08-446-100-21	Sequence 21, Appl
37	370	33.8	614	3	US-08-446-100-22	Sequence 22, Appl
38	370	33.8	614	3	US-08-446-100-23	Sequence 23, Appl
39	370	33.8	614	3	US-08-814-095-2	Sequence 2, Appl
40	370	33.8	614	5	PCT-US92-06106-2	Sequence 2, Appl
41	370	33.8	617	2	US-08-370-156-6	Sequence 6, Appl
42	370	33.8	617	3	US-08-814-095-6	Sequence 6, Appl
43	368	33.6	614	3	US-08-446-100-25	Sequence 25, Appl
44	366.5	33.5	575	1	US-08-348-920-1	Sequence 1, Appl
45	363.5	33.2	575	1	US-08-348-920-2	Sequence 2, Appl

ALIGNMENTS

```
RESULT 1
US-09-068-960-43
; Sequence 43, Application US/09068960A
; Patent No. 6235515
; GENERAL INFORMATION:
; APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.
; TITLE OF INVENTION: MALATHION CARBOXYL ESTERASE
; FILE REFERENCE: Attorney Docket No. 6235515 50179-051
; CURRENT APPLICATION NUMBER: US/09/068,960A
; EARLIER FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: PCT/AU96/00746
; EARLIER FILING DATE: 1996-11-22
; EARLIER APPLICATION NUMBER: AU 6751
; EARLIER FILING DATE: 1995-11-23
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Lucilia cuprina
; US-09-068-960-43

Query Match      100.0%; Score 1095; DB 4; Length 207;
Best Local Similarity 100.0%; Pred. No. 2.3e+124;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVDFITGKVGSEDCILYVYTNLNPEYKRPVLYVYHGGFTIGENHRDMPDYFIKK 60
    |||||||
Db 1 QVDFITGKVGSEDCILYVYTNLNPEYKRPVLYVYHGGFTIGENHRDMPDYFIKK 60
    |||||||

QY 61 DVLVINTQYRIGALGFLTNSDNLVPGNAGLQDVWALRWIKNNCANFGNDNTTVFG 120
    |||||||
Db 61 DVLVINTQYRIGALGFLTNSDNLVPGNAGLQDVWALRWIKNNCANFGNDNTTVFG 120
    |||||||

QY 121 ESAGAASTHMMTLEQYRGLFHRRGILMSGNAICPLANTOCORHAFYTLAKYKGGDNK 180
    |||||||
Db 121 ESAGAASTHMMTLEQYRGLFHRRGILMSGNAICPLANTOCORHAFYTLAKYKGGDNK 180
    |||||||

QY 181 DVEFFLMKARPODLIKLEKVLTEER 207
    |||||||
Db 181 DVEFFLMKARPODLIKLEKVLTEER 207
    |||||||

RESULT 2
US-09-068-960-2
; Sequence 2, Application US/09068960A
; Patent No. 6235515
; GENERAL INFORMATION:
; APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.
; TITLE OF INVENTION: MALATHION CARBOXYL ESTERASE
```



```
FILE REFERENCE: Attorney Docket No. 6235515 50179-051
CURRENT APPLICATION NUMBER: US/09/068,960A
CURRENT FILING DATE: 1998-05-20
EARLIER APPLICATION NUMBER: PCT/AU96/00746
EARLIER FILING DATE: 1996-11-22
EARLIER APPLICATION NUMBER: AU 6751
EARLIER FILING DATE: 1995-11-23
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 2
LENGTH: 570
TYPE: PRT
ORGANISM: Lucilia cuprina
US-09-068-960-2

Query Match          100.0%; Score 1095; DB 4; Length 570;
Best Local Similarity 100.0%; Pred. No. 1e-123;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVDFITGKVGSEDCILSVYTNLNLPETKRPLVYIHGGFTIGENHRDMYGPDPYFIKK 60
    |||
Db 97 QVDFITGKVGSEDCILSVYTNLNLPETKRPLVYIHGGFTIGENHRDMYGPDPYFIKK 156
    |||
QY 61 DVLINIOYRLGALGFLSINSEDLNVPNGAGLKDQYVALRWIKNNCANFGNPDNITVFG 120
    |||
Db 157 DVLINIOYRLGALGFLSINSEDLNVPNGAGLKDQYVALRWIKNNCANFGNPDNITVFG 216
    |||
QY 121 ESAGASTHYMMLTEOTRGLFHRGILMSGNAICPLANTOCOHRAFTLAKLAGYKGEDNDK 180
    |||
Db 217 ESAGASTHYMMLTEOTRGLFHRGILMSGNAICPLANTOCOHRAFTLAKLAGYKGEDNDK 276
    |||
QY 181 DVLFLMKAKPODLIKLEEKVLTLEER 207
    |||
Db 277 DVLFLMKAKPODLIKLEEKVLTLEER 303
    |||

RESULT 3
US-09-068-960-4
Sequence 4, Application US/09068960A
Patent No. 6235515
GENERAL INFORMATION:
APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.
TITLE OF INVENTION: MALATHION CARBOXYL ESTERASE
FILE REFERENCE: Attorney Docket No. 6235515 50179-051
CURRENT APPLICATION NUMBER: US/09/068,960A
CURRENT FILING DATE: 1998-05-20
EARLIER APPLICATION NUMBER: PCT/AU96/00746
EARLIER FILING DATE: 1996-11-22
EARLIER APPLICATION NUMBER: AU 6751
EARLIER FILING DATE: 1995-11-23
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 4
LENGTH: 570
TYPE: PRT
ORGANISM: Lucilia cuprina
US-09-068-960-4

Query Match          100.0%; Score 1095; DB 4; Length 570;
Best Local Similarity 100.0%; Pred. No. 1e-123;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVDFITGKVGSEDCILSVYTNLNLPETKRPLVYIHGGFTIGENHRDMYGPDPYFIKK 60
    |||
Db 97 QVDFITGKVGSEDCILSVYTNLNLPETKRPLVYIHGGFTIGENHRDMYGPDPYFIKK 156
    |||
QY 61 DVLINIOYRLGALGFLSINSEDLNVPNGAGLKDQYVALRWIKNNCANFGNPDNITVFG 120
    |||
Db 157 DVLINIOYRLGALGFLSINSEDLNVPNGAGLKDQYVALRWIKNNCANFGNPDNITVFG 216
    |||
QY 121 ESAGASTHYMMLTEOTRGLFHRGILMSGNAICPLANTOCOHRAFTLAKLAGYKGEDNDK 180
    |||
Db 217 ESAGASTHYMMLTEOTRGLFHRGILMSGNAICPLANTOCOHRAFTLAKLAGYKGEDNDK 276
    |||
QY 181 DVLFLMKAKPODLIKLEEKVLTLEER 207
    |||
Db 277 DVLFLMKAKPODLIKLEEKVLTLEER 303
    |||

RESULT 4
US-09-068-960-6
Sequence 6, Application US/09068960A
Patent No. 6235515
GENERAL INFORMATION:
APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.
TITLE OF INVENTION: MALATHION CARBOXYL ESTERASE
FILE REFERENCE: Attorney Docket No. 6235515 50179-051
CURRENT APPLICATION NUMBER: US/09/068,960A
CURRENT FILING DATE: 1998-05-20
EARLIER APPLICATION NUMBER: PCT/AU96/00746
EARLIER FILING DATE: 1996-11-22
EARLIER APPLICATION NUMBER: AU 6751
EARLIER FILING DATE: 1995-11-23
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 6
LENGTH: 570
TYPE: PRT
ORGANISM: Lucilia cuprina
US-09-068-960-6

Query Match          100.0%; Score 1095; DB 4; Length 570;
Best Local Similarity 100.0%; Pred. No. 1e-123;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVDFITGKVGSEDCILSVYTNLNLPETKRPLVYIHGGFTIGENHRDMYGPDPYFIKK 60
    |||
Db 97 QVDFITGKVGSEDCILSVYTNLNLPETKRPLVYIHGGFTIGENHRDMYGPDPYFIKK 156
    |||
QY 61 DVLINIOYRLGALGFLSINSEDLNVPNGAGLKDQYVALRWIKNNCANFGNPDNITVFG 120
    |||
Db 157 DVLINIOYRLGALGFLSINSEDLNVPNGAGLKDQYVALRWIKNNCANFGNPDNITVFG 216
    |||
QY 121 ESAGASTHYMMLTEOTRGLFHRGILMSGNAICPLANTOCOHRAFTLAKLAGYKGEDNDK 180
    |||
Db 217 ESAGASTHYMMLTEOTRGLFHRGILMSGNAICPLANTOCOHRAFTLAKLAGYKGEDNDK 276
    |||
QY 181 DVLFLMKAKPODLIKLEEKVLTLEER 207
    |||
Db 277 DVLFLMKAKPODLIKLEEKVLTLEER 303
    |||

RESULT 5
US-09-068-960-10
Sequence 10, Application US/09068960A
Patent No. 6235515
GENERAL INFORMATION:
APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.
TITLE OF INVENTION: MALATHION CARBOXYL ESTERASE
FILE REFERENCE: Attorney Docket No. 6235515 50179-051
CURRENT APPLICATION NUMBER: US/09/068,960A
CURRENT FILING DATE: 1998-05-20
EARLIER APPLICATION NUMBER: PCT/AU96/00746
EARLIER FILING DATE: 1996-11-22
EARLIER APPLICATION NUMBER: AU 6751
EARLIER FILING DATE: 1995-11-23
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 10
LENGTH: 570
TYPE: PRT
ORGANISM: Lucilia cuprina
US-09-068-960-10

Query Match          100.0%; Score 1095; DB 4; Length 570;
Best Local Similarity 100.0%; Pred. No. 1e-123;
```

```
QY 181 DVLFLMKAKPODLIKLEEKVLTLEER 207
    |||
Db 277 DVLFLMKAKPODLIKLEEKVLTLEER 303
    |||

RESULT 4
US-09-068-960-6
Sequence 6, Application US/09068960A
Patent No. 6235515
GENERAL INFORMATION:
APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.
TITLE OF INVENTION: MALATHION CARBOXYL ESTERASE
FILE REFERENCE: Attorney Docket No. 6235515 50179-051
CURRENT APPLICATION NUMBER: US/09/068,960A
CURRENT FILING DATE: 1998-05-20
EARLIER APPLICATION NUMBER: PCT/AU96/00746
EARLIER FILING DATE: 1996-11-22
EARLIER APPLICATION NUMBER: AU 6751
EARLIER FILING DATE: 1995-11-23
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 6
LENGTH: 570
TYPE: PRT
ORGANISM: Lucilia cuprina
US-09-068-960-6

Query Match          100.0%; Score 1095; DB 4; Length 570;
Best Local Similarity 100.0%; Pred. No. 1e-123;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVDFITGKVGSEDCILSVYTNLNLPETKRPLVYIHGGFTIGENHRDMYGPDPYFIKK 60
    |||
Db 97 QVDFITGKVGSEDCILSVYTNLNLPETKRPLVYIHGGFTIGENHRDMYGPDPYFIKK 156
    |||
QY 61 DVLINIOYRLGALGFLSINSEDLNVPNGAGLKDQYVALRWIKNNCANFGNPDNITVFG 120
    |||
Db 157 DVLINIOYRLGALGFLSINSEDLNVPNGAGLKDQYVALRWIKNNCANFGNPDNITVFG 216
    |||
QY 121 ESAGASTHYMMLTEOTRGLFHRGILMSGNAICPLANTOCOHRAFTLAKLAGYKGEDNDK 180
    |||
Db 217 ESAGASTHYMMLTEOTRGLFHRGILMSGNAICPLANTOCOHRAFTLAKLAGYKGEDNDK 276
    |||
QY 181 DVLFLMKAKPODLIKLEEKVLTLEER 207
    |||
Db 277 DVLFLMKAKPODLIKLEEKVLTLEER 303
    |||

RESULT 5
US-09-068-960-10
Sequence 10, Application US/09068960A
Patent No. 6235515
GENERAL INFORMATION:
APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.
TITLE OF INVENTION: MALATHION CARBOXYL ESTERASE
FILE REFERENCE: Attorney Docket No. 6235515 50179-051
CURRENT APPLICATION NUMBER: US/09/068,960A
CURRENT FILING DATE: 1998-05-20
EARLIER APPLICATION NUMBER: PCT/AU96/00746
EARLIER FILING DATE: 1996-11-22
EARLIER APPLICATION NUMBER: AU 6751
EARLIER FILING DATE: 1995-11-23
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 10
LENGTH: 570
TYPE: PRT
ORGANISM: Lucilia cuprina
US-09-068-960-10

Query Match          100.0%; Score 1095; DB 4; Length 570;
Best Local Similarity 100.0%; Pred. No. 1e-123;
```



```

ADDRESS: Lowe Price Lebanc & Becker
STREET: 99 Canal Center Plaza, Suite 300
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,524
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Price, Robert L.
REGISTRATION NUMBER: 22,685
REFERENCE/DOCKET NUMBER: 1451-021
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1111
TELEFAX: 703-684-1124
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 570 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-669-524-4

Query Match          97.9%  Score 1072; DB 2; Length 570;
Best Local Similarity 98.1%; Pred. No. 6,3e-121;
Matches 203; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 QVDFITGKVGSGEDCLYISVTNNLNPEKRPVLVYIHGGGFTIGENHRDMYGPDYFIKK 60
DB 97 QVDFITGKVGSGEDCLYISVTNNLNPEKRPVLVYIHGGGFTIGENHRDMYGPDYFIKK 156
QY 61 DVLINIOYRLGALGFLSLNSDLPVPGNAGLKDQVMAKRWKNNCANFGNPDNITVFG 120
DB 157 DVLINIOYRLGALGFLSLNSDLPVPGNAGLKDQVMAKRWKNNCANFGNPDNITVFG 216
QY 121 ESAGASTHYMMLEQTRGLFHRGILMSGNAICPLANTOCQHRATFLAKLAGYKGEDNDK 180
DB 217 ESAGASTHYMMLEQTRGLFHRGILMSGNAICPLANTOCQHRATFLAKLAGYKGEDNDK 276
QY 181 DYLEFLMAKAPQDLIKLEKVLTLER 207
DB 277 DYLEFLMAKAPQDLIKLEKVLTLER 303

RESULT 9
US-09-068-960-15
; Sequence 15, Application US/09068960A
; Patent No. 6235515
; GENERAL INFORMATION:
; APPLICANT: Commonwealth Scientific and Industrial Resrch. Org.
; TITLE OF INVENTION: MALATHION CARBOXYL ESTERASE
; FILE REFERENCE: Attorney Docket No. 6235515 50179-051
; CURRENT APPLICATION NUMBER: US/09/068,960A
; EARLIER FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: PCT/AU96/00746
; EARLIER FILING DATE: 1996-11-22
; EARLIER APPLICATION NUMBER: AU 6751
; EARLIER FILING DATE: 1995-11-23
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Musca domestica
US-09-068-960-15

```

```

Query Match          75.4%  Score 826; DB 4; Length 207;
Best Local Similarity 74.6%; Pred. No. 8.2e-92;
Matches 153; Conservative 25; Mismatches 27; Indels 0; Gaps 0;

QY 1 QVDFITGKVGSGEDCLYISVTNNLNPEKRPVLVYIHGGGFTIGENHRDMYGPDYFIKK 60
DB 1 QVDFITGKVGSGEDCLYISVTNNLNPEKRPVLVYIHGGGFTIGENHRDMYGPDYFIKK 60
QY 61 DVLINIOYRLGALGFLSLNSDLPVPGNAGLKDQVMAKRWKNNCANFGNPDNITVFG 120
DB 61 DVLINIOYRLGALGFLSLNSDLPVPGNAGLKDQVMAKRWKNNCANFGNPDNITVFG 120
QY 121 ESAGASTHYMMLEQTRGLFHRGILMSGNAICPLANTOCQHRATFLAKLAGYKGEDNDK 180
DB 121 ESAGASTHYMMLEQTRGLFHRGILMSGNAICPLANTOCQHRATFLAKLAGYKGEDNDK 180
QY 181 DYLEFLMAKAPQDLIKLEKVLTLER 205
DB 181 DYLEFLMAKAPQDLIKLEKVLTLER 205

RESULT 10
US-09-068-960-13
; Sequence 13, Application US/09068960A
; Patent No. 6235515
; GENERAL INFORMATION:
; APPLICANT: Commonwealth Scientific and Industrial Resrch. Org.
; TITLE OF INVENTION: MALATHION CARBOXYL ESTERASE
; FILE REFERENCE: Attorney Docket No. 6235515 50179-051
; CURRENT APPLICATION NUMBER: US/09/068,960A
; EARLIER FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: PCT/AU96/00746
; EARLIER FILING DATE: 1996-11-22
; EARLIER APPLICATION NUMBER: AU 6751
; EARLIER FILING DATE: 1995-11-23
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Musca domestica
US-09-068-960-13

Query Match          74.8%  Score 819; DB 4; Length 570;
Best Local Similarity 73.7%; Pred. No. 2.7e-90;
Matches 151; Conservative 27; Mismatches 27; Indels 0; Gaps 0;

QY 1 QVDFITGKVGSGEDCLYISVTNNLNPEKRPVLVYIHGGGFTIGENHRDMYGPDYFIKK 60
DB 97 QVDFITGKVGSGEDCLYISVTNNLNPEKRPVLVYIHGGGFTIGENHRDMYGPDYFIKK 156
QY 61 DVLINIOYRLGALGFLSLNSDLPVPGNAGLKDQVMAKRWKNNCANFGNPDNITVFG 120
DB 157 DVLINIOYRLGALGFLSLNSDLPVPGNAGLKDQVMAKRWKNNCANFGNPDNITVFG 216
QY 121 ESAGASTHYMMLEQTRGLFHRGILMSGNAICPLANTOCQHRATFLAKLAGYKGEDNDK 180
DB 217 ESAGASTHYMMLEQTRGLFHRGILMSGNAICPLANTOCQHRATFLAKLAGYKGEDNDK 276
QY 181 DYLEFLMAKAPQDLIKLEKVLTLER 205
DB 277 DYLEFLMAKAPQDLIKLEKVLTLER 301

RESULT 11
US-08-669-524-8
; Sequence 8, Application US/08669524
; Patent No. 5843758
; GENERAL INFORMATION:
; APPLICANT: RUSSELL, Robyn J.
; APPLICANT: NEWCOMB, Richard D.
; APPLICANT: ROBIN, Geoffrey C.
US-08-669-524-8

```

Query Match 74.2%; Score 812.5; DB 2; Length 572.
 Best Local Similarity 73.1%; Pred. No. 1,6e-89;
 Matches 152; Conservative 26; Mismatches 29; Indels 1; Gaps 1.

QY 1 QVDFTGVCSSGSDCLTVSYVTNNINPETKRPVLVYIHGGFPIIGENHRDMXGDPYFIKK 60
 |||:|||||:|||||:|:|||||:|||||:|:|||||:|:
 Db QVOEFEDKVEGSEDDCLTVNVTNNKPKDKARPVWMIHGGFPIIGBANREWGDPYFKK 156
 QY 61 DVLINIDYRIGALGFLSLNSEDLVNPPGAGLKDQVMALRWTKNNCANFGNPDNITYFG 120
 ||||:|||||:|||||:|:|||||:|||||:|||||:|||||:|:
 Db DVLVTTIDYRIGALGFSRLKSPELNPPGAGLKDVLALRWTKNNCASGSDPNCITVFG 216
 QY 121 ESAGASTHYMYLLEOTGGLFHRGILMSGNAICPLA-NTQCHRAFPATLAKGYGGEED 179
 ||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db ESAGASTHYMYLTDQGTGLFHRGILGSGSALCPMAYNODITHNFRIRAKLVGYGGEED 276
 QY 180 KDVEFLMKAKPQDLIKLEKYLITLEER 207
 |||||:|:|||||:|||||:
 Db 277 KDVEFLQNVKAKDLIRVEENVLTLEER 304

RESULT 12
 US-08-747-221B-37
 ; Sequence 37, Application US/08747221B
 ; Patent No. 6063610
 ; GENERAL INFORMATION:
 ; APPLICANT: Silver, Gary W.
 ; APPLICANT: Wisniewski, Nancy
 ; TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid
 ; TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
 ; NUMBER OF SEQUENCES: 66
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Carol Talkington Verser, Ph.D.
 ; ADDRESSEE: Heska Corporation

Query Match	45.38;	Score 496.5;	DB 3;	Length 528;
Best Local Similarity	49.58;	Pred. No. 2.6e-51;		
Matches 97;	Conservative 36;	Mismatches 58;	Indels 5;	Gaps 3;

RESULT 13
 US-09-005-051-37
 : Sequence 37, Application US/09005051
 : Patent No. 6291222
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: Silver, Gary W.
 :
 : APPLICANT: Wisniewski, Nancy
 :
 : TITLE OF INVENTION: No. 6291222el Carboxylesterase Nucleic
 :
 : TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
 :
 : NUMBER OF SEQUENCES: 66
 :
 : CORRESPONDENCE ADDRESS:
 :
 : ADDRESSEE: Carol Talkington Verser, Ph.D.
 :
 : ADDRESSEE: Heska Corporation
 :
 : STREET: 1825 Sharp Point Drive
 :
 : CITY: Fort Collins
 :
 : STATE: Colorado
 :
 : COUNTRY: USA
 :
 : ZIP: 80525
 :
 : COMPUTER READABLE FORM:
 :
 : MEDIUM TYPE: Floppy disk
 :
 : COMPUTER: IBM PC compatible
 :
 : OPERATING SYSTEM: Windows 95
 :
 : SOFTWARE: Wordperfect for Windows, Version 7.0

Query Match	45.3%	Score	496.5	DB	4	Length	528
Best Local Similarity	49.58%	Pred.	No.2,66-51				
Matches	97	Conservative	36	Mismatches	58	Indels	5
						Gaps	3

QY	2	VDEITGKCGS	EDCLVSYTNNLN	PEPKRPVLYI	HGGGEIT	IGENHRDMY	GDPYTIKDD	61
Db	69	VHFIKRKVGA	EDCLVLYNVPKTS	SEKSLP	PWWIHGG	GFMSGSDMY	GGEYLMDDYG	128
QY	62	VYLINIQYR	GAIGFGLT	SEDLNPGNA	GKDDOMAL	RWIKNNK	CANFGNPDI	121
Db	129	IVLTFENYR	LGAVIGFGLT	SEDLNPGNA	GKDDOMAL	RWIKNNK	CANFGNPDI	186
QY	122	SAGASATHY	MMLEQTQRL	FHRGILM	SGNAICP	--LANTQ	COHRAFTLAKI	179
Db	187	SAGASATHY	IMLSDLSK	GFHKAI	SQSGCA	FNPMAID	ONHNKERA	245
QY	180	KDYLEFL	PMKAKK	PODLI	195			
Db	246	TEAKLIT	ROAP	IDDLI	261			

```

REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 530 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-747-221b-53

Query Match      39.5%; Score 432; DB 3; Length 530;
Best Local Similarity 43.9%; Pred. No. 1,7e-43;
Matches      86; Conservative      32; Mismatches      74; Indels      4; Gaps      3.

Oy      2 VDFITGVCVSGECILSYVTNNINPEFKRPVLYIHGGSGFIIEGNRDYAGPDYFKKD 61
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      68 LNFELKRIEDEDCELLVNAVAPRTSSDKLPVFVWVGSGFVTSGLIEQSPDYLVND 127
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy      62 VLLINIRYRGAAGFSLNSEDLNPVGNAGLKDQYMALRMKNCANFGNPDNITVFE 121
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      128 VIFTFNRYRGRPLGFIINLELE--GAPGVNGLIDYVALKWKTEIKERFGDPENITIGV 185
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy      122 SAGAATHYVMLTEQYRGLEPHRGILMSGALCPRLA-NQCCHRAFTLAKAGKGEDNOK 180
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      186 SAGASVHYLLHTTGTGLYKRALQSGSLALPMVAFORHPYKRSLLQAEILGHP-TWNTQ 244
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy      181 DYLEFLMKAKRPDILK 196
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      245 DAEFLQKAPYDSILK 260

RESULT 15
US-09-005-051-53
: Sequence 53, Application US/09005051
: Patent No. 6291222
: GENERAL INFORMATION:
: APPLICANT: Silver, Gary W.
: APPLICANT: Wisniewski, Nancy
: TITLE OF INVENTION: No. 6291222e1 Carboxylesterase Nucleic Acid
: TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
: NUMBER OF SEQUENCES: 66
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Carol Talkington Verser, Ph.D.
: STREET: 1825 Sharp Point Drive
: CITY: Fort Collins
: STATE: Colorado
: COUNTRY: USA
: ZIP: 80525
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: Windows 95
: SOFTWARE: Wordperfect for Windows, Version 7.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/005,051
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/747,221
: FILING DATE: No. 6291222ember 12, 1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Verser, Carol Talkington
: REGISTRATION NUMBER: 37,459
: REFERENCE/DOCKET NUMBER: FC-1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 970/493-7272
: TELEFAX: 970/484-9505
: INFORMATION FOR SEQ ID NO: 53:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 530 amino acids

```

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-051-53

Query Match 39.5%; Score 432; DB 4; Length 530;
Best Local Similarity 43.9%; Pred. No. 1.7e-43;
Matches 86; Conservative 32; Mismatches 74; Indels 4; Gaps 3;

OY 2 VDFITGKVGSGEDCLVSYTNNLNPEYKRPVLYIHGGFTIGENHMDTGPDYFIKRD 61
Db 68 LNFETLKIEGDEDCLVNVAAPKTSDDRKPVEFWVHGSGFVTSQNLFEQSPDYLVND 127
OY 62 VVLTINQVRIAGLGFSLNSDDLNVPGNAGLKDQVVALRWIKNNCANFGNDNTVFGE 121
Db 128 VIEVFENYRLGPLEGFLNELE--GAPGNVGLDQVAAALKTKENTIEKGGDPENITIGV 185
OY 122 SAGASTHMTTEQTRGIFHRGIIISGNATCPLA-NTOCQHRFTLAKLAGYKGEDNDK 180
Db 186 SAGGASVHLLSHSTTGLYKRAIAQSGSALNPMAFORHPVKRSIQLAETILGHP-TNNTQ 244
OY 181 DYLEFLMKAKPODLTK 196
Db 245 DALFEFLQKRPVDSLK 260

Search completed: April 4, 2003, 09:18:12
Job time: 7.7278 secs

GenCore version 5.1.4-p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2003, 09:16:33 ; Search time 8.92471 Seconds
(without alignments)
1417.991 Million cell updates/sec

Title: US-09-776-910-43

Perfect score: 1095
Sequence: 1 OVDFITGKVGSEDLVLSV.....KAKPOLIKLEKVLLEER 207

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 248812 segs, 61136040 residues

Total number of hits satisfying chosen parameters: 248812

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published_Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCF_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/PCFUS_PUBCOMB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	401.5	36.7	574	9	US-10-023-515-4
2	401.5	36.7	612	9	US-09-875-353-4
3	391	33.7	585	10	US-09-934-323-4
4	361.5	33.0	574	10	US-09-748-739A-21
5	359.5	32.8	574	10	US-09-748-739A-23
6	356.5	32.6	574	10	US-09-748-739A-22
7	353.5	32.3	574	10	US-09-748-739A-4
8	353.5	32.3	574	10	US-09-748-739A-6
9	353.5	32.3	574	10	US-09-748-739A-8
10	353.5	32.3	574	10	US-09-748-739A-17
11	353.5	32.3	574	10	US-09-748-739A-18
12	353.5	32.3	574	10	US-09-748-739A-19
13	353.5	32.3	574	10	US-09-748-739A-20
14	353.5	32.3	602	10	US-09-748-739A-2
15	331.5	30.3	568	9	US-09-418-176-4
16	331.5	30.3	722	9	US-09-418-176-3
17	331.5	30.3	745	9	US-09-418-176-2
18	323.5	29.5	537	9	US-09-738-626-4754
19	322.5	29.5	549	9	US-10-102-806-689

20	322.5	29.5	565	10	US-09-895-860-5	Sequence 5, Appl 1
21	321.5	29.4	545	9	US-09-978-295A-254	Sequence 234, App
22	321.5	29.4	545	9	US-09-978-697-254	Sequence 254, App
23	321.5	29.4	545	9	US-09-978-192A-254	Sequence 254, App
24	321.5	29.4	545	9	US-09-999-832A-254	Sequence 254, App
25	321.5	29.4	545	9	US-09-978-189-254	Sequence 254, App
26	321.5	29.4	545	9	US-10-174-550-58	Sequence 58, Appl
27	321.5	29.4	545	9	US-10-174-758-58	Sequence 58, Appl
28	321.5	29.4	545	9	US-10-175-737-58	Sequence 58, Appl
29	321.5	29.4	545	9	US-10-173-706-58	Sequence 58, Appl
30	321.5	29.4	545	9	US-10-175-738-58	Sequence 58, Appl
31	321.5	29.4	545	9	US-10-175-752-58	Sequence 58, Appl
32	321.5	29.4	545	9	US-10-176-482-58	Sequence 58, Appl
33	321.5	29.4	545	9	US-10-176-757-58	Sequence 58, Appl
34	321.5	29.4	545	9	US-10-176-913-58	Sequence 58, Appl
35	321.5	29.4	545	9	US-10-180-552-58	Sequence 58, Appl
36	321.5	29.4	545	9	US-10-180-557-58	Sequence 58, Appl
37	321.5	29.4	545	9	US-10-173-700-58	Sequence 58, Appl
38	321.5	29.4	545	9	US-10-174-572-58	Sequence 58, Appl
39	321.5	29.4	545	9	US-10-174-579-58	Sequence 58, Appl
40	321.5	29.4	545	9	US-10-174-582-58	Sequence 58, Appl
41	321.5	29.4	545	9	US-10-174-588-58	Sequence 58, Appl
42	321.5	29.4	545	9	US-10-175-739-58	Sequence 58, Appl
43	321.5	29.4	545	9	US-10-175-740-58	Sequence 58, Appl
44	321.5	29.4	545	9	US-10-175-743-58	Sequence 58, Appl
45	321.5	29.4	545	9	US-10-176-488-58	Sequence 58, Appl

ALIGNMENTS

RESULT 1

US-10-023-515-4

Sequence 4, Application US/10023515

Publication No. US20020182636A1

GENERAL INFORMATION:

APPLICANT: Curtiss, Rory A. J.

TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYL ESTERASE

TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF

FILE REFERENCE: 10448-122001

CURRENT APPLICATION NUMBER: US/10/023, 515

CURRENT FILING DATE: 2001-12-18

PRIOR APPLICATION NUMBER: 60/256, 369

PRIOR FILING DATE: 2000-12-18

PRIOR APPLICATION NUMBER: 60/279, 508

PRIOR FILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 4

LENGTH: 574

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Consensus sequence

US-10-023-515-4

Query Match

Best Local Similarity 36.7%; Score 401.5; DB 9; Length 574;

Matches 86; Conservative 43; Mismatches 64; Indels 15; Gaps 6;

Db

12 SEDVLVSVYV-NNLINETKRPVLVYIHGGFTIGENHR---DMYGDYTRK-DVLLIN 66

Db

91 SEDVLVSVYVTRKTRKNSKLPMVWYHGGGFMFGSCHSLPLSDGESLARGNVIYVS 150

Db

67 IQRRLGALGFLSUNSEDLVNGNAGLKDQYVALRWIKNNCANFGNPDNITVYESAGAA 126

Db

151 INYRLGFLGLSTGDDKLPSGNGVYGLDRLATLKWODNIAFGGDPNSVTIGESAGAA 210

Db

127 STVHNMTE-----QRRGFHRIIGILMSGNAICPLA---NTQQRHAFITLAKIGKED 177

Db

211 SVSILLTSLNGNDNPPSKGLFHRATISGSGALSPMAIQSESNARGAKELARLLGC-NET 269

; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 23
 ; LENGTH: 574
 ; TYPE: PRF
 ; ORGANISM: Rattus sp.
 US-09-748-739A-23

Query Match
 Best Local Similarity 41.6%; Score 359.5; DB 10; Length 574;
 Matches 82; Conservative 42; Mismatches 62; Indels 11; Gaps 6;

QY 12 SEDCLYLSVTNNLNPETRKPVLYIHGGFIIENHRDMYGPDYFIKDD-VVLINIOYR 70
 Db 89 SEDCLYLNWIPAPKPK-NATVLMWIVGGGFGTGTSSLPYDGKFLARVERIVVSMNMR 147
 QY 71 LGALGFSL--NSEDLVNPGNAGLKDYVALRWIKNNCANFGNDNITVFGESAGAST 128
 Db 148 VGALGFSLPGNSE--APGNMGLFDQDLALOWYOKNIAAFGKPSVTLFGESAGASV 204
 QY 129 HYMLTEQTRGLFHRGILMSGNAICPLA--NTQOHRAPFLAKLAGYKGGENDKDYLEF 185
 Db 205 SLHLSPGSHSLFTRALIOGSSNAPMAVKHPEAKRNTLTIAKFGC-SKENEKEITTC 263
 QY 186 LMAKAPDILKEEVL 202
 Db 264 LRKNDPQELILNEKLVL 280

RESULT 6
 US-09-748-739A-22
 ; Sequence 22, Application US/09748739A
 ; Patent No. US20020119489A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lockridge, Oksana
 ; TITLE OF INVENTION: Butyrylcholinesterase Variants and
 ; FILE REFERENCE: P-IX 4143
 ; CURRENT APPLICATION NUMBER: US/09/748, 739A
 ; CURRENT FILING DATE: 2000-12-06
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 22
 ; LENGTH: 574
 ; TYPE: PRF
 ; ORGANISM: Felis catus
 US-09-748-739A-22

Query Match
 Best Local Similarity 40.0%; Score 356.5; DB 10; Length 574;
 Matches 76; Conservative 47; Mismatches 56; Indels 11; Gaps 6;

QY 12 SEDCLYLSVTNNLNPETRKPVLYIHGGFIIENHRDMYGPDYFIKDD-VVLINIOYR 70
 Db 89 SEDCLYLNWIPAPKPK-NATVLMWIVGGGFGTGTSSLPYDGKFLARVERIVVSMNMR 147
 QY 71 LGALGFSL--NSEDLVNPGNAGLKDYVALRWIKNNCANFGNDNITVFGESAGAST 128
 Db 148 VGALGFSLPGNSE--APGNMGLFDQDLALOWYOKNIAAFGKPSVTLFGESAGASV 204
 QY 129 HYMLTEQTRGLFHRGILMSGNAICPLA--NTQOHRAPFLAKLAGYKGGENDKDYLEF 185
 Db 205 SLHLSPGSHSLFTRALIOGSSNAPMAVKHPEAKRNTLTIAKFGC-SKENEKEITTC 263
 QY 186 LMAKAPDILKEEVL 195
 Db 264 LRKNDPQELIL 273

RESULT 7
 US-09-748-739A-4
 ; Sequence 4, Application US/09748739A

; Patent No. US20020119489A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lockridge, Oksana
 ; TITLE OF INVENTION: Butyrylcholinesterase Variants and
 ; FILE REFERENCE: P-IX 4143
 ; CURRENT APPLICATION NUMBER: US/09/748, 739A
 ; CURRENT FILING DATE: 2000-12-06
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 574
 ; TYPE: PRF
 ; ORGANISM: Artificial Sequence
 ; OTHER INFORMATION: Human Butyrylcholinesterase variant
 US-09-748-739A-4

Query Match
 Best Local Similarity 41.1%; Score 353.5; DB 10; Length 574;
 Matches 81; Conservative 41; Mismatches 64; Indels 11; Gaps 6;

QY 12 SEDCLYLSVTNNLNPETRKPVLYIHGGFIIENHRDMYGPDYFIKDD-VVLINIOYR 70
 Db 89 SEDCLYLNWIPAPKPK-NATVLMWIVGGGFGTGTSSLPYDGKFLARVERIVVSMNMR 147
 QY 71 LGALGFSL--NSEDLVNPGNAGLKDYVALRWIKNNCANFGNDNITVFGESAGAST 128
 Db 148 VGALGFSLPGNSE--APGNMGLFDQDLALOWYOKNIAAFGKPSVTLFGESAGASV 204
 QY 129 HYMLTEQTRGLFHRGILMSGNAICPLA--NTQOHRAPFLAKLAGYKGGENDKDYLEF 185
 Db 205 SLHLSPGSHSLFTRALIOGSSNAPMAVKHPEAKRNTLTIAKFGC-SKENEKEITTC 263
 QY 186 LMAKAPDILKEEVL 202
 Db 264 LRKNDPQELILNEAFVY 280

RESULT 8
 US-09-748-739A-6
 ; Sequence 6, Application US/09748739A
 ; Patent No. US20020119489A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lockridge, Oksana
 ; TITLE OF INVENTION: Butyrylcholinesterase Variants and
 ; FILE REFERENCE: P-IX 4143
 ; CURRENT APPLICATION NUMBER: US/09/748, 739A
 ; CURRENT FILING DATE: 2000-12-06
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 6
 ; LENGTH: 574
 ; TYPE: PRF
 ; ORGANISM: Artificial Sequence
 ; OTHER INFORMATION: Human Butyrylcholinesterase variant
 US-09-748-739A-6

Query Match
 Best Local Similarity 41.1%; Score 353.5; DB 10; Length 574;
 Matches 81; Conservative 41; Mismatches 64; Indels 11; Gaps 6;

QY 12 SEDCLYLSVTNNLNPETRKPVLYIHGGFIIENHRDMYGPDYFIKDD-VVLINIOYR 70
 Db 89 SEDCLYLNWIPAPKPK-NATVLMWIVGGGFGTGTSSLPYDGKFLARVERIVVSMNMR 147
 QY 71 LGALGFSL--NSEDLVNPGNAGLKDYVALRWIKNNCANFGNDNITVFGESAGAST 128
 Db 148 VGALGFSLPGNSE--APGNMGLFDQDLALOWYOKNIAAFGKPSVTLFGESAGASV 204

```
OY 129 HYMLTEOTRGLEFHRGILMSGNAICPLANT---QOHRATFLAKLAGYGEDNDKDVLEF 185
      : : : | | | | | : : : | | | | | : : : | | | | | : : : |
Db 205 SLHLSPGSHSLFTTRALLOSGSFNAPWAVTSLEYEARNTLNLAKLIGCSRE-NETETIKC 263

OY 186 LMAKAPDOLIKLEEKVL 202
      | | | : : | :
Db 264 LNKDPQETILLNEAFV 280

RESULT 9
US-09-748-739A-8
; Sequence 8, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
; APPLICANT: Lockridge, Oksana
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: P-IX 4143
; CURRENT APPLICATION NUMBER: US/09/748,739A
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Human Butyrylcholinesterase variant
US-09-748-739A-8

Query Match
Best Local Similarity 41.1%; Score 353.5; DB 10; Length 574;
Matches 81; Conservative 41; Mismatches 64; Indels 11; Gaps 6;

OY 12 SEDCLYLVYTNLNPETKRPVLYVYIHGGFTIGENHDMYGPDYFIKRD-VVLINIOYR 70
      | | | | | : : | | | | | : : | | | | | : : | | | | | : : |
Db 89 SEDCLYLVWVLPAPKPK-NATVLIWYGGFGQTGSSLIHYDGKFLARVERIYVSMNYR 147

OY 71 LGALGFSL--NSEDLVNPGNAGLKDOVMALRMKNNCANFGNPDNITVFGESAGAST 128
      : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 148 VGALGFALPGNPE--APGNMGLFDQALQWOKNIAAFGNPKSVTLFGESAGASV 204

OY 129 HYMLTEOTRGLEFHRGILMSGNAICPLANT---QOHRATFLAKLAGYGEDNDKDVLEF 185
      : : : | | | | | : : : | | | | | : : : | | | | | : : : |
Db 205 SLHLSPGSHSLFTTRALLOSGSFNAPWAVTSLEYEARNTLNLAKLIGCSRE-NETETIKC 263

OY 186 LMAKAPDOLIKLEEKVL 202
      | | | : : | :
Db 264 LNKDPQETILLNEAFV 280

RESULT 10
US-09-748-739A-17
; Sequence 17, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
; APPLICANT: Lockridge, Oksana
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: P-IX 4143
; CURRENT APPLICATION NUMBER: US/09/748,739A
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-748-739A-17
```

```
Query Match
Best Local Similarity 41.1%; Score 353.5; DB 10; Length 574;
Matches 81; Conservative 41; Mismatches 64; Indels 11; Gaps 6;

OY 12 SEDCLYLVYTNLNPETKRPVLYVYIHGGFTIGENHDMYGPDYFIKRD-VVLINIOYR 70
      | | | | | : : | | | | | : : | | | | | : : | | | | | : : |
Db 89 SEDCLYLVWVLPAPKPK-NATVLIWYGGFGQTGSSLIHYDGKFLARVERIYVSMNYR 147

OY 71 LGALGFSL--NSEDLVNPGNAGLKDOVMALRMKNNCANFGNPDNITVFGESAGAST 128
      : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 148 VGALGFALPGNPE--APGNMGLFDQALQWOKNIAAFGNPKSVTLFGESAGASV 204

OY 129 HYMLTEOTRGLEFHRGILMSGNAICPLANT---QOHRATFLAKLAGYGEDNDKDVLEF 185
      : : : | | | | | : : : | | | | | : : : | | | | | : : : |
Db 205 SLHLSPGSHSLFTTRALLOSGSFNAPWAVTSLEYEARNTLNLAKLIGCSRE-NETETIKC 263

OY 186 LMAKAPDOLIKLEEKVL 202
      | | | : : | :
Db 264 LNKDPQETILLNEAFV 280

RESULT 11
US-09-748-739A-18
; Sequence 18, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
; APPLICANT: Lockridge, Oksana
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: P-IX 4143
; CURRENT APPLICATION NUMBER: US/09/748,739A
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-748-739A-18

Query Match
Best Local Similarity 41.1%; Score 353.5; DB 10; Length 574;
Matches 81; Conservative 41; Mismatches 64; Indels 11; Gaps 6;

OY 12 SEDCLYLVYTNLNPETKRPVLYVYIHGGFTIGENHDMYGPDYFIKRD-VVLINIOYR 70
      | | | | | : : | | | | | : : | | | | | : : | | | | | : : |
Db 89 SEDCLYLVWVLPAPKPK-NATVLIWYGGFGQTGSSLIHYDGKFLARVERIYVSMNYR 147

OY 71 LGALGFSL--NSEDLVNPGNAGLKDOVMALRMKNNCANFGNPDNITVFGESAGAST 128
      : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 148 VGALGFALPGNPE--APGNMGLFDQALQWOKNIAAFGNPKSVTLFGESAGASV 204

OY 129 HYMLTEOTRGLEFHRGILMSGNAICPLANT---QOHRATFLAKLAGYGEDNDKDVLEF 185
      : : : | | | | | : : : | | | | | : : : | | | | | : : : |
Db 205 SLHLSPGSHSLFTTRALLOSGSFNAPWAVTSLEYEARNTLNLAKLIGCSRE-NETETIKC 263

OY 186 LMAKAPDOLIKLEEKVL 202
      | | | : : | :
Db 264 LNKDPQETILLNEAFV 280

RESULT 12
US-09-748-739A-19
; Sequence 19, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
; APPLICANT: Lockridge, Oksana
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: P-IX 4143
; CURRENT APPLICATION NUMBER: US/09/748,739A
```

```
? CURRENT FILING DATE: 2000-12-06
? NUMBER OF SEQ ID NOS: 31
? SOFTWARE: FastSeq for Windows Version 4.0.
? SEQ ID NO: 19
? LENGTH: 574
? TYPE: PRN
? ORGANISM: Homo sapiens
US-05-748-739A-19
```

Query Match	32.3%;	Score	353.5;	DB	10;	Length	574;
Best Local Similarity	41.1%;	Pred. No.	9e-30;				
Matches	81;	Conservative	41;	Mismatches	64;	Indels	11;
						Gaps	6

```
QY      12 SEDCLYLSVYTNNLNAPETKRPVLVIHGCGFICGENHRDMYGPDYFIKKD-VLINTQYR 70
        |||||::: | : ||:::|||| | : : : : : ||
Db      89 SEDCLYLNIWIPAPRK-NATVLIWITGGGFQTGTSSLHYDDGKFARVERIVISMNRY 147
```

Db 148 VGLALGFLALPGNPE--APGNMGLEDDOLALQWQKNIAAFGNGPKSVTLFGESAGASV 204

Db 205 SLHLSPGSHSLFRAILQSSFNAPAVTSLEYARNRFLNLAKLTGCSRE NETETIIC 263

```
QY      186 LMKAKPQDLIKLEEKVL 202
      |  ||::: |  |:
Db      264 LRNKDPQETLLNEAFV 280
```

RESULT 13
US-09-748-739A-20

```

sequence 20, Application US/09/48/739A
Patent No. US20020119489A1
GENERAL INFORMATION:
APPLICANT: lockridge, oksana
APPLICANT: Watkins, Jeffrey D.
TITLE OF INVENTION: Butyrylcholinesterase Variants and
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: P-IX 4143
CURRENT APPLICATION NUMBER: US/09/748,739A
CURRENT FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 20
LENGTH: 574
TYPE: PRT
ORGANISM: Homo sapiens
OS-09-748-739A-20

```

Query Match	32.3%;	Score 353.5;	DB 10;	Length 574;
Best Local Similarity	41.1%;	Pred. No. 9e-30;		
Matches	81;	Conservative	41;	Mismatches 64;
			Indels	11;
			Gaps	6

QY 12 SEDCLYSVYTNLNLPETKRPVLVYIHGGGFTIGENHRDMGYDPIKRD-VVLINIQYR 70
 |||||:| : ||::||| | : :| : : : : : ||
 Db 89 SEDCLYNWIPAPPK-NATVLINVIYGGGQTGTSLSHVYDGKFLARYERVIIVSMNYR 147

```

148 VGALGFLALPGNE--APGNMGLEDDQLALQWVQKNTAAFGGNPKSVTLFGESAGASV 204
      :::::|      ||| |||:::| |:::|:::|:::|:::|:::|:::|:::|:::|:::|
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

```

Db 205 SLHLSPGSHSLFTRAILQSGSFENAPWAVSYLEARNRTLNLAKLQSGRE-NETETIIKC 263

Db 264 LRNKDPQELLNEAFV 2800

RESULT 14
US-09-748-739A-2

Sequence 2, Application US/09748739A
Patent No. US20020119489A1
GENERAL INFORMATION:
ADDITONAL INFORMATION:

1
 2
 3
 4
 5
 6
 7
 8
 9
 10
 11
 12
 13
 14
 15
 16
 17
 18
 19
 20
 21
 22
 23
 24
 25
 26
 27
 28
 29
 30
 31
 32
 33
 34
 35
 36
 37
 38
 39
 40
 41
 42
 43
 44
 45
 46
 47
 48
 49
 50
 51
 52
 53
 54
 55
 56
 57
 58
 59
 60
 61
 62
 63
 64
 65
 66
 67
 68
 69
 70
 71
 72
 73
 74
 75
 76
 77
 78
 79
 80
 81
 82
 83
 84
 85
 86
 87
 88
 89
 90
 91
 92
 93
 94
 95
 96
 97
 98
 99
 100
 101
 102
 103
 104
 105
 106
 107
 108
 109
 110
 111
 112
 113
 114
 115
 116
 117
 118
 119
 120
 121
 122
 123
 124
 125
 126
 127
 128
 129
 130
 131
 132
 133
 134
 135
 136
 137
 138
 139
 140
 141
 142
 143
 144
 145
 146
 147
 148
 149
 150
 151
 152
 153
 154
 155
 156
 157
 158
 159
 160
 161
 162
 163
 164
 165
 166
 167
 168
 169
 170
 171
 172
 173
 174
 175
 176
 177
 178
 179
 180
 181
 182
 183
 184
 185
 186
 187
 188
 189
 190
 191
 192
 193
 194
 195
 196
 197
 198
 199
 200
 201
 202
 203
 204
 205
 206
 207
 208
 209
 210
 211
 212
 213
 214
 215
 216
 217
 218
 219
 220
 221
 222
 223
 224
 225
 226
 227
 228
 229
 230
 231
 232
 233
 234
 235
 236
 237
 238
 239
 240
 241
 242
 243
 244
 245
 246
 247
 248
 249
 250
 251
 252
 253
 254
 255
 256
 257
 258
 259
 260
 261
 262
 263
 264
 265
 266
 267
 268
 269
 270
 271
 272
 273
 274
 275
 276
 277
 278
 279
 280
 281
 282
 283
 284
 285
 286
 287
 288
 289
 290
 291
 292
 293
 294
 295
 296
 297
 298
 299
 300
 301
 302
 303
 304
 305
 306
 307
 308
 309
 310
 311
 312
 313
 314
 315
 316
 317
 318
 319
 320
 321
 322
 323
 324
 325
 326
 327
 328
 329
 330
 331
 332
 333
 334
 335
 336
 337
 338
 339
 340
 341
 342
 343
 344
 345
 346
 347
 348
 349
 350
 351
 352
 353
 354
 355
 356
 357
 358
 359
 360
 361
 362
 363
 364
 365
 366
 367
 368
 369
 370
 371
 372
 373
 374
 375
 376
 377
 378
 379
 380
 381
 382
 383
 384
 385
 386
 387
 388
 389
 390
 391
 392
 393
 394
 395
 396
 397
 398
 399
 400
 401
 402
 403
 404
 405
 406
 407
 408
 409
 410
 411
 412
 413
 414
 415
 416
 417
 418
 419
 420
 421
 422
 423
 424
 425
 426
 427
 428
 429
 430
 431
 432
 433
 434
 435
 436
 437
 438
 439
 440
 441
 442
 443
 444
 445
 446
 447
 448
 449
 450
 451
 452
 453
 454
 455
 456
 457
 458
 459
 460
 461
 462
 463
 464
 465
 466
 467
 468
 469
 470
 471
 472
 473
 474
 475
 476
 477
 478
 479
 480
 481
 482
 483
 484
 485
 486
 487
 488
 489
 490
 491
 492
 493
 494
 495
 496
 497
 498
 499
 500
 501
 502
 503
 504
 505
 506
 507
 508
 509
 510
 511
 512
 513
 514
 515
 516
 517
 518
 519
 520
 521
 522
 523
 524
 525

```

;
; CURRENT APPLICATION NUMBER: US/09/748,739#
;
; CURRENT FILING DATE: 2000-12-06
;
; NUMBER OF SEQ ID NOS: 31
;
; SOFTWARE: FastSeq for Windows Version 4.0

```

```

; SEQ ID NO 2
;
; LENGTH: 602
; TYPE: PRT
; ORGANISM: Artificial Sequence

```

```

; FEATURE:
; OTHER INFORMATION: Human Butyrylcholinesterase variant
US-09-748-739A-2

```

Query Match	32.3%;	Score 353.5;	DB 10;	Length 602;
Best Local Similarity	41.1%;	Pred. No. 9.6e-30;		
Matches	81;	Conservative 41;	Mismatches 64;	Indels 11;
				Gaps 6

12 SEDCLISLVIINNLPETAKRPVYIHGGGFIIGSENHRRDYGPDYTIKD-VLINIIGYR 70
 117 SEDCLYLNWIPAKRPK-NATVILIMYIGGGFQIGTSSLHYVDGKFLERVERVIIVSMNR 170

176 VGALGFLALPGNP-E--APGNNGLPDQLALQWQKNIAAFGGNPKRSVTLFGESAGASV 230

233 SHLLSPSHSLFTRAILÖSSFNAPMAVTSLEYARNRPTNLAKLTGCSRE-NETETIKC 29

```
QY      186 LMKAPQDLIKLEKVL 202
        |  |::: |  |:
Db      292 LRNKDPQELLNEAFV 308
```

RESULT 15
US-09-418-176-4
: Sequence 4, Application NS/09418176

```

; APPLICATION NO.: 022007004901
;
; GENERAL INFORMATION:
;
; APPLICANT: Das, Goutam
;
; TITLE OF INVENTION: DNA Molecules for Expression of

```

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case

```

; CITY: New York
; STATE: New York
; COUNTRY: United States
; RD: 1000 3707

```

```

;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: MS-DOS

```

SOFTWARE: patentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/418,176
FILING DATE:

CLASSIFICATION: /
PRIOR APPLICATION DATA: /
APPLICATION NUMBER: 08/624,398 /
FILING DATE: 04-APR-1996 /

APPLICATION NUMBER: PCT/SE96/00318
FILING DATE: 12-MAR-1996
PRIOR APPLICATION DATA:

```

APPLICATION NUMBER: SE 9501939-4
FILING DATE: 24-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Thelma A. Chen Cleland
REGISTRATION NUMBER: 40,948
REFERENCE/DOCKET NUMBER: 1103326-0206
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8200
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 568 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: Mammary gland
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..568
OTHER INFORMATION: /label= Variant_C
PUBLICATION INFORMATION:
AUTHORS: Hansson, Lennart
AUTHORS: Blackberg, Lars
AUTHORS: Edlund, Michael
AUTHORS: Lundberg, Lennart
AUTHORS: Stromqvist, Mats
AUTHORS: Hernell, Olle
TITLE: Recombinant Human Milk Bile Salt-stimulated
        lipase
JOURNAL: J. Biol. Chem.
VOLUME: 268
ISSUE: 35
PAGES: 26692-26698
DATE: Dec. 15-1993
US-09-418-176-4

```

```

Query Match          30.3%; Score 331.5; DB 9; Length 568;
Best Local Similarity 37.4%; Pred. No. 2.1e-27;
Matches 76; Conservative 31; Mismatches 53; Indels 43; Gaps 7;

QY 11 GSEDCYLYSVYTNLNLPETRR--PVLVYIHGGFIIGENHRDMY-----GPDYFIKKD 61
DB 76 GDEDCILINWVPGRKQVSRDLPMIWIYGAFLMSGHGANFLNNYLYDGEIATRCN 135

QY 62 VVLINIQYRLGALGFLSLNSEDINVPGNAGLKDQVALRWIKNKCANFGSNPDNITVEGE 121
DB 136 VIVVFENYRVGPGFLS--TGDANLPNGNYGLRDQHMALWVKRNIATAFGDPNNITLFE 193

QY 122 SAGASHTVWMLTEQTRGLFHGILMSGNAI-----CPLAN--- 157
DB 194 SAGGASVSLQTLSPYKGLIRRAISQSGVALSPWVIOKNPLFWAKKVAEKVGCPCVDAR 253

QY 158 -TOC---QHRAPFLA---KLAG 172
DB 254 MAQCLKVTDPRALTLAYKVPVLAG 276

```

Search completed: April 4, 2003, 09:34:08
Job time : 10.9247 secs

Matches 153; Conservative 25; Mismatches 27; Indels 0; Gaps 0;

```
QY 1 QTFDISGKPTGSEDCLYLNTYNDLNDPKRPMVFHGGGFIPEGANRMWGPDPYFMK 60
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 97 QVDFITGKVGSGEDCLYLSYTNLNPETKRPLVYIHGGGFIPEGANRMWGPDPYFIK 156
QY 61 PVLVTVQYRLGVLGFLSLKSENLNPGNAGLKDQVMALEWFKSNIAIFGGDVNDITVFG 120
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 157 DVVLINQYRLGALGFLSLNSEDNLNPGNAGLKDQVMALEWFKSNIAIFGGDVNDITVFG 216
QY 121 ESAGGASTHYMMITTEOTRGLFHRGIMSGNSMCSASTECOSRALTMKRVYKGEENEK 180
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 217 ESAGGASTHYMMITTEOTRGLFHRGIMSGNACPLANTQCOHRAFTLAKLAGYGEDNDK 276
QY 181 DLEFLMKANPYDLIKEEPOVLTPE 205
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 277 DYLEFLMKAKKPODLIKLEKVTLE 301
```

RESULT 6
US-09-068-960-6
Sequence 6, Application US/09068960A
Patent No. 6235515

GENERAL INFORMATION:

APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.
TITLE OF INVENTION: MALATHION CARBOXYL ESTERASE
FILE REFERENCE: Attorney Docket No. 6235515 50179-051
CURRENT FILING DATE: 1998-05-20
EARLIER FILING DATE: 1996-11-22
EARLIER APPLICATION NUMBER: PCT/AU96/00746
EARLIER FILING DATE: 1995-11-23
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 6
LENGTH: 570
TYPE: PRT
ORGANISM: Lucilia cuprina
US-09-068-960-6

Query Match 75.6%; Score 826; DB 4; Length 570;
Best Local Similarity 74.6%; Pred. No. 2,8e-92;

Matches 153; Conservative 25; Mismatches 27; Indels 0; Gaps 0;

```
QY 1 QTFDISGKPTGSEDCLYLNTYNDLNDPKRPMVFHGGGFIPEGANRMWGPDPYFMK 60
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 97 QVDFITGKVGSGEDCLYLSYTNLNPETKRPLVYIHGGGFIPEGANRMWGPDPYFIK 156
QY 61 PVLVTVQYRLGVLGFLSLKSENLNPGNAGLKDQVMALEWFKSNIAIFGGDVNDITVFG 120
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 157 DVVLINQYRLGALGFLSLNSEDNLNPGNAGLKDQVMALEWFKSNIAIFGGDVNDITVFG 216
QY 121 ESAGGASTHYMMITTEOTRGLFHRGIMSGNSMCSASTECOSRALTMKRVYKGEENEK 180
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 217 ESAGGASTHYMMITTEOTRGLFHRGIMSGNACPLANTQCOHRAFTLAKLAGYGEDNDK 276
QY 181 DLEFLMKANPYDLIKEEPOVLTPE 205
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 277 DYLEFLMKAKKPODLIKLEKVTLE 301
```

RESULT 7
US-09-068-960-10

Sequence 10, Application US/09068960A
Patent No. 6235515

GENERAL INFORMATION:

APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.
TITLE OF INVENTION: MALATHION CARBOXYL ESTERASE
FILE REFERENCE: Attorney Docket No. 6235515 50179-051
CURRENT FILING DATE: 1998-05-20
EARLIER APPLICATION NUMBER: PCT/AU96/00746

EARLIER FILING DATE: 1996-11-22
EARLIER APPLICATION NUMBER: AU 6751
EARLIER FILING DATE: 1995-11-23
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 10
LENGTH: 570
TYPE: PRT
ORGANISM: Lucilia cuprina
US-09-068-960-10

Query Match 75.6%; Score 826; DB 4; Length 570;
Best Local Similarity 74.6%; Pred. No. 2,8e-92;

Matches 153; Conservative 25; Mismatches 27; Indels 0; Gaps 0;

```
QY 1 QTFDISGKPTGSEDCLYLNTYNDLNDPKRPMVFHGGGFIPEGANRMWGPDPYFMK 60
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 97 QVDFITGKVGSGEDCLYLSYTNLNPETKRPLVYIHGGGFIPEGANRMWGPDPYFIK 156
QY 61 PVLVTVQYRLGVLGFLSLKSENLNPGNAGLKDQVMALEWFKSNIAIFGGDVNDITVFG 120
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 157 DVVLINQYRLGALGFLSLNSEDNLNPGNAGLKDQVMALEWFKSNIAIFGGDVNDITVFG 216
QY 121 ESAGGASTHYMMITTEOTRGLFHRGIMSGNSMCSASTECOSRALTMKRVYKGEENEK 180
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 217 ESAGGASTHYMMITTEOTRGLFHRGIMSGNACPLANTQCOHRAFTLAKLAGYGEDNDK 276
QY 181 DLEFLMKANPYDLIKEEPOVLTPE 205
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 277 DYLEFLMKAKKPODLIKLEKVTLE 301
```

RESULT 8
US-08-669-524-3

Sequence 3, Application US/08669524
Patent No. 5843758

GENERAL INFORMATION:

APPLICANT: RUSSELL, Robyn J.
APPLICANT: NEWCOMB, Richard D.
APPLICANT: ROBIN, Geoffrey C.
APPLICANT: BOYCE, Thomas M.
APPLICANT: CAMPBELL, Peter M.
APPLICANT: PARKER, Anthony G.
APPLICANT: OAKESHOT, John G.
APPLICANT: SMYTH, Kerrie A.
TITLE OF INVENTION: ENZYME BASED BIOREMEDIATION
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lowe Price Lebland & Becker
STREET: 99 Canal Center Plaza, Suite 300
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,524
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Price, Robert L.
REGISTRATION NUMBER: 22,685
REFERENCE/DOCKET NUMBER: 1451-021
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1111
TELEFAX: 703-684-1124
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 570 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-669-524-3

Query Match 75.5%; Score 825; DB 2; Length 570;
Best Local Similarity 74.6%; Pred. No. 3.7e-92;
Matches 153; Conservative 25; Mismatches 27; Indels 0; Gaps 0;

QY 1 QDFTSGKPTGSEDCLYLVNVTNDLNDPKRPVVFTHGGGFTFGEANRNMVGPDPYEMK 60
DB 97 QVDFITGKVCSEDCLYLVNVTNNLNPETKRPLVYIHGGGFTFGEANRNMVGPDPYEMK 156
QY 61 PVLVTVQYRLGVGLSLKSENLPVGNAGLKDQVMAIRWFKSNIAIFGGDVNDITVFG 120
DB 157 DVLLINIOYRLGALGLSLNSDELNVPGNAGLKDQVMAIRWIKNNCANGCPNDITVFG 216
QY 121 ESAGGASTHYMMITDQTRGLFHRGIMSGNSCSASTECOSRALTMAKRVYKGEENK 180
DB 217 ESAGGASTHYMMITDQTRGLFHRGIMSGNATCPWANTOCOHRAFTLAKLAGYKGEDMDK 276
QY 181 DILEFLKAKNPDLIKEPOVLTPE 205
DB 277 DVLEFLKAKNPDLIKEPVLTLE 301

RESULT 9
US-09-068-960-8
Sequence 8, Application US/09068960A
Patent No. 6235513
GENERAL INFORMATION:
APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.
TITLE OF INVENTION: MALATHION CARBOXYL ESTERASE
FILE REFERENCE: Attorney Docket No. 6235513 50179-051
CURRENT APPLICATION NUMBER: US/09/068,960A
CURRENT FILING DATE: 1998-05-20
EARLIER APPLICATION NUMBER: PCT/AU96/00746
EARLIER FILING DATE: 1996-11-22
EARLIER APPLICATION NUMBER: AU 6751
EARLIER FILING DATE: 1995-11-23
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 8
LENGTH: 570
TYPE: PRT
ORGANISM: Lucilia cuprina
US-09-068-960-8

Query Match 75.5%; Score 825; DB 4; Length 570;
Best Local Similarity 74.6%; Pred. No. 3.7e-92;
Matches 153; Conservative 25; Mismatches 27; Indels 0; Gaps 0;

QY 1 QDFTSGKPTGSEDCLYLVNVTNDLNDPKRPVVFTHGGGFTFGEANRNMVGPDPYEMK 60
DB 97 QVDFITGKVCSEDCLYLVNVTNNLNPETKRPLVYIHGGGFTFGEANRNMVGPDPYEMK 156
QY 61 PVLVTVQYRLGVGLSLKSENLPVGNAGLKDQVMAIRWFKSNIAIFGGDVNDITVFG 120
DB 157 DVLLINIOYRLGALGLSLNSDELNVPGNAGLKDQVMAIRWIKNNCANGCPNDITVFG 216
QY 121 ESAGGASTHYMMITDQTRGLFHRGIMSGNSCSASTECOSRALTMAKRVYKGEENK 180
DB 217 ESAGGASTHYMMITDQTRGLFHRGIMSGNATCPWANTOCOHRAFTLAKLAGYKGEDMDK 276
QY 181 DILEFLKAKNPDLIKEPOVLTPE 205
DB 277 DVLEFLKAKNPDLIKEPVLTLE 301

RESULT 10
US-08-669-524-4
Sequence 4, Application US/08669524

Patent No. 5843758
GENERAL INFORMATION:
APPLICANT: RUSSELL, Robyn J.
APPLICANT: NEWCOMB, Richard D.
APPLICANT: ROBIN, Geoffrey C.
APPLICANT: BOYCE, Thomas M.
APPLICANT: CAMPBELL, Peter M.
APPLICANT: PARKER, Anthony G.
APPLICANT: OAKESHOTY, John G.
APPLICANT: SMYTH, Kerrie A.
TITLE OF INVENTION: ENZYME BASED BIOREMEDIATION
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lowe Price Leblanc & Becker
STREET: 99 Canal Center Plaza, Suite 300
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,524
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Price, Robert L.
REGISTRATION NUMBER: 22,685
REFERENCE/DOCKET NUMBER: 1451-021
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1111
TELEFAX: 703-684-1124
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 570 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-669-524-4

Query Match 74.2%; Score 811; DB 2; Length 570;
Best Local Similarity 73.7%; Pred. No. 1.9e-90;
Matches 151; Conservative 25; Mismatches 29; Indels 0; Gaps 0;

QY 1 QDFTSGKPTGSEDCLYLVNVTNDLNDPKRPVVFTHGGGFTFGEANRNMVGPDPYEMK 60
DB 97 QVDFITGKVCSEDCLYLVNVTNNLNPETKRPLVYIHGGGFTFGEANRNMVGPDPYEMK 156
QY 61 PVLVTVQYRLGVGLSLKSENLPVGNAGLKDQVMAIRWFKSNIAIFGGDVNDITVFG 120
DB 157 DVLLINIOYRLGALGLSLNSDELNVPGNAGLKDQVMAIRWIKNNCANGCPNDITVFG 216
QY 121 ESAGGASTHYMMITDQTRGLFHRGIMSGNSCSASTECOSRALTMAKRVYKGEENK 180
DB 217 ESAGGASTHYMMITDQTRGLFHRGIMSGNATCPWANTOCOHRAFTLAKLAGYKGEDMDK 276
QY 181 DILEFLKAKNPDLIKEPOVLTPE 205
DB 277 DVLEFLKAKNPDLIKEPVLTLE 301

RESULT 11
US-08-669-524-8
Sequence 8, Application US/08669524
Patent No. 5843758
GENERAL INFORMATION:
APPLICANT: RUSSELL, Robyn J.
APPLICANT: NEWCOMB, Richard D.
APPLICANT: ROBIN, Geoffrey C.

APPLICANT: BOYCE, Thomas M.
 APPLICANT: CAMPBELL, Peter M.
 APPLICANT: PARKER, Anthony G.
 APPLICANT: OAKSHOTT, John G.
 APPLICANT: SMITH, Kerrie A.
 TITLE OF INVENTION: ENZYME BASED BIOREMEDIATION
 NUMBER OF SEQUENCES: 22
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lowe Price Leblanc & Becker
 STREET: 99 Canal Center Plaza, Suite 300
 CITY: Alexandria
 STATE: Virginia
 COUNTRY: USA
 ZIP: 22314
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/669,524
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Price, Robert L.
 REGISTRATION NUMBER: 22,685
 REFERENCE/DOCKET NUMBER: 1451-021
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-684-1111
 TELEFAX: 703-684-1124
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 572 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-669-524-8

Query Match 67.3%; Score 736; DB 2; Length 572;
 Best Local Similarity 67.5%; Pred. No. 2,9e-81;
 Matches 141; Conservative 25; Mismatches 41; Indels 2; Gaps 2;
 QY 1 QTFISGKPTGSEDCLYLNYNTNDLPKRRPVWFTIHGGFTFGANRWYGPDYFMKKPVY 60
 DB 97 QVQFPEKDESEDCLYLNYNTNNPKAPVWVWTHGGFTFGANRWYGPDYFMKE 156
 QY 61 PVLVTVOYRLGVGLFSLKSENINVPNGAGIKDOVMALRMFKSNIAIFGSDVNITVFG 120
 DB 157 DVVLVTIOYRLGALGFMSLKSPELVNPGNAGLKDOVLALKIKNNCASFGSDPNCITVFG 216
 QY 121 ESAGASHTYMMTEORTGLFHRGIMSGNSMCSA-STECQSRALTMKRVYKGEENE 179
 DB 217 ESAGASHTYMMTEORTGLFHRGILDSGSAICPMAYNGDITNHPYRIAKLVYKGDND 276
 QY 180 KDLFLMKANPYDLKEEPOVLT-PEPM 207
 DB 277 KDVLFLQNVAKADLIRVEENVLTLEERM 305

RESULT 12
 US-08-747-221B-37
 Sequence 37, Application US/08747221B
 Patent No. 6063610
 GENERAL INFORMATION:
 APPLICANT: Silver, Gary W.
 APPLICANT: Wisniewski, Nancy
 TITLE OF INVENTION: No. 6063610e1 Carboxylesterase Nucleic Acid
 TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
 NUMBER OF SEQUENCES: 66
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Carol Talkington Verser, Ph.D.
 ADDRESSEE: Heska Corporation

STREET: 1825 Sharp Point Drive
 CITY: Fort Collins
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80525
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: WordPerfect for Windows, Version 7.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/747,221B
 FILING DATE: No. 6063610ember 12, 1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Verser, Carol Talkington
 REGISTRATION NUMBER: 37,459
 REFERENCE/DOCKET NUMBER: FC-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 970/493-7272
 TELEFAX: 970/484-9505
 INFORMATION FOR SEQ ID NO: 37:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 528 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-747-221B-37

Query Match 42.4%; Score 463.5; DB 3; Length 528;
 Best Local Similarity 47.3%; Pred. No. 5.9e-48;
 Matches 98; Conservative 34; Mismatches 64; Indels 11; Gaps 4;
 QY 4 FISKPTGSEDCLYLNYNTNDLPKRRPVWFTIHGGFTFGANRWYGPDYFMKKPVY 63
 DB 71 FIKRIKVGAEBCLYLNYVPTSEKSLPVWVTHGGFTFGANRWYGPDYFMKKPVY 130
 QY 64 LVTVYQYRLGVGLFSLKSENINVPNGAGIKDOVMALRMFKSNIAIFGSDVNITVFGESA 123
 DB 131 LVTFNYRLGVGLFSLKSENINVPNGAGIKDOVMALRMFKSNIAIFGSDVNITVFGESA 188
 QY 124 GASTHYMMTEORTGLFHRGIMSGNSMCSASTECQSR-ALTMKRVYKGEENE 181
 DB 189 GASTHYMMTEORTGLFHRGILDSGSAICPMAYNGDITNHPYRIAKLVYKGDND 247
 QY 182 ILFLMKANPYDLKEEPOVLT-PEPM 202
 DB 248 ALKILRQAPIDLDLNRKPKDKGOLI 274

RESULT 13
 US-09-005-051-37
 Sequence 37, Application US/09005051
 Patent No. 6291222
 GENERAL INFORMATION:
 APPLICANT: Silver, Gary W.
 APPLICANT: Wisniewski, Nancy
 TITLE OF INVENTION: No. 6291222e1 Carboxylesterase Nucleic Acid
 TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
 NUMBER OF SEQUENCES: 66
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Carol Talkington Verser, Ph.D.
 ADDRESSEE: Heska Corporation
 STREET: 1825 Sharp Point Drive
 CITY: Fort Collins
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80525
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: WordPerfect for Windows, Version 7.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,051
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/747,221
FILING DATE: No. 6291222ember 12, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 528 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-051-37

Query Match 42.4%; Score 463.5; DB 4; Length 528;
Best Local Similarity 47.3%; Pred. No. 5.9e-48;
Matches 98; Conservative 34; Mismatches 64; Indels 11; Gaps 4;

QY 4 FISKPTGSEDCILYLVNTDLPDKRPVWFIHGGGFTFGANRWYGPDYFMKRPV 63
DB 71 FIKRKGAECDCLYLVNTYVKTSEKSLPVMWVHGGGFTGSGNSMYPPELMDGYI 130
QY 64 LVTVQVRLGVGLFSLKSENLNPGNAGLDQVVALRFRKSNIAIFGADVNTIVGES 123
DB 131 LVTVNRYRLGVGLFNLGLE--EAPGNVGLMDQVVALKRVKNNIASFGDDNNNTIFESA 188
QY 124 GGASTHWMITQTRGLFHRGIMSGNSMSSASTECQSR--ALTMARVGYGKEENKD 181
DB 189 GGASVHYLMISDLKGLFHKRAISQSGAFNFWALQHDNNKNAFLCKLGLHP-VDMETE 247
QY 182 ILFLMKANPYDLI-----KEEQVL 202
DB 248 ALKIRQAPIDLIDNRIRKPKDGLI 274

RESULT 14
US-08-747-221B-53
Sequence 53, Application US/08747221B
Patent No. 6063610
GENERAL INFORMATION:
APPLICANT: Silver, Gary W.
APPLICANT: Wisniewski, Nancy
TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESS: Hesk Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,221B
FILING DATE: No. 6063610ember 12, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459

REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 530 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-747-221B-53

Query Match 39.2%; Score 428; DB 3; Length 530;
Best Local Similarity 46.0%; Pred. No. 1.3e-43;
Matches 91; Conservative 29; Mismatches 74; Indels 4; Gaps 3;

QY 3 DFISKPTGSEDCILYLVNTDLPDKRPVWFIHGGGFTFGANRWYGPDYFMKRPV 62
DB 69 NFELKKGDEDCILYLVNAPKTTSDKLPVFWYHGGGFTGSGNLEFGSPDYLVWYDV 128
QY 63 LVTVQVRLGVGLFSLKSENLNPGNAGLDQVVALRFRKSNIAIFGADVNTIVGES 122
DB 129 LVTVNRYRLGVGLFNLGLE--EAPGNVGLMDQVVALKRVKNNIASFGDDNNNTIFES 186
QY 123 GGASTHWMITQTRGLFHRGIMSGNSMSSASTECQSRALTMARVGYGKEENKD 181
DB 187 GGASVHYLLSHTTTGLYKRAIQAOSGALNFWAFQRRHPKRSJOLALGLHP-TNNTQD 245
QY 182 ILFLMKANPYDLIKEEP 199
DB 246 ALFLQKAPVDSLKNMP 263

RESULT 15
US-09-005-051-53
Sequence 53, Application US/09005051
Patent No. 6291222
GENERAL INFORMATION:
APPLICANT: Silver, Gary W.
APPLICANT: Wisniewski, Nancy
TITLE OF INVENTION: No. 6291222el Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESS: Hesk Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,051
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/747,221
FILING DATE: No. 6291222ember 12, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 530 amino acids

```

;      TYPE: amino acid
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
US-09-005-051-53

```

Query Match	39.28;	Score 428;	DB 4;	Length 530;
Best Local Similarity	46.08;	Pred. No. 1	3e-43.	

Matches	91;	Conservative	29;	Mismatches	74;	Indels	4;	Gaps	3;
---------	-----	--------------	-----	------------	-----	--------	----	------	----

3 DFISGKPTGSEDCLYLNVTNDLNDPKKRPVMVFIIHGGEIFGEANRNWIGPDYEMKKPV 62

69 NPELKIEGDEDCLLVNVYAPKITSDKLPVFFFWHGGSFVTGSGNIEFQSPDYLNVYDV 128

63 VLVTQYRLGVLGFLSKSENINLPGNAGLKDQVMAIRWFKSNIAIFGGVDNITVEGES 122

Db 129 IFVTENYRLGPIGLNLELE--GAPGNVGLLDQYALKWTKENIEREGGDPENITIGGVS 186

123 AGCA¹THYMITEQ²TRGLF³HRCIMSGNSMCSA-STECOSRAITMAKPVYCKEENEK⁴ 101

Db

187 AGGASVHYLLISHTTGLYKRAIAOSSALNPMAEORHDKVPEIOLATLTCUD ERMRE 345

182 ILEETIMKANPYDI,IKFED 100
OY

	1975
pb	: :	
245	ALEI OKA DINGCT IYWAH	553

230 RUDOLF VON SUTLINMP 263

Search completed: April 4, 2003, 09:18:10
Job time : 7.7278 secs

Job time : 7.7278 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2003, 09:16:33 ; Search time 8.92471 Seconds
(without alignments)
1417.991 Million cell updates/sec

Title: US-09-776-910-15

Perfect score: 1093

Sequence: 1 QTDPIGSKPTGSEDCILYLVN.....KANPDYLIKEPQVLTPEEM 207

Scoring table: BLOSUM62

Searched: Gapex 10.0, Gapex 0.5

Total number of hits satisfying chosen parameters: 248812

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCIT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/PCITUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	365.5	33.4	574	9	US-10-023-515-4	Sequence 4, Appl 1
2	365.5	33.4	612	9	US-09-875-353-4	Sequence 4, Appl 1
3	357.5	32.7	574	10	US-09-748-739A-21	Sequence 21, Appl 1
4	355	32.5	585	10	US-09-934-323-4	Sequence 4, Appl 1
5	347.5	31.8	574	10	US-09-748-739A-23	Sequence 23, Appl 1
6	343.5	31.4	574	10	US-09-748-739A-22	Sequence 22, Appl 1
7	336	30.7	574	10	US-09-748-739A-17	Sequence 17, Appl 1
8	336	30.7	574	10	US-09-748-739A-18	Sequence 18, Appl 1
9	336	30.7	574	10	US-09-748-739A-19	Sequence 19, Appl 1
10	336	30.7	574	10	US-09-748-739A-20	Sequence 20, Appl 1
11	336	30.7	602	10	US-09-748-739A-20	Sequence 20, Appl 1
12	335.5	30.7	545	9	US-09-978-295A-254	Sequence 254, Appl 1
13	335.5	30.7	545	9	US-09-978-697-254	Sequence 254, Appl 1
14	335.5	30.7	545	9	US-09-978-192A-254	Sequence 254, Appl 1
15	335.5	30.7	545	9	US-09-999-832A-254	Sequence 254, Appl 1
16	335.5	30.7	545	9	US-09-978-189-254	Sequence 254, Appl 1
17	335.5	30.7	545	9	US-10-174-590-58	Sequence 58, Appl 1
18	335.5	30.7	545	9	US-10-176-758-58	Sequence 58, Appl 1
19	335.5	30.7	545	9	US-10-176-758-58	Sequence 58, Appl 1

20	335.5	30.7	545	9	US-10-175-737-58	Sequence 58, Appl 1
21	335.5	30.7	545	9	US-10-173-706-58	Sequence 58, Appl 1
22	335.5	30.7	545	9	US-10-175-738-58	Sequence 58, Appl 1
23	335.5	30.7	545	9	US-10-175-752-58	Sequence 58, Appl 1
24	335.5	30.7	545	9	US-10-176-482-58	Sequence 58, Appl 1
25	335.5	30.7	545	9	US-10-176-757-58	Sequence 58, Appl 1
26	335.5	30.7	545	9	US-10-176-913-58	Sequence 58, Appl 1
27	335.5	30.7	545	9	US-10-180-552-58	Sequence 58, Appl 1
28	335.5	30.7	545	9	US-10-180-552-58	Sequence 58, Appl 1
29	335.5	30.7	545	9	US-10-173-700-58	Sequence 58, Appl 1
30	335.5	30.7	545	9	US-10-174-572-58	Sequence 58, Appl 1
31	335.5	30.7	545	9	US-10-174-579-58	Sequence 58, Appl 1
32	335.5	30.7	545	9	US-10-174-582-58	Sequence 58, Appl 1
33	335.5	30.7	545	9	US-10-174-588-58	Sequence 58, Appl 1
34	335.5	30.7	545	9	US-10-175-739-58	Sequence 58, Appl 1
35	335.5	30.7	545	9	US-10-175-740-58	Sequence 58, Appl 1
36	335.5	30.7	545	9	US-10-175-743-58	Sequence 58, Appl 1
37	335.5	30.7	545	9	US-10-176-488-58	Sequence 58, Appl 1
38	335.5	30.7	545	9	US-10-176-492-58	Sequence 58, Appl 1
39	335.5	30.7	545	9	US-10-176-747-58	Sequence 58, Appl 1
40	335.5	30.7	545	9	US-10-176-750-58	Sequence 58, Appl 1
41	335.5	30.7	545	9	US-10-176-985-58	Sequence 58, Appl 1
42	335.5	30.7	545	9	US-10-176-987-58	Sequence 58, Appl 1
43	335.5	30.7	545	9	US-10-176-991-58	Sequence 58, Appl 1
44	335.5	30.7	545	9	US-10-176-992-58	Sequence 58, Appl 1
45	335.5	30.7	545	9	US-10-176-993-58	Sequence 58, Appl 1

ALIGNMENTS

RESULT 1	
US-10-023-515-4	
Sequence 4, Application US/10023515	
Publication No. US20020182636A1	
GENERAL INFORMATION:	
APPLICANT: Curtiss, Roy A. J.	
APPLICANT: Sinos-Santiago, Immaculada	
TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLTERASE	
FILE REFERENCE: 10448-122001	
CURRENT APPLICATION NUMBER: US/10/023,515	
PRIOR FILING DATE: 2001-12-18	
PRIOR APPLICATION NUMBER: 60/256,369	
PRIOR FILING DATE: 2000-12-18	
PRIOR APPLICATION NUMBER: 60/279,508	
PRIOR FILING DATE: 2001-03-28	
NUMBER OF SEQ ID NOS: 6	
SOFTWARE: FastSeq for Windows Version 4.0	
SEQ ID NO 4	
LENGTH: 574	
TYPE: PRT	
ORGANISM: Artificial Sequence	
FEATURE:	
OTHER INFORMATION: Consensus sequence	
US-10-023-515-4	
Query Match	33.4% Score 365.5; DB 9; Length 574;
Best Local Similarity	39.7% Pred. No. 2.5e-31;
Matches	79; Conservative 42; Mismatches 63; Indels 15; Gaps 5;
12 SEDCLYLWVY-NDLNPDKRPVWFHGGGFGEAN----	RMVGPDPVFMKKPVLYV 66
11 SEDCLYLWVYIPKPKPKPSKLPVWVHGGGFGEAN----	PLSYDESLAREGNVYVS 150
67 VOYRIGVGLFSLKSENINLVGNGKLDQVWALRFRKSNIAIFGVDNITVGSAGGA 126	
151 INVRIGLPGFLSTDDDKLPKSGNGGLDORIALKWKVDNIAAFGDPNSVTIPGESAGGA 210	
127 STHWMLTE-----QTRGLFHRGIMGNSM-----CSSASTEGQSALIMAKVNGKE 177	
211 SVSLLLSNGSDNPPSSKGLFHRALISGSGSALSPWALQSESNARAKELARLLGC-NET 269	

```

; FILE REFERENCE: P-IX 4143
; CURRENT APPLICATION NUMBER: US/09/748,739A
; CURRENT FILING DATE: 2000-12-06
;

```

100

100

DB 207 HILSPGSHSLFTRAILILOGSGFNAPMAVTSLEYARNRTLNIAKLTCG-SRENTEIILKCLR 265
QY 188 KANPYDLIKEPOVL---TP 204
DB 266 NKDPOEILLNEAFVVPYGT 285

RESULT 9
US-09-748-739A-18
Sequence 18, Application US/09748739A
Patent No. US20020119489A1

GENERAL INFORMATION:
APPLICANT: Lockridge, Oksana
APPLICANT: Watkins, Jeffrey D.
TITLE OF INVENTION: Butyrylcholinesterase Variants and
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: P-IX 4143
CURRENT APPLICATION NUMBER: US/09/748,739A
CURRENT FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 18
LENGTH: 574
TYPE: PRT
ORGANISM: Homo sapiens
US-09-748-739A-18

Query Match
Best Local Similarity 30.7%; Score 336; DB 10; Length 574;
Best Local Similarity 39.5%; Pred. No. 4,1e-28;
Matches 79; Conservative 41; Mismatches 70; Indels 10; Gaps 6;

QY 12 SEDCLVLYNTDNDLPDKRPVWFTHGGGFTFGEANRMWGPDPYEMK-KPVLYVTVQYR 70
DB 89 SEDCLVLYNTDNDLPDKRPVWFTHGGGFTFGEANRMWGPDPYEMK-KPVLYVTVQYR 147
QY 71 LCVLGFSLKSENLVPGNAGLKDQVMAIRFKSNIAIFGGDVNTITVFGSAGASTHY 130
DB 148 VGALGFALPG-NPEAPGNMGLFDQDLALOWYOKNIAAFGKNKSVTLFGESAGASVSL 206
QY 131 MMITBOTRGLEFRGIMSGNSMCSAST--ECOSRALTMARKVYKGEENEKDIIEFLM 187
DB 207 HILSPGSHSLFTRAILILOGSGFNAPMAVTSLEYARNRTLNIAKLTCG-SRENTEIILKCLR 265
QY 188 KANPYDLIKEPOVL---TP 204
DB 266 NKDPOEILLNEAFVVPYGT 285

RESULT 10
US-09-748-739A-19
Sequence 19, Application US/09748739A
Patent No. US20020119489A1

GENERAL INFORMATION:
APPLICANT: Lockridge, Oksana
APPLICANT: Watkins, Jeffrey D.
TITLE OF INVENTION: Butyrylcholinesterase Variants and
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: P-IX 4143
CURRENT APPLICATION NUMBER: US/09/748,739A
CURRENT FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 19
LENGTH: 574
TYPE: PRT
ORGANISM: Homo sapiens
US-09-748-739A-19

Query Match
Best Local Similarity 30.7%; Score 336; DB 10; Length 574;
Best Local Similarity 39.5%; Pred. No. 4,1e-28;
Matches 79; Conservative 41; Mismatches 70; Indels 10; Gaps 6;

QY 12 SEDCLVLYNTDNDLPDKRPVWFTHGGGFTFGEANRMWGPDPYEMK-KPVLYVTVQYR 70
DB 89 SEDCLVLYNTDNDLPDKRPVWFTHGGGFTFGEANRMWGPDPYEMK-KPVLYVTVQYR 147
QY 71 LCVLGFSLKSENLVPGNAGLKDQVMAIRFKSNIAIFGGDVNTITVFGSAGASTHY 130
DB 148 VGALGFALPG-NPEAPGNMGLFDQDLALOWYOKNIAAFGKNKSVTLFGESAGASVSL 206
QY 131 MMITBOTRGLEFRGIMSGNSMCSAST--ECOSRALTMARKVYKGEENEKDIIEFLM 187
DB 207 HILSPGSHSLFTRAILILOGSGFNAPMAVTSLEYARNRTLNIAKLTCG-SRENTEIILKCLR 265
QY 188 KANPYDLIKEPOVL---TP 204
DB 266 NKDPOEILLNEAFVVPYGT 285

RESULT 11
US-09-748-739A-20
Sequence 20, Application US/09748739A
Patent No. US20020119489A1

GENERAL INFORMATION:
APPLICANT: Lockridge, Oksana
APPLICANT: Watkins, Jeffrey D.
TITLE OF INVENTION: Butyrylcholinesterase Variants and
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: P-IX 4143
CURRENT APPLICATION NUMBER: US/09/748,739A
CURRENT FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 20
LENGTH: 574
TYPE: PRT
ORGANISM: Homo sapiens
US-09-748-739A-20

Query Match
Best Local Similarity 30.7%; Score 336; DB 10; Length 574;
Best Local Similarity 39.5%; Pred. No. 4,1e-28;
Matches 79; Conservative 41; Mismatches 70; Indels 10; Gaps 6;

QY 12 SEDCLVLYNTDNDLPDKRPVWFTHGGGFTFGEANRMWGPDPYEMK-KPVLYVTVQYR 70
DB 89 SEDCLVLYNTDNDLPDKRPVWFTHGGGFTFGEANRMWGPDPYEMK-KPVLYVTVQYR 147
QY 71 LCVLGFSLKSENLVPGNAGLKDQVMAIRFKSNIAIFGGDVNTITVFGSAGASTHY 130
DB 148 VGALGFALPG-NPEAPGNMGLFDQDLALOWYOKNIAAFGKNKSVTLFGESAGASVSL 206
QY 131 MMITBOTRGLEFRGIMSGNSMCSAST--ECOSRALTMARKVYKGEENEKDIIEFLM 187
DB 207 HILSPGSHSLFTRAILILOGSGFNAPMAVTSLEYARNRTLNIAKLTCG-SRENTEIILKCLR 265
QY 188 KANPYDLIKEPOVL---TP 204
DB 266 NKDPOEILLNEAFVVPYGT 285

RESULT 12
US-09-748-739A-2
Sequence 2, Application US/09748739A
Patent No. US20020119489A1

GENERAL INFORMATION:
APPLICANT: Lockridge, Oksana
APPLICANT: Watkins, Jeffrey D.
TITLE OF INVENTION: Butyrylcholinesterase Variants and
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: P-IX 4143
CURRENT APPLICATION NUMBER: US/09/748,739A
CURRENT FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2

us-09-776-910-15.rapb

PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632

PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649

PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR ADDITION NUMBER: 60/077791

PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20

PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294

PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079654

PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689

PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27

PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-30

PRIOR APPLICATION NUMBER: 60/079923
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/080105
PRIOR FILING DATE: 1998-03-30

PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080165

PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/080194
 PRIOR FILING DATE: 1998-03-31
 APPLICATION NUMBER: 60/080194

PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080328
PRIOR FILING DATE: 1998-04-01

PRIOR FILING DATE: 1998-04-01
 PRIOR APPLICATION NUMBER: 60/080334
 PRIOR FILING DATE: 1998-04-01

PRIOR APPLICATION NUMBER: 60/081070
 PRIOR FILING DATE: 1998-04-08
 PRIOR APPLICATION NUMBER: 60/081049

PRIOR APPLICATION NUMBER: 60/081071
 PRIOR FILING DATE: 1998-04-08
 PRIOR APPLICATION NUMBER: 60/081195

PRIOR FILING DATE: 1998-04-08
 PRIOR APPLICATION NUMBER: 60/081203
 PRIOR FILING DATE: 1998-04-09
 ADDITIONAL NUMBER: 00000000

PRIOR FILING DATE: 1998-04-09
 PRIOR APPLICATION NUMBER: 60/081955
 PRIOR FILING DATE: 1998-04-15

PRIOR FILING DATE: 1998-04-15
 PRIOR APPLICATION NUMBER: 60/081819

Page 5

Mon Apr 14 10:18:14 2003

us-09-776-910-15.rapb

PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081952
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081838
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082568
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082569
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082704
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082700
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083495
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083496
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083499
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083554
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083558
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083559
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083500
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083742
PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366
PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084637
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084639
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084640
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084598
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084627
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084643
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085339
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085338
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085582
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15

PRIOR APPLICATION NUMBER: 60/085689
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 30.7%; Score 335.5; DB 9; Length 545;
Best Local Similarity 44.2%; Pred. No. 4.3e-28;
Matches 80; Conservative 29; Mismatches 63; Indels 9; Gaps 5;

QY 12 SEDCLYNTYNDLP-DKKRPYVFIHGGGFEGEANKRWGPDYFMKRPVLYTVQYR 70
DB 217 SEDCLYNTYVAPARAPDPPQPVWVFPFGCAFIVGAAS-SYEGSDLAAREKVVLFQHR 275
QY 71 LGVIGFLSKSENLNVGNAGLKDQVALRMFKSNITAFGVDYDITTVGESAGASTHY 130
DB 276 LGIFGFLS--TDSHANGNGLDQMAALFWOENIAFGDGNVTLFGQSAGMSISG 333
QY 131 MMTTEOTRGLEFHGCIIMSGSMCSASTECQSRALTMARVGYKG--EENKDIIEFLMK 188
DB 334 LMSPLASGLFHRALISOSGALFRFLT---SNPLKAKVAILAGCNHNSTQILVNCILR 390
QY 189 A 189
DB 391 A 391

RESULT 14
US-09-978-697-254
Sequence 254, Application US/09978697
Patent No. US20020169284A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fond, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Wally E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Iyar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Wally A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC27
CURRENT FILING DATE: 2001-10-16
CURRENT APPLICATION NUMBER: US/09/978,697
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250

us-09-776-910-15.rapb

1	PRIOR FILING DATE: 1997-10-17
2	PRIOR APPLICATION NUMBER: 60/064245
3	PRIOR FILING DATE: 1997-11-03
4	PRIOR APPLICATION NUMBER: 60/065311
5	PRIOR FILING DATE: 1997-11-13
6	PRIOR APPLICATION NUMBER: 60/066366
7	PRIOR FILING DATE: 1997-11-21
8	PRIOR APPLICATION NUMBER: 60/077450
9	PRIOR FILING DATE: 1998-03-10
10	PRIOR APPLICATION NUMBER: 60/077632
11	PRIOR FILING DATE: 1998-03-11
12	PRIOR APPLICATION NUMBER: 60/077641
13	PRIOR FILING DATE: 1998-03-11
14	PRIOR APPLICATION NUMBER: 60/077649
15	PRIOR FILING DATE: 1998-03-11
16	PRIOR APPLICATION NUMBER: 60/077791
17	PRIOR FILING DATE: 1998-03-12
18	PRIOR APPLICATION NUMBER: 60/078004
19	PRIOR FILING DATE: 1998-03-13
20	PRIOR APPLICATION NUMBER: 60/078886
21	PRIOR FILING DATE: 1998-03-20
22	PRIOR APPLICATION NUMBER: 60/078936
23	PRIOR FILING DATE: 1998-03-20
24	PRIOR APPLICATION NUMBER: 60/078910
25	PRIOR FILING DATE: 1998-03-20
26	PRIOR APPLICATION NUMBER: 60/078939
27	PRIOR FILING DATE: 1998-03-20
28	PRIOR APPLICATION NUMBER: 60/079294
29	PRIOR FILING DATE: 1998-03-25
30	PRIOR APPLICATION NUMBER: 60/079656
31	PRIOR FILING DATE: 1998-03-26
32	PRIOR APPLICATION NUMBER: 60/079664
33	PRIOR FILING DATE: 1998-03-27
34	PRIOR APPLICATION NUMBER: 60/079689
35	PRIOR FILING DATE: 1998-03-27
36	PRIOR APPLICATION NUMBER: 60/079663
37	PRIOR FILING DATE: 1998-03-27
38	PRIOR APPLICATION NUMBER: 60/079728
39	PRIOR FILING DATE: 1998-03-27
40	PRIOR APPLICATION NUMBER: 60/079786
41	PRIOR FILING DATE: 1998-03-27
42	PRIOR APPLICATION NUMBER: 60/079920
43	PRIOR FILING DATE: 1998-03-30
44	PRIOR APPLICATION NUMBER: 60/079923
45	PRIOR FILING DATE: 1998-03-30
46	PRIOR APPLICATION NUMBER: 60/080105
47	PRIOR FILING DATE: 1998-03-31
48	PRIOR APPLICATION NUMBER: 60/080107
49	PRIOR FILING DATE: 1998-03-31
50	PRIOR APPLICATION NUMBER: 60/080165
51	PRIOR FILING DATE: 1998-03-31
52	PRIOR APPLICATION NUMBER: 60/080194
53	PRIOR FILING DATE: 1998-03-31
54	PRIOR APPLICATION NUMBER: 60/080327
55	PRIOR FILING DATE: 1998-04-01
56	PRIOR APPLICATION NUMBER: 60/080328
57	PRIOR FILING DATE: 1998-04-01
58	PRIOR APPLICATION NUMBER: 60/080333
59	PRIOR FILING DATE: 1998-04-01
60	PRIOR APPLICATION NUMBER: 60/080334
61	PRIOR FILING DATE: 1998-04-01
62	PRIOR APPLICATION NUMBER: 60/081070
63	PRIOR FILING DATE: 1998-04-08
64	PRIOR APPLICATION NUMBER: 60/081049
65	PRIOR FILING DATE: 1998-04-08
66	PRIOR APPLICATION NUMBER: 60/081071
67	PRIOR FILING DATE: 1998-04-08
68	PRIOR APPLICATION NUMBER: 60/081195
69	PRIOR FILING DATE: 1998-04-08
70	PRIOR APPLICATION NUMBER: 60/081203
71	PRIOR FILING DATE: 1998-04-09
72	PRIOR APPLICATION NUMBER: 60/081229
73	PRIOR FILING DATE: 1998-04-09

1	PRIOR APPLICATION NUMBER: 60/08195535
2	PRIOR FILING DATE: 1998-04-15
3	PRIOR APPLICATION NUMBER: 60/08181717
4	PRIOR FILING DATE: 1998-04-15
5	PRIOR APPLICATION NUMBER: 60/08181819
6	PRIOR FILING DATE: 1998-04-15
7	PRIOR APPLICATION NUMBER: 60/0819552
8	PRIOR FILING DATE: 1998-04-15
9	PRIOR APPLICATION NUMBER: 60/081838
10	PRIOR FILING DATE: 1998-04-15
11	PRIOR APPLICATION NUMBER: 60/082568
12	PRIOR FILING DATE: 1998-04-21
13	PRIOR APPLICATION NUMBER: 60/082569
14	PRIOR FILING DATE: 1998-04-21
15	PRIOR APPLICATION NUMBER: 60/082704
16	PRIOR FILING DATE: 1998-04-22
17	PRIOR APPLICATION NUMBER: 60/082804
18	PRIOR FILING DATE: 1998-04-22
19	PRIOR APPLICATION NUMBER: 60/082700
20	PRIOR FILING DATE: 1998-04-22
21	PRIOR APPLICATION NUMBER: 60/082797
22	PRIOR FILING DATE: 1998-04-22
23	PRIOR APPLICATION NUMBER: 60/082796
24	PRIOR FILING DATE: 1998-04-23
25	PRIOR APPLICATION NUMBER: 60/083336
26	PRIOR FILING DATE: 1998-04-27
27	PRIOR APPLICATION NUMBER: 60/083322
28	PRIOR FILING DATE: 1998-04-28
29	PRIOR APPLICATION NUMBER: 60/083392
30	PRIOR FILING DATE: 1998-04-29
31	PRIOR APPLICATION NUMBER: 60/083495
32	PRIOR FILING DATE: 1998-04-29
33	PRIOR APPLICATION NUMBER: 60/083496
34	PRIOR FILING DATE: 1998-04-29
35	PRIOR APPLICATION NUMBER: 60/083499
36	PRIOR FILING DATE: 1998-04-29
37	PRIOR APPLICATION NUMBER: 60/083545
38	PRIOR FILING DATE: 1998-04-29
39	PRIOR APPLICATION NUMBER: 60/083554
40	PRIOR FILING DATE: 1998-04-29
41	PRIOR APPLICATION NUMBER: 60/083558
42	PRIOR FILING DATE: 1998-04-29
43	PRIOR APPLICATION NUMBER: 60/083559
44	PRIOR FILING DATE: 1998-04-29
45	PRIOR APPLICATION NUMBER: 60/083500
46	PRIOR FILING DATE: 1998-04-29
47	PRIOR APPLICATION NUMBER: 60/083742
48	PRIOR FILING DATE: 1998-04-30
49	PRIOR APPLICATION NUMBER: 60/084366
50	PRIOR FILING DATE: 1998-05-05
51	PRIOR APPLICATION NUMBER: 60/084414
52	PRIOR FILING DATE: 1998-05-06
53	PRIOR APPLICATION NUMBER: 60/084441
54	PRIOR FILING DATE: 1998-05-06
55	PRIOR APPLICATION NUMBER: 60/084637
56	PRIOR FILING DATE: 1998-05-07
57	PRIOR APPLICATION NUMBER: 60/084639
58	PRIOR FILING DATE: 1998-05-07
59	PRIOR APPLICATION NUMBER: 60/084640
60	PRIOR FILING DATE: 1998-05-07
61	PRIOR APPLICATION NUMBER: 60/084627
62	PRIOR FILING DATE: 1998-05-07
63	PRIOR APPLICATION NUMBER: 60/084643
64	PRIOR FILING DATE: 1998-05-07
65	PRIOR APPLICATION NUMBER: 60/085339
66	PRIOR FILING DATE: 1998-05-13
67	PRIOR APPLICATION NUMBER: 60/085338
68	PRIOR FILING DATE: 1998-05-13
69	PRIOR APPLICATION NUMBER: 60/085323

PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: 60/085582
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085700
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085689
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085579
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085580
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085573
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 30.7%; Score 335.5; DB 9; Length 545;
 Best Local Similarity 44.2%; Pred. No. 4.3e-28;
 Matches 80; Conservative 29; Mismatches 63; Indels 9; Gaps 5;

QY 12 SEDCLYLVNVTNDLP-DKRRPVVFIHGGFEGEAMRMVYGPDMKPPVLTVOYR 70
 |||||
 DB 217 SEDCLYLVNVPARAPGDPQLPVWVWPGAFIVGAAS-STEGSDLAAREKVVLFQHR 275
 QY 71 LGVIGFLSKENLVNPGNAGLKDVVALRWFKSNIAIFSGDVNITVFGSAGASTHY 130
 |||||
 DB 276 LGIFFLS--IDDSHARNWGLIDDMALRWQENIAAFGDPGVVTLFGSAGASTISG 333
 QY 131 NMITEOTGLFHRGIMSGNSKCSASTECOSRALTMMKRYGYKG--DENKEDLIEFLMK 188
 |||||
 DB 334 LKMSPLASGLFHRALISQSTALEFLRFT---SNPLKVKAKVAHLGACHNHSQILVNLRL 390
 QY 189 A 189
 DB 391 A 391

RESULT 15
 US-09-978-192A-254
 Sequence 254, Application US/09978192A
 Patent No. US2002017753A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleon
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerilsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth J.
 APPLICANT: Kijavlin, Ivar J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2630P1C9

CURRENT APPLICATION NUMBER: US/09/978,192A
 PRIOR FILING DATE: 2001-10-15
 PRIOR APPLICATION NUMBER: 09/918585
 PRIOR FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/064249
 PRIOR FILING DATE: 1997-11-03
 PRIOR APPLICATION NUMBER: 60/065311
 PRIOR FILING DATE: 1997-11-13
 PRIOR APPLICATION NUMBER: 60/066364
 PRIOR FILING DATE: 1997-11-21
 PRIOR APPLICATION NUMBER: 60/077450
 PRIOR FILING DATE: 1998-03-10
 PRIOR APPLICATION NUMBER: 60/077632
 PRIOR FILING DATE: 1998-03-11
 PRIOR APPLICATION NUMBER: 60/077641
 PRIOR FILING DATE: 1998-03-11
 PRIOR APPLICATION NUMBER: 60/077649
 PRIOR FILING DATE: 1998-03-11
 PRIOR APPLICATION NUMBER: 60/077791
 PRIOR FILING DATE: 1998-03-12
 PRIOR APPLICATION NUMBER: 60/078004
 PRIOR FILING DATE: 1998-03-13
 PRIOR APPLICATION NUMBER: 60/078886
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/078936
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/078910
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/078939
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/079294
 PRIOR FILING DATE: 1998-03-25
 PRIOR APPLICATION NUMBER: 60/079656
 PRIOR FILING DATE: 1998-03-26
 PRIOR APPLICATION NUMBER: 60/079664
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/079689
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/079663
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/079728
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/079786
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/079920
 PRIOR FILING DATE: 1998-03-30
 PRIOR APPLICATION NUMBER: 60/079923
 PRIOR FILING DATE: 1998-03-30
 PRIOR APPLICATION NUMBER: 60/080105
 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/080107
 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/080165
 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/080194
 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/080327
 PRIOR FILING DATE: 1998-04-01
 PRIOR APPLICATION NUMBER: 60/080328
 PRIOR FILING DATE: 1998-04-01
 PRIOR APPLICATION NUMBER: 60/080333
 PRIOR FILING DATE: 1998-04-01
 PRIOR APPLICATION NUMBER: 60/080334
 PRIOR FILING DATE: 1998-04-01
 PRIOR APPLICATION NUMBER: 60/081070
 PRIOR FILING DATE: 1998-04-08
 PRIOR APPLICATION NUMBER: 60/081049
 PRIOR FILING DATE: 1998-04-08
 PRIOR APPLICATION NUMBER: 60/081071
 PRIOR FILING DATE: 1998-04-08
 PRIOR APPLICATION NUMBER: 60/081195

PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081819
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081952
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081838
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082568
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082569
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082704
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082700
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083495
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083496
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083499
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083554
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083558
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083559
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083500
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083742
PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366
PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084637
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084639
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084640
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084598
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084627
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084643
PRIOR FILING DATE: 1998-05-07

PRIOR APPLICATION NUMBER: 60/085339
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085338
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085582
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085689
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match

Best Local Similarity 30.7%; Score 335.5; DB 9; Length 545;
Matches 80; Conservative 29; Mismatches 63; Indels 9; Gaps 5;

QY 12 SEDCLYINVTNDLNP-DKKRPVVFTHGGCFTEGANNRWGPDYEMKPPVLYTVQYR 70
DB 217 SEDCLYINVTNDLNP-DKKRPVVFTHGGCFTEGANNRWGPDYEMKPPVLYTVQYR 275
QY 71 LGVIGFSLKSENINVPNGNGLDQVWALFWEKSNIAIFGGVDNITVGEAGASTHY 130
DB 276 LGVIGFSLKSENINVPNGNGLDQVWALFWEKSNIAIFGGVDNITVGEAGASTHY 130
QY 131 MITEQTRGLFHGIMSGNSMSSASTECOSRALTMAKRVYKG--EENKDIIEFLMK 188
DB 334 LMSPILASGLFHGIMSGNSMSSASTECOSRALTMAKRVYKG--EENKDIIEFLMK 188
QY 189 A 189
DB 391 A 391

Search completed: April 4, 2003, 09:34:06
Job time: 11.9247 secs

